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February 12, 2003, 10:03:55; Search time 13.4328 Seconds (without alignments) 198.395 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1 IVGGYTCGANTVPYQVSLNS 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	N-terminus of bovi	Amino terminal sed	Bovine TRYP peptid	TRYP protein. Bos	Bovine trypsin. B	Bovine trypsinogen	Bovine trypsinogen	Recombinant trypsi	Bovine met-phe-try	Trypsinogen analog
SUMMARIES	AAB03086	AAB31574	AAW81767	AAY69973	AAR53637	AAY77494	AAR53638	AAY91926	AAB80953	AAY91925
EQ.	21	22	50	21	12	21	15	21	22	21
% Query Match Length	20	20	223	223	224	229	230	231	231	233
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Score	107	107	107	107	107	107	107	107	107	107
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22 77 75 40	Human sp. Human sp. Human p. H	01 Human	003	Human Human	60 Human 21 Human	58 Human	93 Human 46 Atlan	65 Salmo	36 N-terminal of an N-terminal of an	57 Salmon enzyme	544 546	360 Atlantic c	Engraulis	937	943 N-terminal	944 N-terminal	348 Krill-derived	366 Atlantic c	967 Atlantic cod 358 Atlantic cod
23 ABB83: 18 AAW08- 21 AAY78: 21 AAY78: 19 AAW577	AAP8124		2010	-	6	m	m o	~ ,	40	(1)	~ -	4 m	m	v	7	N C	0	μ,	21 AAB22 23 AAO21.
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No.9064. The N-terminus of this protease is given in AAB03085. The novel protease has trypsin-like activity, specifically cleaving peptide chains on the carboxyl side of a basic amino acid (e.g., arginine or lysine). It has a pH optimum of 7-8, and is stable between pH 5 and pH10. It has a temperature optimum of approximately 40 degrees Celsius, and is stable between 40 and 50 degrees Celsius. The invention also relates to a method for the preparation of he novel serion protease, and the use of the protease in protein degrees Celsius. The enzyme has coagulant, hypertensive and anti-inflammatory effects. It may also be used in the preparation of leather, for raw silk treatment and for the preparation of protein hydrolysate. Sequences AAB03086-B03089 represent the N-terminal 20 amino acids of trypsin from a variety of organisms.
      85666666666665568
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20 AA; Seguence

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Gaps
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 Length 20;
                        Indels
100.0%; Score 107; DB 21;
100.0%; Pred. No. 1.9e-09;
ive 0; Mismatches 0;
                                                20
                                                                   1 ivggyrcganrvPYQVSLNS 20
                                                1 IVGGYTCGANTVPYQVSLNS
           Local Similarity 100.
 Query Match
             Best Loca
Matches
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AAB31574 standard; peptide; 20 AA. RESULT

(first entry) 20-APR-2001 AAB31574;

Amino terminal sequence of bovine trypsins.

Fish, serine proteinase, pain, acute inflammation, chronic inflammation, arthritis; inflamed joint; bursitis; osteoarthritis; septic arthritis; rheumatoid arthritis; juvenile rheumatoid arthritis; fibromyalgia, systemic lupus erythematosus; phiebitis; tendinitis; rash; psoriasis; acne; eczema; facial seborrheic eczema; foreskin infection; achetete septon; fistulae infection; ulcer; navel infection; wrinkle; scar; kelloid; boil; wart; allergic itch; hemorrhoid; wound; fungal infection; autoimmune disease.

Вов вр.

WO200078332-A2

28-DEC-2000

15-JUN-2000; 2000WO-IS00005

18-JUN-1999;

(BJAR/) BJARNASON J B.

Bjarnason JB

WPI; 2001-091493/10.

Fish serine proteinase, useful as a cosmetic, medicament for treating eczema, psoriasis, arthritis, and in the manufacture of the medicament for treating, preventing pathogenic diseases involving receptor mediated binding

Disclosure, Page 5; 38pp, English.

The specification describes a fish serine proteinase. The proteinases are useful as medicaments, for treating and preventing a disease in a human or an animal such as pain, acute inflammation, chronic inflammation, arthritis, inflamed joints, bursatis, osteoarthritis, theunatoid arthritis, juvenile rheumatoid arthritis, juvenile rheumatoid arthritis, systemic lupus erthematosus, phlebitis, tendinitis, rash, psoriasis, acue, eczema, facial seborrheic eczema, eczema of the hands,

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face or neck, foreskin infections, athlete's foot, fistulae infections, infected topical ulcers, navel infections in newborns, wrinkles, scars, kelloids, boils, wartes and allergic itch, hemorrhoids, wounds, wounds infections, wounds from burns, fungal infections and immunological and autoimmune diseases. They are also useful for removing dead or peeling skin from otherwise healthy skin, and for treating or preventing a disease in which pathogenesis is caused by bacteria, virus, fungus, parasite or a protozoan or a receptor mediated binding is involved. The present sequence represents the amino terminal of bovine trypsins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein function; trypsin; bovine; homology; resemblance.
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Pred. No. 2.9e-08;
; Mismatches 0;
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Pred. No. 1.9e-09;
Mismatches 0;
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ribonuclease; myoglobin; database;
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Best Local Similarity 100.
Matches 20, Conservative
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Best Local Similarity
Matches 20; Conserv
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N-PSDB; AAQ63794.
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           Bovine trypsin.
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                                                                                       EP597681-A.
                                                                  Bos taurus
                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the TRYP protein.

The invention relates to a database containing information on the amino acid (as) sequences of proteins of which I or more biological functions are known. The database also contains additional information on the score of importance of each as residue in the whole as sequence in determining the known biological functions. The invention also relates to a method of preparing an alignment between as sequences contained in the database and those of the unknown polypeptide. This is represented as the homology amongst various sites, each being identified as having a high score of importance in determining potential biological functions. The method is used to enable an efficient estimation of the biological functions used to enable an efficient estimation of the biological functions their as equences. Suitable proteins can then be isolated and purified by various means. This could be of considerable use in a biological and medical context. The computerised procedure is efficient, fast and
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                                                                                                                                 Protein sequence database; biological function determination; enzymatic activity; signaling activity; protein function determination; TRYP protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 107; DB 21; Length 223; 100.0%; Pred. No. 2.9e-08; cive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                (MEDI-) INST MEDICINAL MOLECULAR DESIGN INC.
                                                                                                                                                                                                                                                                                                                        Imamura M;
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                                               AAY69973 Btandard; protein; 223 AA.
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                                                                                                                                                                                                                                                                                                                        Tomioka N, Itai R,
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nes 20; Conservative
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                                                                                                                TRYP protein.
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Bovine, trypsinogen, heterologous protease, expression, transgenic plant,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expression vectors for bovine trypsin and bovine trypsinogen for cleavage of zymogens into active drugs, e.g. pro-insulin conversion into insulin
Cattle; cow; trypsin; enzyme; protease; proinsulin; insulin; hormone; plasmid pRMG4.
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Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 20; Conservative 0; Mismatches 0;
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The invention relates to a transgenic plant that comprises DNA encoding an active or inactive form of a heterologous protease (e.g., trypsin) The nuclectide sequence encoding the protease is operably linked to a promoter to effect expression of the protease in the plant. The transgenic plant is used in a method of producing protease in commercial quantities, comprising the extraction of the protease in commercial blomass. The current source of trypsin is the organs of animals. One of the main difficulties with this source is that there is considerable contamination by other proteases. Chymotrypsin is one of the additional overcomes the product in an undesired manner. The method of the invention overcomes the problem of contamination by other additional proteases. By directing the expression of the protease and contamination by contamination by contamination overcomes the problem of expression of the protease and having it digest the proteins in the plant, resulting in cell death is overcome. The proteins in the plant, resulting in cell death is overcome. The proteins in the plant, resulting in cell death is construction of a plant expression plasmid in the exemplifications of the invention.
                                                                                                                              encoding a heterologous protein, used
                                                                                                                    Transgenic plant containing DNA encoding a for the commercial production of protease
                                                                                                                                                                                            Example 1; Page 28-29; 32pp; English
                                              WPI; 2000-195105/17
     Hood E;
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                                                                          N-PSDB; AAZ92585.
  Howard JA,
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100.0%; Score 107; DB 21; Length 229; 100.0%; Pred. No. 38-08; 1ve 0; Mismatches 0; Indels 0. 20 7 IVGGYTCGANTVPYQVSLNS 26 1 IVGGYTCGANTVPYQVSLNS Query Match
Best Local Similarity 100.
Matches 20; Conservative 쉱 ઠ

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Gaps

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AAR53638 standard; Protein; 230 AA. (first entry) Bovine trypsinogen. 01-DEC-1994 AAR53638;

Cattle, cow; trypsinogen; enzyme; protease; proinsulin; insulin; hormone; plasmid pRWG4.

Bos taurus.

EP597681-A.

18-MAY-1994.

93EP-0308959 10-NOV-1993;

92US-0977703 13-NOV-1992;

(ELIL) LILLY & CO ELI

Greaney MG, Rosteck PR;

WPI; 1994-160671/20.

Expression vectors for bovine trypsin and bovine trypsinogen for cleavage of zymogens into active drugs, e.g. pro-insulin conversion into insulin

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produced by cleavage of a trypsinogen analogue (AAY91925). A wild type bovine trypsinogen was mutated to destroy the trypsin cleavage site. The lys residue present in the leader sequence of the native bovine trypsinogen was mutated to an Asp residue. The vector was constructed such that DNA encoding a (Glu-Ala)2 peptide was inserted between the C-terminus of the alpha factor signal and the N-terminus of the trypsinogen analogue leader sequence to improve the yield of the secreted protein. The specification claims an isolated trypsinogen analogue leader the secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New trypsinogen analog useful for the production of recombinant trypsin has a modified leader sequence not cleavable by trypsin or trypsin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pain ia
A wild type
                                                                                                                                                                                                                                                                                                                                                        Recombinant trypsin, trypsinogen analogue; mutated bovine trypsinogen; leader sequence; trypsin activity; recombinant protein production; inactive zymogen.
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosteck PR;
                       This protein may be expressed by E. coli/plasmid pRMG7 and is able to cleave zymogens into active drugs, e.g. pro-insulin conversion into insulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The trypsin
                                                                                                                                   ö
                                                                                                          Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "optionally absent, see disclosure"
                                                                                                                                   Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desplancq D, Larson JL,
                                                                                                      Score 107; DB 15;
Pred. No. 3e-08;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence shows a claimed recombinant trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= leader_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8..231
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 22; Page 51-52; 56pp; English.
Disclosure; Page 27; 35pp; English.
                                                                                                                                                                                                                                                AAY91926 standard; Protein; 231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Socation/Qualifiers
                                                                                                                                  ö
                                                                                                      100.0%;
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                                                                                                                                                         1 IVGGYTCGANTVPYQVSLNS 20
                                                                                                                                                                          8 IVGGYTCGANTVPYQVSLNS 27
                                                                                        Query Match
Best Local Similarity 100.0%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US21047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0101213
                                                                                                                                                                                                                                                                                                     19-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIL ) LILLY & CO BLI.
                                                                                                                                                                                                                                                                                                                              Recombinant trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-283565/24.
                                                                             230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-283565/
N-PSDB; AAA08526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200017332-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                             Sequence
                                                                                                                                                                                                                                                                            AAY91926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                         RESULT 8
AAY91926
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us-10-036-371-2.rag

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produced by expressing trypsinogen inside a prokaryotic cell which is then isolated and activated to form trypsin.
                                                                                                                                                                                                      AAY91925 Btandard; Protein; 233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "trypsin'
                                                                                        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanquier JM, Hershberger CL,
                                                                100.0%;
                                                                           100.08;
                                                                                                                 1 IVGGYTCGANTVPYQVSLNS 20
                                                                                                                                        28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US21047.
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                                                                                                                                9 IVGGYTCGANTVPYQVSLNS
                                                                                                                                                                                                                                                        (first entry)
                                                                                         20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11..233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-283565/24.
                                                                                                                                                                                                                                                                                 Trypsinogen analogue
                                                                Query Match
Best Local Similarity
                                         231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA08525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200017332-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-1998;
                                                                                                                                                                                                                                                        19-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2000
                                                                                                                                                                                                                                                                                                                                             Synthetic.
Bos taurus.
                                                                                                                                                                                                                               AAY91925;
                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enzymes
                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                              Best Loca
Matches
                                                                                                                                                                               RESULT 10
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  sequence having at least two amino acids which are not Lys or Arg.
The trypsin derived from the recombinant trypsinogen is useful for the characterization of other proteins, and in the manufacture of other recombinant bioproducts, for example to cleave leader sequences from small recombinant proteins expressed initially as fusion proteins. The present method provides for expression of an inactive zymogen form that is soluble and properly folded yet is not activated until after purification from fermentation broth or cell extracts. This is accomplished through the expression of a single chain trypsinogen analogue where the leader sequence is modified such that it lacks a rangous of the present invention lack a lysin or arginine in the netwant leader sequence of the protein to prevent auto-activation or activation by endougenous host cell enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is bovine met-phe-trypsinogen. Trypsin is a serine protease which cleaves the peptide bond on the carboxy-terminus of basic amino acid residues. Trypsin is synthesised in a slightly longer catalytically inactive form: trypsinogen, which itself is cleaved (leader sequence removed) to give trypsin. The leader sequence of the present protein consists of ((Asp)4-Lyps) and is present at the amino-terminus. This protein has two additional residues at the amino-terminus. Phe. Bovine met-phe-trypsinogen is useful for the manufacture of recombinant protein pharmaceuticals. High purity trypsin products are
                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New chymotrypsin-free trypsin and trypsinogen useful for manufacturing recombinant protein pharmaceuticals and pure trypsin -
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Leader peptide, cleaved to produce trypsin"
                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                  Score 107; DB 21; Length 231;
Pred. No. 3e-08;
Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosteck PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypsinogen; bovine; trypsin; serine protease.
                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                               AAB80953 standard; Protein; 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Fig 1; 55pp; English
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                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                        1 IVGGYTCGANTVPYOVSLNS 20
                                                                                                                                                                                                                                                                                            9 IVGGYTCGANTVPYQVSLNS 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine met-phe-trypsinogen.
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                               20; Conservative
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                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                 231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAF81479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200119970-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                        AAB80953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New trypsinogen analog useful for the production of recombinant trypsin
has a modified leader sequence not cleavable by trypsin or trypsin-like
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosteck PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypsinogen analogue, mutated bovine trypsinogen, leader sequence, trypsin activity, recombinant protein production; inactive zymogen.
                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "native bovine trypsinogen protein was
Score 107; DB 22; Length 231;
Pred. No. 3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "optionally absent, see disclosure"
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Larson JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutated to an Asp residue"
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                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= linker_peptide
/note= "increases yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label = leader_sequence
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trypsingen analogue leader sequence to improve the yield of the secreted protein. The specification claims an isolated trypsinogen analogue leader sequence to improve the yield of the secreted protein. The specification claims an isolated trypsinogen analogue comprising a protein having trypsin activity and a leader sequence having at least two amino acids which are not lys or Arg. A recombinantly produced trypsin (AAY91926) is also claimed. The trypsin (derived from the recombinant trypsinogen is useful for the claracterization of other proteins, and in the manufacture of other recombinant proteins, and in the manufacture of other recombinant proteins expressed initially as fusion proteins. The present method provides for expression of an inactive zymogen form that is soluble and properly folded yet is not activated until after purification from fermenteation broth or cell extracts. This is a complished through the expression of a single chain trypsinogen analogue where the leader sequence is modified such that it lacks a rippin-like enzyme cleavage site. Specifically the trypsinogen analogues of the present invention lack a lysin or arginine in the Netwinship was a leader sequence of the protein to prevent auto-activation or activation by endougenous host cell enzymes. C-terminus of the alpha factor signal and the N-terminus of the 233 AA; Sequence 88888888888888888888888888888

Gaps ö Score 107; DB 21; Length 233; Pred. No. 3e-08; Nismatches 0; Indels 0. 0; Indels ö 100.0%; 50 11 IVGGYTCGANTVPYQVSLNS 30 1 IVGGYTCGANTVPYQVSLNS Local Similarity 100. les 20; Conservative Query Match Matches 셤 ઠે

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ABB83322 standard; protein; 223 AA ABB83322;

(first entry 30-AUG-2002

Partial trypsin sequence

Trypsin; three dimensional structure; protein structure analysis; serine protease.

Unidentified

US2002035434-A1

21-MAR-2002.

23-JUL-2001; 2001US-0910054.

92JP-0021012. 92JP-0331703. 93US-0014867. 06-FEB-1992; 38-FEB-1993; 11-DEC-1992;

(FUIT) FUJITSU LTD.

Matsuzawa Tomikawa M, Aikawa S,

WPI; 2002-507172/54.

Analysis of three-dimensional structures by generating combination of correspondence satisfying restriction condition, and calculating root mean square distance between elements in the combination of correspondence.

Disclosure, Fig 38; 65pp; English.

The present invention relates to a method for analysis of three dimensional structures. The method involves generating a combination of correspondence satisfying a restriction condition between the elements belonging to a first and second point sets from among all candidates for

1 IVGGYTCGANTVPYQVSLNS 20

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ö ö the combination of correspondence, and calculating a root mean square distance between the elements corresponding in the combination of correspondence. The method is useful for analysing three-diamensional structures of molecules, particularly proteins. To illustrate the invention, the serine proteases trypsin and elastase were used. The present sequence is a partial sequence for trypsin. The histidine and serine active sites of trypsin and elastase were used. The serine active sites of trypsin and elastase were analysed using the method of the invention. An almost complete pig trypsinogen (AAW08475) lacking the very N-terminal end of the signal peptide is the product of a cDNA clone (AAT49878) isolated from a pig pancreas cDNA library. The cDNA clone can be fused to a signal sequence (e.g. from the native enzyme or from a specified amylase gene) and used for prodn. of recombinant trypsin in transformed host cells, esp. filamentous fungus, e.g. Aspergillus oryzae or Aspergillus niger. Levels of trypsin secreted by Aspergillus spp. are several-fold higher than those obtd. using other microbial systems. Gaps Gaps fused to signal with recombinant DNA comprising trypsinogen sequence fused to signarequence, provides higher level of expression than other expression Prodn. of trypsin or trypsinogen in filamentous fungi - transformed ö Trypsinogen; trypsin; protease; filamentous fungus; Asperillus. ö Length 223; 89.7%; Score 96; DB 18; Length 247; 85.0%; Pred. No. 1.5e-06; Live 2; Mismatches 1; Indels Score 98; DB 23; Length 22.
Pred. No. 6.6e-07; AAW08475 standard; Protein; 247 AA Example 2; Page 15; 28pp; English. . 0 91.6%; 20 20 96WO-DK00253. 95DK-0000693 1 IVGGYTCCANTVPYQVSLNS (first entry) 1 IVGGYTCGANTVPYQVSLNS Local Similarity 95.0 nes 19; Conservative Conservative (NOVO) NOVO-NORDISK AS. DNA WPI; 1997-077523/07. N-PSDB; AAT49878. Porcine trypsinogen 223 AA; Local Similarity tes 17; Conserv 247 AA; with recombinant Kjeldsen TB, 10-JUN-1996; 16-JUN-1995; WO9700316-A1 28-MAR-1997 03-JAN-1997. Sus scrofa. Seguence Sequence Query Match Query Match Bystems Matches Best Loc Matches RESULT 12 ò 셤

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Ashida Y, Yamada T;
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                                                                                                                                                                                                                                                                                                                      (FUJY ) FUJI YAKUHIN KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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Best Local Similarity 85.0
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-206018/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 AA;
                                                                                               Canis familiaris.
                                                                                                                                     WO200009739-A1.
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                                                                                                                                                                                                                                                                                                                                                              Waritani T,
                                                                                                                                                                                                                      09-AUG-1999;
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                                                                                                                                                                                                                                                            10-AUG-1998;
                                                                                                                                                                              24-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW57740;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents an immunogenic fragment of the canine anionic trypsinogen amino acid sequence. The fragment corresponds to amino acid residues 24 to 43 of the anionic trypsinogen protein sequence (see AAY78975). The invention relates to monoclonal antibodies with specificity against canine trypsin, or canine trypsin-related substances. The antibodies are highly specific and can be used as reagent for quick and accurate detection and quantitation of canine trypsin and canine trypsin-like immunoreactants in various forms. The antibodies can be used in the diagnosis of diseases such as pancreatitis, pancreatic cancer, renal insufficiency and extrapancreatic hyposecretion.
                                                                                                                                                                                                                                          Canine anionic trypsinogen immunogenic fragment #2 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-canine trypsin monoclonal antibody, useful as reagent for quick and accurate detection and quantitation of trypsin and/or trypsin-like immunoreactants in various forms in diagnosis e.g. of pancreatic
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85.0%; Pred, No. 3.6e-07;
.ive 1; Mismatches 2; Indels
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                                                                                                                        AAY78977 standard; protein; 20 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FUJY ) FUJI YAKUHIN KOGYO KK.
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Matches 17; Conservative
25 IVGGYTCAANSIPYQVSLNS
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                                                                                                                                                                                                                                                                                                                                                                                                             WO200009739-A1.
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10-MAR-1999;
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                                                                                                                                                              AAY78977;
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ID AAY79977

XX AAY79

XX AAY79

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XX AAY70

DD Canin

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KW A
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This sequence represents the canine anionic trypsinogen amino acid sequence. The protein was isolated from the canine pancreas. The invention relates to monoclonal antibodies with specificity against canine trypsin, or canine trypsin-related substances. The antibodies are highly specific and can be used as reagent for quick and accurate detection and quantitation of canine trypsin and canine trypsin-like immunoreactants in various forms. The antibodies can be used in the diagnosis of diseases such as panoreatitis, pancreatic cancer, renal insufficiency and extrapancreatic hyposecretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-canine trypgin monoclonal antibody, useful as reagent for quick and accurate detection and quantitation of trypsin and/or trypsin-like immunoreactants in various forms in diagnosis e.g. of pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Anionic trypsinogen; dog; monoclonal antibody production; detect; diagnose; pancreatitis; pancreatic cancer; renal insufficiency; extrapancreatic hyposecretion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 64-65; 67pp; Japanese.
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Search completed: February 12, 2003, 10:22:22 Job time : 15.4328 secs

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APPLICANT: Franklin, Richard L.
APPLICANT: Cowling, Didier S.P.
APPLICANT: Hubbel, Jeffrey A.
APPLICANT: van de Wetering, Petra
TITLE OF INVENTION: Treatment of Trauma
FILE REFERENCE: 314572-105
CURRENT APPLICATION NUMBER: US/09/938,269
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US-09-938-269-16
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US-09-938-269-15
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Sequence 16, Appl
Sequence 17, Appl
Sequence 1, Appl
Sequence 14, Appl
Sequence 154, Appl
Sequence 154, Appl
Sequence 164, Appl
Sequence 103, Appl
Sequence 103, Appl
Sequence 96, Appl
Sequence 96, Appl
Sequence 97, Appl
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Sequence 1, Appli
Sequence 4, Appli
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                                                                                                           February 12, 2003, 10:22:36; Search time 3.04478 Seconds (without alignments) 167.821 Million cell updates/sec
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CGTG 6/ptodata/1/pubpaa/USOB NEW PUB.pep: *
CGTG 6/ptodata/1/pubpaa/USOB NEW PUB.pep: *
CGTG 6/ptodata/1/pubpaa/USOB NEW PUB.pep: *
CGTG 6/ptodata/1/pubpaa/USOT NEW PUB.pep: *
CGTG 6/ptodata/1/pubpaa/USOT NEW PUB.pep: *
CGTG 6/ptodata/1/pubpaa/USOT NEW PUB.pep: *
CGTG 6/ptodata/1/pubpaa/USOB PUBCOMB.pep: *
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-938-269-17
US-09-938-269-14
US-09-938-269-14
US-09-938-269-14
US-09-932-779-154
US-09-925-779-154
US-09-925-300-1093
US-09-925-300-1093
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US-09-928-300-1093
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US-09-822-827-946
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Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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Sequence 745, App Sequence 11, App Sequence 11, App Sequence 117, App Sequence 617, App Sequence 617, App Sequence 617, App Sequence 978, App Sequence 978, App Sequence 982, App Sequence 395, App Sequence 396, 
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10 US-09-988-975A-7

10 US-09-955-297-745

10 US-09-855-297-745

10 US-09-895-814-617

10 US-09-895-814-617

10 US-09-895-814-617

10 US-09-895-814-617

10 US-09-895-814-617

10 US-09-895-817-978

10 US-09-895-793-978

10 US-09-895-793-978

10 US-09-895-793-978

10 US-09-895-793-978

10 US-09-895-793-978

10 US-09-978-195A-395

10 US-09-978-195A-395

10 US-09-98-189-395

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APPLICANT: Cowling, Didier S.P.
APPLICANT: Cowling, Didier S.P.
APPLICANT: Hubbel, Jeffrey A.
TITLE OF INVENTION: Treatment of Trauma TITLE OF INVENTION: Treatment of Trauma FILE REFRENCE: 14572-105
CURRENT APPLICATION NAMBER: US/09/938,269
CURRENT FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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Publication No. US20030007951A1
GENERAL INFORMATION:
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Publication No. US20030007951Al
GENERAL INFORMATION:
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Matches 17; Conservative
        TYPE: PRT
ORGANISM: Atlantic cod
US-09-938-269-15
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NAME/KEY: MOD RES
LOCATION: (33)
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LOCATION: (204)
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US-10-036-171-8

i Sequence 8, Application US/10036371

i Patent No. US20020141987A1

i GENERAL INFORMATION:

i APPLICANT: BARRARSON, JON B.

i TITLE OF INVENTION: COSMETIC USE

i TITLE OF INVENTION: COSMETIC USE

i TITLE OF INVENTION: UMBER: US/10/036,371

CURRENT APPLICATION WHMER: US/10/036,371

CURRENT PILING DATE: 1999-10-12

i PRIOR PAPLICATION NUMBER: 5066/99

PRIOR PILING DATE: 1999-06-18

i PRIOR PILING DATE: 1999-06-18

i SOFTWARE: Patentin Ver: 2.1

i SRQ ID NOS: 8

i SRQ ID NOS: 8

i SRQ ID NOS: 8

i SRQ ID NOS: 8
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94.7%; Score 90; DB 9; Length 25;
Best Local Similarity 85.0%; Pred. No. 9.8e-09;
Matches 17; Conservative 0; Mismatches 3; Indels
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85.0%; Pred. No. 1.5e-08;
Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/08938269
Publication No. US20030007951A1
GENERAL INFORMATION:
APPLICANT: Franklin, Richard L.
APPLICANT: Cowling, Didier S.P.
APPLICANT: Hubbel, Jeffrey A.
APPLICANT: van de Wetering, Petra
ITILE OF INVENTION: Treatment of Trauma
FILE REFERENCE: 314572-105
CURRENT PELLING DATE: 2001-08-23
CURRENT FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 17
LENGTH: 37
TYPE: PRT
CREANISM: Atlantic cod
US-09-938-269-17
CURRENT FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FRRESEQ for Windows Version 4.0
LENGTH: 25
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FEATURE:
NAME/KEY: MOD_RES
LOCATION: (9)
OTHER INFORMATION: K or R
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Matches 17; Conservative
                                                                                                           TYPE: PRT

ORGANISM: Atlantic cod

US-09-938-269-16
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US-10-036-371-1
; Sequence 1, Application US/10036371
; Patent No. US20020141987A1
; GENERAL INFORMATION:
; APPLICATION:
; TILE OF INVENTION: FISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND
; TILE OF INVENTION: COSNETIC USE
; TILE OF INVENTION: USCANETIC USE
; FILE REFERENCE: 81691/284960
; CURRENT APPLICATION NUMBER: US/10/036,371
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                                                                                                                                                                                                                                                                                            NAME/KEY: MOD RES
LOCATION: (71)
OTHER INFORMATION: I or unknown
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NAME/KEY: MOD RES
LOCATION: (212)
OTHER INFORMATION: M, V or C
                                                         NAME/KEY: MOD RES
LOCATION: (32)
OTHER INFORMATION: K OF E
FEATURE:
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NAME/KEY: MOD_RES
LOCATION: (136)
OTHER INFORMATION: V or C
                                                                                                                                                     LOCATION: (33)
OTHER INFORMATION: D or Q
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NAME/KEY: MOD RES
LOCATION: (82)
OTHER INFORMATION: N OF D
FEATURE:
NAME/KEY: MOD RES
LOCATION: (92)
OTHER INFORMATION: K OF E
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; OTHER INFORMATION: N or S
US-10-036-371-8
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LOCATION: (647
OTHER INFORMATION: Y or
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NAME/KEY: MOD RES
LOCATION: (129)
OTHER INFORMATION: A or
LOCATION: (24)
OTHER INFORMATION: Y
FEATURE:
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LOCATION: (138)
OTHER INFORMATION: N
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Gaps
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GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jianghun
APPLICANT: Xu,
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Best Local Similarity 65.0%; Pred. No. 0.0019;
Matches 13; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 69.5%; Score 66; DB 12; Length 271; Best Local Similarity 53.6%; Pred. No. 0.00099; Matches 15; Conservative 1; Mismatches 4; Indels
                                                                                                                                                     COMPUTRY: USA
ZIP: 0210-2804.

ZIP: 0210-2804.

COMPUTRR: RADABLE FORM:
COMPUTRR: IBM PC compatible
COMPUTRR: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/10/021,368
FILING DATE: 12-Pec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: <a href="https://doi.org/10.038">https://doi.org/10.038</a>
ATTORNEY/AGENT INPORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30.162
REPERENCE/DOCKET NUMBER: 00398/100002
TELEPRAY: 617/542-5070
TELEPRAX: 617/542-8906
                  ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 IVGGYSSTRYPIIECKAYSQPHQVSLNS 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-09-923-779-154
Sequence 154, Application US/09923779
; Patent No. US20020076721A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 271 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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US-09-923-779-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-021-368-10
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Patent No. US20020106367A1
GENERAL INFORMATION:
APPLICANT: Band, Vimla
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 93.7%; Score 89; DB 12; Length 20; Best Local Similarity 100.0%; Pred. No. 1.1e-08; Matches 20; Conservative 0; Mismatches 0; Indels
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82.1%; Score 78; DB 9; Length 25;
Best Local Similarity 75.0%; Pred. No. 9.2e-07;
Matches 15; Conservative 2; Mismatches 3; Indels
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US-09-938-269-14
Sequence 14, Application US/09938269
Sequence 14, Application US/09938269
Publication No. US20030007951A1
GENERAL INFORMATION:
APPLICANT: Franklin, Richard L.
APPLICANT: Cowling, Didier S.P.
APPLICANT: van de Wetering, Petra
TITLE OF INVENTION: Treatment of Trauma
FILE REFERENCE: 314572-105
CURRENT APPLICATION NUMBER: US/09/938,269
CURRENT FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 17
SOCTWARE: FactSEQ for Windows Version 4.0
SEQ ID NO 14
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 09/411,688
PRIOR PILIOR DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 5066/99
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO I
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COTHER INFORMATION: K or R
US-10-036-371-1
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NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: E OF T FEATURE:
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US-09-938-269-14
                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Gadus sp.
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NAME/KEY: MOD_RES
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                           AL INFORMATION:
APPLICANT: Band, Vimla
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 57.9%; Score 55; DB 10; Length 235; Best Local Similarity 55.0%; Pred. No. 0.055; Matches 11; Conservative 3; Mismatches 6; Indels
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MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
ODBERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U2.Dec-2001
CLASSIFICATION ATA:
APPLICATION NUMBER: 09/201,038
FILING DATE: 12-Dec-2001
CLASSIFICATION NUMBER: 09/201,038
ATORNEY/AGENT INFORMATION:
NAME: CLAEX'
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET WINBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1914 & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/10021368
Patent No. US20020106367A1
GENERAL INFORMATION:
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SEQUIBNE CHARACTERISTICS:
LENGTH: 286 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 IVGGWECEKHSQPWQVAVYS 106
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STATE: MA
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APPLICANT: Tomikawa Mayumi
APPLICANT: Tomikawa Seiichi
APPLICANT: Tomikawa Seiichi
APPLICANT: Tomikawa Seiichi
APPLICANT: Mateuzawa, Funiko
TITLE OF INVENTION: Method and Apparatus for Extracting and Evaluating Mutually Simil
TITLE OF INVENTION: Structures of Molecules
TITLE OF INVENTION: Structures of Molecules
TITLE OF INVENTION: MUMBER: US/09/910,071
CURRENT APPLICATION NUMBER: US/09/910,071
CURRENT FILING DATE: 2001-07-23
PRIOR PILING DATE: 2001-07-23
RIVER APPLICATION NUMBER: US/09/910,071
PRIOR FILING DATE: 1093-02-08
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
LENGTH: 223
                                                                      RESULT 9
US-10-036-171-2
; Sequence 2, Application US/10036371
; Patent No. US2002014198741
; GENERAL INFORMATION:
; APPLICANT: BUARNARCON, JON B.
; TITLE OF INVENTION: PISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND TITLE OF INVENTION: COGNETIC USE
; TITLE OF INVENTION: COGNETIC USE
; TITLE OF INVENTION: COGNETIC USE
; FILE REFERENCE: 81691/284960
; CURRENT APPLICATION NUMBER: 109/411,688
; PRIOR APPLICATION NUMBER: 09/411,688
; PRIOR PILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 5086/99
; PRIOR FILING DATE: 1999-66-18
; WUMBER OF SEQ ID NOS: 8
; SEOTWARE: Patentin Ver: 2.1
; ELENGTH: 20
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65.3%; Score 62; DB 10; Length 223;
Best Local Similarity 60.0%; Pred. No. 0.0037;
Matches 12; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.3%; Score 63; DB 12; Length 20; 60.0%; Pred. No. 0.00021; Live 3; Mismatches 5; Indels
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US-09-910-071-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-09-925-300-1093
; Sequence 1093, Application US/09925300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09910071
Patent No. US20020116146A1
GENERAL INFORMATION:
  24 IVGGYICEENSVPYOVSLNS 43
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Best Local Similarity 60.01
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) TYPE: PRT
; ORGANISM: Bovine ep.
US-10-036-371-2
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ORGANISM: unknown
FEATURE:
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US-09-796-294-10
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54.7%; Score 52; DB 9; Length 261;

Best Local Similarity 55.0%; Pred. No. 0.19;

Matches 11; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09796294
; Patent No. US20020037581A1
; GRENEAL INFORMATION:
; APPLICANT: O'STIGN. Timochy J.;
; APPLICANT: Underwood, Lowell J.;
; TITLE OF INVENTION: Extracellular Serine Protease;
; FILE OF INVENTION: Extracellular Serine Protease;
; FILE OF INTENTION NUMBER: US/09/796,294
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/618,259
; PRIOR FILING DATE: 2000-07-18
; SEQ ID NO 10
: LENGTH: 261
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PRIOR FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR PILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENT VEYSION 3.1
SEQ ID NO 62
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US-10-131-241-62
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                         TYPE: PRT
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US-10-131-241-62
US-10-131-241-62
Sequence 62. Application US/10131241
Sequence 62. Application No. US2003001279281
SERVERAL INFORMATION
APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/413,049
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APPLICANT: Foy, Teresa
APPLICANT: Copy R. Teresa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT APPLICATION 009: 982
SURBERS OF SEC ID NOS: 982
SOFTWARE: PASLSEQ for Windows Version 3.0
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                                                     Query Match
57.9%; Score 55; DB 12; Length 286;
Best Local Similarity 46.4%; Pred. No. 0.067;
Matches 13; Conservative 2; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                                      1 IVGGY-----XCXXHSQAHQVSLNS 20
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Publication No. US20020192763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
McNeill, Patricia D.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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US-09-895-793-946
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LENGTH: 261
               US-10-021-368-9
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                        ; FAZENT NO. &&AZUUBS.
; GENERAL INFORMATION:
APPLICANT: Richard L. Franklin
APPLICANT: Richard L. Franklin
; APPLICANT: Publard L. Franklin
; APPLICANT: Vees St. Pierre
TITLE OF INVENTION: Treatment and Prevention of Immune
TITLE OF INVENTION: Rejection Reactions
FILE REFERNCE: 314572-101D
CURRENT APPLICATION NUMBER: US/09/220,731A
CURRENT PILING DATE: 1998-12-24
EARLIER PILING DATE: 1993-05-21
EARLIER PILING DATE: 1993-05-21
EARLIER FILING DATE: 1994-11-22
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1995-06-07
EARLIER PILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: REALSEQ FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-385-540A-19

Sequence 19, Application US/08385540A
Patent No. 5945102
GENERAL INFORMATION:
APPLICANT: de Faire, Johan
TITLE OF INVENTION: Round Care With Multifunctional
TITLE OF INVENTION: Enzyme
INUMER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
US-08-487-167-9
US-08-482-816-9
US-08-296-149-9
US-08-601-499-9
US-08-074-659-9
US-09-074-659-9
US-09-106-468-9
US-09-106-468-9
US-09-106-467-9
US-09-106-467-9
US-09-106-467-9
US-09-106-467-9
US-09-106-467-9
US-08-108-85$A-21
US-08-768-85$A-21
US-08-767-820A-16
US-08-767-820A-16
US-08-767-920A-16
US-08-767-920A-16
US-08-767-920A-16
US-08-767-920A-16
US-08-767-920A-16
US-08-767-920A-16
US-08-622-046B-1
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                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 18, Application US/09220731A; Patent No. 6232088
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Best Local Similarity 85.0
Matches 17; Conservative
   ; TYPE: PRT
; ORGANISM: Atlantic cod
US-09-220-731-18
 US-09-220-731-18
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LENGTH: 23
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Sequence 17,
Sequence 24,
Sequence 20,
Sequence 10,
Sequence 10,
Sequence 10,
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Sequence 13,
Sequence 5, A
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Sequence 9,
Sequence 9,
Sequence 9,
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Sequence 1
Sequence 3
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-385-546A-19
US-08-365-546A-20
US-08-600-273A-19
US-08-600-273A-19
US-08-68-820-19
US-08-486-820-19
US-08-486-820-19
US-08-486-820-19
US-08-600-273A-18
US-08-600-273A-18
US-08-68-194-11
US-08-956-267A-2
US-08-956-267A-2
US-08-956-267A-2
US-08-956-267A-3
US-08-956-267A-3
US-08-954-483-35
US-08-944-483-35
US-08-944-483-35
US-08-944-483-35
US-08-944-483-35
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US-08-944-483-36
US-08-944-683-36
US-08-944-683-36
US-08-944-683-36
US-08-944-683-36
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Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
                                                                                                                                                     US-10-036-371-1
95
1 IVGGYXCXXHSQAHQVSLNS 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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US-08-600-273A-19
is Sequence 19, Application US/08600273A
is Patent No. 5958406
is GENERAL INFORMATION:
APPLICANT:
APPLICANT: Franklin, Richard L.
ITILE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lemox Drive, Building 3, Suite 210
COTTY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.7%; Score 90; DB 2; Length 25;
                                                                                                                                                                                                                                                                                                               94.7%; Score 90; DB 2; Length 25;
85.0%; Pred. No. 8.7e-10;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY: USA
ZIF: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketer
COMPUTER: IBM Compatible
OPREATING SYSTEM: Windows 95
SOFTWARE: FRAESEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,273A
FILING DATE: 08-FEB-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/486,820
FILING DATE: 07-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,820
FILING DATE: 07-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,820
FILING DATE: 07-UNN-1995
ATTORNEY/AGENT INFORMATION:
AND ATTORNEY/AGENT INFORMATION:
AND ATTORNEY/AGENT INFORMATION:
                    REPERENCE/DOCKET NUMBER: 314572-101A
TELECOMUNICATION INFORMATION:
TELEPHONE: 609-520-3114
TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314572-101C
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REGISTRATION NUMBER: 3145
REFERENCE/DOCKET NUMBER: 3145
TELECOMMUNICATION INFORMATION:
TELEFONE: 609-620-3214
TELEFAX: 609-620-3259
    REGISTRATION NUMBER: 29,135
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: gingle
TOPOLOGY: linear
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USA
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TOPOLOGY:
US-08-385-540A-20
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Sequence 20, Application US/08385540A

Sequence 20, Application US/08385540A

Falent No. 5945102

JILLO SPASIOS

TITLE OF INVENTION: Wound Care With Multifunctional

TITLE OF INVENTION: Enzyme

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Deckert Price & Rhoads

STATE: 10

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

IP 08543

COMPUTER: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/385,540A
ADDRESSER: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
                                                                                      COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: ISM Compatible
COMPUTER: ISM Compatible
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,540A
                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/600,273
FILING DATE: 08-FEB-1996
ATTONNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REPRENENCE/DOCKET NUMBER: 314572-101A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/600,273
FILING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: amino acid sTRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IVGGYXCXXHSQAHQVSLNS 20
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US-08-385-540A-19
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US-08-486-820-20
Sequence 20, Application US/08486820
Sequence 20, Application US/08486820
Sequence 20, Application US/08486820
Settle No. 603612
APPLICANT: Franklin: Aichard L. APPLICANT: Franklin: Richard L. APPLICANT: AV. John
TITLE OF INVENTION: Antimicrobial Uses Of Multifunctional
TITLE OF INVENTION: BRIYME
MUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lemox Drive, Building 3, Suite 210
CITY: Lawrenceville
  APPLICANT: Kay, John
TITLE OF INVENTION: Antimicrobial Uses Of Multifunctional
TITLE OF INVENTION: Enzyme
TITLE OF INVENTION: Enzyme
TOWNER OF SECURNCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechart Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
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                                                                                                                                                                                         COUNTRY: USA
ZIP: USA
ZIP: USA
ZIP: USA
ZIP: 08543
COMPUTER: READABLE FORM:
COMPUTER: LIBM COMPACTION
CORPUTER: LIBM COMPACTION
CORRATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,820
FILING DATE:
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MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: Windows 95
SOFFWARE: FastSEG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,820
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REFERENCE/DOCKET NUMBER: 314572-101B
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,820
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IVGGYXCXXHSQAHQVSLNS 20
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SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
TOPOLOGY: linear
US-08-486-820-19
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY:
STATE:
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                                                                                                                                                                                                                             Sequence 20, Application US/08600273A
Patent No. 5958406
GENERAL INFORMATION:
APPLICANT: Franklin, Richard L.
APPLICANT: Kay, John
TITLE OF INVENTION: Acne Treatment With Multifunctional
TITLE OF INVENTION: BIZZYME
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STRET: 997 Lenox Drive, Building 3, Suite 210
STY: Lawrenceville
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
COMPARE: FastSEQ for Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,273A
FILING DATE: 08-FEB-1996
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
FILING DATE: 08-FEB-1995
APPLICATION NUMBER: 08/385,540
FILING DATE: 08-FEB-1995
APPLICATION NUMBER: 29,135
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 314572-101C
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION NUMBER: 314572-101C
TELECOMMUNICATION INPORMATION:
Best Local Similarity 85.0%; Pred. No. 8.7e-10; Matches 17; Conservative 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-08+486-820-19
US-08+486-820-19
Sequence 19, Application US/08486820
Patent No. 6030612
GENERAL INFORMATION:
APPLICANT: Franklin, Richard L.
                                                                                                     1 IVGGYECTKHSQAHQVSLNS 20
                                                                   1 IVGGYXCXXHSQAHQVSLNS 20
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SEQUENCE CHARACTERISTICS:
TYPE: amino acid
STRANDEDNESS: single
TOPOLCGY: linear
US-08-600-273A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.04
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
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US-08-600-273A-20
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Sequence 18, Application US/08600273A
; Sequence 18, Application US/08600273A
; Patent No. 5958406
; GENERAL INFORMATION:
APPLICANT: de Faire, Johan
APPLICANT: Ray, John
TITLE OF INVENTION: Acne Treatment With Multifunctional
TITLE OF INVENTION: Acne Treatment With Multifunctional
TITLE OF INVENTION: Enzyme
NUMBER OF SEQUENCES: 20
CORRESPONDENCES: 20
; CORRESPONDENCES: Dechert Price & Rhoade
STREET: 997 Lemox Dive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.1%; Score 78; DB 2; Length 25; 75.0%; Pred. No. 1.2e-07; tive 2; Mismatches 3; Indels
   Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows 95
SOFTWARE: FastSEQ for Windows 95
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/600,273A
FILING DATE: 08-FEB-1996
CLASSIFFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,820
FILING DATE: 07-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/385,540
FILING DATE: 08-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: BLOOM, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 314572-101C
TELECHOME: 609-620-3214
   82,1%; Score 78; DB 2; I 75.0%; Pred. No. 1.2e-07; Live 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/08486820; Patent No. 6030612; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVGGYXCXXHSQAHQVSLNS 20
                                                                                                                                                1 IVGGYXCXXHSQAHQVSLNS 20
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SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
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Best Local Similarity 75.0
Matches 15; Conservative
       Query Match
Best Local Similarity 75.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-600-273A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08543
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US-08-486-820-18
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US-08-385-540A-18
Sequence 18, Application US/08385540A
Factor No. 5945102
Factor No. 5945108
Facto
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COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
SOFTWARE: FastSEQ for Windows Version 2.0b
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,540A
FILING DATE: WB/600,273
PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/600,273
PRILING DATE: 08-FEB-1996
ATTORNEY/AGENT INPORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REGISTRATION NUMBER: 29,135
REFERENCE/POCKET NUMBER: 314572-101A
TELEPHONE: 609-520-2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.7%; Score 90; DB 3; 1
85.0%; Pred. No. 8.7e-10;
tive 0; Mismatches 3,
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PPLICATION NUMBER: 08/486,820
FILING DATE: 07-JUNE-1995.
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 314572-101B
TELECOMMUNICATION INFORMATION:
TELEFRONE: 609-620-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IVGGYXCXXHSQAHQVSLNS 20
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                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 20;
SEQUENCE CHRACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.0 Matches 17; Conservative
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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US-08-385-540A-18
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Query Match
74.7%; Score 71; DB 2; Length 246;
Best Local Similarity 70.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                    82.1%; Score 78; DB 4; Length 25; 75.0%; Pred. No. 1.2e-07; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-08-978-404B-44

i Sequence 44, Application US/08978404B

i Patent No. 5568782

i GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

TITLE OF INVENTION: FIBRINOGEN

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

CITY: Boston

CONTRY: U.S.A.

ZIP: 02210-221

COMPUTER READBRIE FORM:

MEDIUM TYPE: DISKette

COMPUTER: IBM Compatible

COMPUTER: BMC Compatible

COMPUTER: STREED for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,404B

FILING DATE: 25-NOV-97

CLASSIFICATION NUMBER: 60/032,354

FILING DATE: 1 NPORMATION:

NAME: PLUMET INFORMATION:

NAME: PLUMET INFORMATION:

NAME: PLUMET INFORMATION:

NAME: BUMET. BIZABER: 36,637

REGESTRATION NUMBER: 36,637

TELEPROMMICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3550
                ) NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
; LENGTH: 25
; TYPE: PRT
; CRGANISM: Salmon
US-09-220-731-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5968782e
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SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acid
                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0°
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-720-2441
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US-08-956-267A-2
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APPLICANT: de Faire, Johan
APPLICANT: Franklin, Richard L.
APPLICANT: Kay, John
TITLE OF INVENTION: Britmicrobial Uses Of Multifunctional
TITLE OF INVENTION: Britme
NUMBER OF SEQUENCES: 20
NUMBER OF SEQUENCES: 20
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.1%; Score 78; DB 3; Length 25; Best Local Similarity 75.0%; Pred. No. 1.2e-07; Matches 15; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-220-731-7
Sequence 17, Application US/09220731A
Sequence 17, Application US/09220731A
Fatent No. 6232088
GENERAL INFORMATION:
APPLICANT: Phairson Medical, Inc.
APPLICANT: Richard L. Franklin
TITLE OF INVENTION: Teatment and Prevention of Immune
TITLE OF INVENTION: Treatment and Prevention of Immune
TITLE OF INVENTION: Treatment and Prevention of Immune
TITLE OF INVENTION: Treatment and Prevention of Immune
CURRENT PLICATION NUMBER: US/09/220,731A
CURRENT PLING DATE: 1998-12-24
EARLIER PLING DATE: 1993-05-11
EARLIER PLING DATE: 1993-05-11
EARLIER PLING DATE: 1994-11-22
EARLIER PLING DATE: 1995-02-08
EARLIER PLING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: STATEM: Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,820
FILING DATE:
CLASSIFICATION TAY
PROFICATION NUMBER: 08/486,820
FILING DATE: 07-UNB-1995
ATTORNEY/AGENT INPORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REGISTRATION NUMBER: 29,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 314572-101B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-620-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISOTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-486-820-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IVGGYXCXXHSQAHQVSLNS 20
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TELEX:
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69.5%; Score 66; DB 2; Length 271; 53.6%; Pred. No. 0.00026;
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Retent No. 5843694
GENERAL INFORMATION:
GENERAL INFORMATION:
TILE OF INVENTION: MOLECULES AND METHODS
ITILE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

ZIP: 0210-2804

COMPUTER: ERADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/628,198
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 69.5%; Score 66, DB 1; I
Best Local Similarity 53.6%; Pred. No. 0.00026;
Matches 15; Conservative 1; Mismatches 4;
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                                                                                                  00398/100001
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APPLICATION NUMBER: 08/467,155
FLING DATE: 06-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, Paul T.
REGISTRATION NUMBER: 00398/10
TELECOMMUNCATION INFORMATION:
TELEPAX: 617/542-8906
                                                NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFRENCE/DOCKET NUMBER: 00391
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                   TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acida
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
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                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-467-155A-10
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MOLECULE TYPE: protein
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STRANDEDNESS: no
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Best Local Similarity
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Sequence 2, Application US/08956267A

Patent No. 5945328

GENERAL INFORMATION:

APPLICANT: WOLDIKE, Helle Fabricius

APPLICANT: KJELDSEN, Thomas Borglum

TITLE OF INVENTION: (Trypsinogen)

TITLE OF INVENTION: (Trypsinogen)

TITLE OF INVENTION: (Trypsinogen)

CORRESPONDENCE ALDIRESS:

ADDRESSEE: No. 59453280 No. 5945328disk of No. 5945328th America, Inc.

STREE: A 405 Lexington Avenue

CITY: New York

STATE: NY

COUNTY: USA
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65.0%; Pred. No. 0.00023;
tive 2; Mismatches 5; Indels
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COUNTRY: USA

ZIP: 0210-2804

COMPUTER RELOABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rolease #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,155A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: ISM COMPATION
SOCIETATION SOCIETATION DATA:
APPLICATION NUMBER: US/08/956,267A
FILING DATE: 22-0CT-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: ROZEK, CAPOIN SOCIETATION NUMBER: 36,993
REGISTRATION NUMBER: 36,993
REGISTRATION NUMBER: 4500.204-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 2478-9655
JINPORMATION FOR SEG ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08467155A
Patent No. 5736377
GENERAL INFORMATION:
APPLICANT: Band, Vimla
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES:
CORRESPONDENCE 3. 11
CORRESPONDENCE 3. 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IVGGYXCXXHSQAHQVSLNS 20
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Best Local Similarity 65.0 Matches 13; Conservative
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// MOLECULE TYPE: protein
US-08-956-267A-2
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      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                           OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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1 IVGGYXCXHSQAHQVSLNS 20
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
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2: sp_bacteria:*
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5: sp_invertebrate:*
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Maximum DB seq length: 200000000
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                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MON-2002 (TrEMBLrel. 21, Last annotation update)
11-Typainogen 2 (Tremment).
Gillichthys seta (Shortjaw mudsucker).
Gillichthys seta (Shortjaw mudsucker).
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Gobiidae; Gillichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthomorpha; Percomorpha; Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDDINE=21117151; PubMed=11172064; Gracey A.Y., Troll J.V., Somero G.N.; Gracey A.Y., Troll J.V., Somero G.N.; Gracey A.Y., Troll J.V., Somero G.N.; Gillichthys mirablis."; Proc. Natl. Acad. Sci. U.S.A. 98:1993-1998(2001).

-I. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYBEIN PAMILY.

EMBL; AF266240; AGG13359.1; --
HSSP; P35031; 1BIT.

MEROPS; 501.125; --
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TISSUB-INTESTINE, PYLORIC CAECA, AND PANCREAS;
Douglas S.E., Gallant J.W.;
"Isolation of convas for Trypsinogen from the Winter Flounder, Pleuronectes americanus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
Local Similarity 85.0%; Pred. No. 2.2e-09;
Let 17; Conservative 0; Mismatches 3; Indels
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Trypsinogen 2 precursor (EC 3.4.21.4).
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InterPro; IPR001234; Ser_protease_Try.
Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SFC; I.
PROSITE; PS50240; TRYPSIN DOW; I.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_I.
Hydrolase; Serine protease.
                                                                                                                               117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVGGYXCXXHSQAHQVSLNS 20
  20 IVGGYECTICHSQAHQVSLNS 39
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                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=79683;
                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Q9DFJ6,
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Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei, Clupeomorpha, Engraulidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=PYLORIC CAECA;
Watabe S., Ahsan M.N., Funabara D.;
"Anchovy trypsinogen mRNA";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
J. Mar. Biotechnol. 0:0-0(1998).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.7%; Score 89; DB 13; Length 242; 85.0%; Pred. No. 4.8e-09; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EWBL; AB04129; BAB40329.1; -.

R HSSP; P00763; 1DP0.

R MEROPS; S01.125; -.

R InterPro; 1PR001314; Chymotrypsin.

R InterPro; 1PR00134; Ser_protease_Try.

R FARNYS; PR00722; CTWOTRYPSIN.

R PRNYS; SM00020; Tryp SPC; 1.

R PROSITE; PS00134; TRYPSIN_DOM; 1.

R PROSITE; PS00134; TRYPSIN_DOM; 1.

R PROSITE; PS00135; TRYPSIN_DOM; 1.

R PROSITE; PS00135; TRYPSIN_ER; 1.

R PROSITE; PS00135; TRYPSIN_ER; 1.

R PROSITE; PS00135; TRYPSIN_ER; 1.

R PROSITE; PS00136; TRYPSIN_ER; 1.

R PROSITE; PS00136; TRYPSIN_ER; 1.

R PROSITE; PS00136; TRYPSIN_ER; 1.
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Best Local Similarity 75.0%; Pred. No. 4.1e-07;
Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN 21 242 TRYPSINOGEN 2.
SEQUENCE 242 AA, 26180 MW; 08D2A834FB289080 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           098TH0;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Trypsinogen.
                                                                                                                                                               MERCEPEO, 1PR001314; Chymotrypain.
InterPro; 1PR001254; Ser_protease_Try.
Pfam; PF00089; trypain; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Signal.
SIGNAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                        EMBL; AF012463; AAC32752.1; -. HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                              MEROPS; 801.125; -.
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us-10-036-371-1.rspt

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PRELIMINARY;
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TISSUE=PYLORIC CAECA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=42892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; S01.258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypsinogen II.
ATRYII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (
01-JUN-2001 (
01-JUN-2002 (
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                                                                                                                                                                                                                                          Matches
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042159
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                                                                                                                                                          Paralichthys olivaceus (Flounder).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Necteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                            Suzuki T., Srivaetava A.S., Kurokawa T.;
"Japanese flounder mRNA for trypsinogen 2.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE EMBL; ABO29751; BAA82363.1; --
HSSP: PO0763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygli, Neopterygli, Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygli; Percomorpha; Pleuronectiformes; Pleuronectoidei; Paralichthydae; Paralichthys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suzuki T., Srivastava A.S., Kurokawa T.;
"Japanese flounder mRNA for trypsinogen 1.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.1%; Score 78; DB 13; Length 238; 75.0%; Pred. No. 6.3e-07; Live 1; Mismatches 4; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 AA; 26071 MW; F2B8908085B8D062 CRC64;
                   09W706 PRELIMINARY, PRT; 238 AA. 09W706; 01.NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-UNV-2002 (TrEMBLrel. 21, Last annotation update) Trypsinogen 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001354; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp_SPc; 1.
PR0SITE; PS00134; TRYPSIN DOM; I.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN HIS; UNKNOWN_I.
Hydrolase; Serine protease.
NON TER.
SEQUENCE 238 AA; 26071 MW; F2BB908085BBD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001114; Chymotrypsin.
InterPro; IPR001254; Ser protease_Try.
Pfam; PF00089; trypsin; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trypsinogen 1.
Paralichthys olivaceus (Flounder).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB029750; BAA82362.1; -. HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 75.0
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; S01.125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE = PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S01,125;
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Matches
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907W90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Engraulis japonicus (Japanese anchovy).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Engraulidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watabe S., Ahsan M.N., Funabara D.;
"Anchovy trypsinogen mRNA.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TYPEN FAMILY.
EWBS; ABO41930; BAB40330.1; -- HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Petromyzon marinus (Sea lamprey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
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                                                                                                                                                                                                       Length 242;
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                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; TYPPS SEC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
Hydrolase; Serine protease.
SEQUENCE 242 AA; 26548 MW; 6DA722C80BC194A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26282 MW; FE362D39CAEEB2F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                042159, PRELIMINARY, PRT; 244 AA.
042159, 01-37A-1998 (TrEMBLrel. 05, Created)
01-3AN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-1998 (TrEMBLrel. 21, Last annotation update)
Trypsinogen B1 precursor (Fragment).
                                                                                                                                                                                                  ch 82.1%; Score 78; DB 13;
1 Similarity 75.0%; Pred. No. 6.4e-07;
15; Conservative 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001214; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfan; PP00089; trypsin; I
PRINTS; PR00729; Tryp SPC; 1.
SMRT; SM00020; Tryp SPC; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
HYGNOSTE; PS00135; TRYPSIN SER; 1.
HYGNOSTE; PS00135; TRYPSIN SER; 1.
HYGNOSTE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                   1 IVGGYXCXXHSQAHQVSLNS 20
                                                                                                                                                                                                                                                                                                                                   21 IVGGYECTPYSQPHQVSLNS 40
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Gape

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5; Indels

73.7%; Pred. No. 9.4e-06;

0; Mismatches

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1 IVGGYXCXXHSQAHQVSLN 19
                                                                                                                                                         22 IVGGYECAAHSÓPWÓVSĽN 40
                          14; Conservative
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trypsinogen 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91515
Q91515;
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Q9W7Q5;
                              Matches
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                                                                                                                                                                                                                                                      RESULT 10
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"The Molecular Evolution of the Vertebrate Trypsinogens.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL, AF011901; AAB69657.1; -.
                                                                                                                                     Roach J.C.;
The Molecular Evolution of the Vertebrate Trypsinogens.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-i. SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1; ALSO KNOWN AS THE TRYPESIN FAMILY.
EMBL; AF011900; AAB69656.1; -.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petromyzon marinus (Sea lamprey).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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Pred. No. 9.4e-06;
0; Mismatches 5; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 POTENTIAL.
245 TRYPSIN B2.
26001 MW; 9A932508B896C93E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C4582EE07E3B8007 CRC64;
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01-JAN-1998 (TrEWBLrel. 05, Created)
01-JAN-1998 (TrEWBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Trypainogen b2 precursor (Fragment).
      Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; 19701314; Chymotrypsin.
Interpro; 1PR001354; Ser protease_Try.
Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSTE; PS50240; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN HIS; UNKNOWN_1.
Hydrolase; Serine protease; Signal.
NON TER 1
1 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 AA
                                                                                                                                                                                                                                                                                                                                                    MEROPS; 501.128; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001284; Ser_protease_Try.
InterPro; IPR001284; Ser_protease_Try.
InterPro; IPR00129; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN DOM, 1.
PROSITE; PS00134; TRYPSIN HIS; UNROWN_1.
PROSITE; PS00135; TRYPSIN SRR, 1.
Hydrolase; Serine protease; Signal.
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TRYPSIN B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.8%;
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                                                                                                SEQUENCE PROM N.A.
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                                        NCBI_TaxID=7757;
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Length 245;

DB 13;

75.8%; Score 72;

Query Match

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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last sequence update)
1-UDM-2002 (TrEMBLrel. 21, Last annotation update)
Trypsinogen (Fragment)
Pugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii, Neopterygii, Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha; Tetraodontiformes; Tetraodontiformes;
                                                                                                                                           Paralichthys Olivaceus (Flounder).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;

Eukaryota, Metyerygli, Teleostei, Buteleostei, Neoteleostei,

Acanthomorpha, Acanthopterygli, Percomorpha, Pleuronectiformes;

Pleuronectoidei, Paralichthyidae; Paralichthys.
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Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                            TISSUE=PANCREAS;
Suzuki T., Srivastava A.S., Kurokawa T.;
Japanese flounder mRNA for trypsinogen 3.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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74.7%; Score 71; DB 13; Lv
Best Local Similarity 73.7%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 AA
247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001314; Chymotrypsin, InterPro; IPR001254; Ser protease_Try. Pfam; PF00089; trypsin; IPR001254; Ser protease_Try. PRINTS; PR00722; CHYMOTRYPSIN. SWART; SW00020; Tryp. SPC; 1. PROSITE; PS00134; TRYPSIN. HIS; UNKNOWN. 1. PROSITE; PS00134; TRYPSIN. HIS; UNKNOWN. 1. Hydrolase; Serine protease. SEQUENCE 247 AA; 26948 MW; DC48647179DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
  PRT;
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                          Q9CPN7
        09CPN7
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TISSUE=PYLORIC CAECA,
MEDLINE=97104330; PubMed=8948488;
Genicot S., Rentier-Delrue F., Edwards D., Van Beeumen J., Gerday C.;
"Trypsin and trypsinogen from an antarctic fish: molecular basis of cold adaptation.";
                                                                                                                                                                                                                                                                                                                                                      Gaps
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01-NOV-1996 (TERMBLrel. 01, Last sequence update)
01-NOV-1996 (TERMBLrel. 21, Last sequence update)
101-UTN-2002 (TERMBLrel. 21, Last annotation update)
Trypsin precursor (BC 3.4.21.4).
Parantothenia magellanica (Maori cod)
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha, Acanthoperygii; Teleostei; Percomorpha;
Notothenioldai; Nototheniidae; Paranotothenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 1298:45-57(1996).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
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                                                                                                                                                                                                                                                                                                        72.6%; Score 69; DB 13; Length 237; 70.0%; Pred. No. 3.5e-05; Live 2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                  SEQUENCE 237 AA; 25726 MW; 30D2DBAAC39080C2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 242 AA
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
EMBL; U25747; AAA75001.1; -.
HSSP; P35031; 1BIT.
                                                                                                                                                                                                                                                                                                                                                                                          1 IVGGYXCXXHSQAHQVSLNS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                16 IVGGYECRKNSVAYOVSLNS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X82223; CAA57701.1; -. HSSP; P00763; IDPO.
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                                                                                                                                                                                                                                                                                                                            Local Similarity 70.0
Les 14, Conservative
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                                        MEROPS; S01.125;
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Matches
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Matches
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SEQUENCE FROM N.A.

REMAIN-C57BL/6J; TISSUE=PANCREAS;

MEDINE-2.1085660; Daibata R., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Shinagawa A., Shinadara R., Konno H., Adachi J., Fukuda S., A Arawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Saito R., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Saburner M., Batalov S., Casavant T., A Rubhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno W., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Black J., Bult C., Fletcher C., Fulita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Asaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whishaw-Boris A., Yebhida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki S., Hayashizaki S., Matsuki S., Mats
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen F., Rowen L., Hood L., Rothenberg E.V.;
"Differential transcriptional regulation of individual TCR Vbeta
"Sifferential before gene rearrangement.";
J. Immunol. 166:1771-1780(2001)
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
-TRYPEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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PROSTIE; PSSO240; TRYPSIN DOM; I. PROSTIE; PSSO134; TRYPSIN HIS; UNKNOWN I. PROSTIE; PSSO135; TRYPSIN ER; I. Hydrolase; Serine protease.

Hydrolase; Serine protease.

SEQUENCE 247 AA; 26503 MW; EDF5F7696833C7BC CRC64;
                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
1310009J06Rik protein (Trypsinogen 4).
247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1920876; 1810009J06Rik.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
PRT;
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MEDLINE=21103195; PubMed=11160223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 68.4
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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SEQUENCE PROM N.A.
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RESULT 14 Q8QGW3

RESULT 13

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Rowen L., Hood L.;
"Comparison between strains Balb/C and 129 in a region of the mouse T
cell receptor beta locus.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

TISSUE-PANCREAS;

KINCKAWA T., Suzuki T., Ohta H., Kagawa H., Tanaka H., Unuma T.;

KINCKAWA T., Suzuki T., Ohta H., Kagawa H., Tanaka H., Unuma T.;

Expression of pancreatic enzyme genes during the early larval stage of Japanese eel, Anguilla japonica.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AB070720; BAB85634.1; -.

FAMTORIASE.

SEQUENCE 244 AA; 26317 MW; 0EB3B68E8706D52D CRC64;
                                                                                                                                                                 Anguilla japonica (Japanese eel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
Anguilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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-i. SIMMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 69.5%; Score 66; DB 13; Length 244; Local Similarity 65.0%; Pred. No. 0.00014; e9 13; Conservative 1; Mismatches 6; Indels
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Last annotation update)
                                                       Created)
Last sequence update)
Last annotation update)
244 AA.
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MGD; MGI:2148749; Trygnl6.
MGD; MGI:2148749; Trygnl6.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001354; Ser protease_Try.
Pfam; PF00089; trypsin; I
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
PRT;
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                                                    01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                           Trypsinogen (EC 3.4.21.4).
TRY.
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7937;
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                              Q8QGW3 ;
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0921R9
1D 0921R9
DT 01-MA
DT 
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Matches
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DR PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.

DR PROSTE; PS00135; TRYPSIN_SER; 1.

KW Hydrolase; Serine protease.

SQ SEQUENCE 246 AA; 26134 WW; 34E173B18CA2F463 CRC64;

Query Match
Best Local Similarity 65.0%; Pred. No. 0.00021;

Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps

Oy 1 IVGGYXCXXHSOAHQVSLNS 20

Oy 1 IVGGYYCRENSVPYQVSLNS 43
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Search completed: February 12, 2003, 10:27:17 Job time : 16:1493 secs

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                  P07647 rattus norv
P036376 rattus norv
P00758 rattus norv
O9ukr3 homo sapien
P08259 homo sapien
P15947 mus musculu
P04071 mus musculu
   rattus norv
rattus norv
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mus musculu
                                                                                                                                                     mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eur. J. Biochem. 180:85-94(1989).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Pyloric caeca;
MEDLINE=89210867; PubMed=2707266;
Asgeirsson B., Fox J.W., Bjarnason J.B.;
"Purification and characterization of trypsin from the poikliotherm
Gadus morhua.";
                                                                                                                                                                                                                                                                                                                 TRYI_GADMO STANDARD; PRT; 241 AA.
P1676, Q2104, Q22156;
P1676, Q2104, Q22156;
P1676, Q2104, Q22156;
P1676, Q2104, Q22156;
P1670, Q2104, Q22156;
P1670, Q202, Created)
P1670, Q202, Created)
P170, P202, Created, C
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InterPro; IPR001254; Ser_protease_Try.
Pfan, PF00089; trypsin, 1.
SMART; SM00020; Tryp_SPC; 1.
PR0SITE; PS50240; TRYPSIN DW; 1.
PR0SITE; PS00134; TRYPSIN_HIS; 1.
PR0SITE; PS00135; TRYPSIN_HIS; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
                                                                                                               P04071 n
P19799 >
P07628 n
P36374 1
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              KLK9 RAT
KLKC RAT
KLKD HUMAN
KLKB HUMAN
KLK8 HUMAN
KLK1 MOUSE
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MOUSE
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MEROPS; S01.151; -.
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Hydrolase; Serine
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8049;
 TRY1_GADMO
rattus norv
homo sapien
homo sapien
homo sapien
hom sapien
bos taurus
bos taurus
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gallus gall
gallus gall
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091041 gadus morhu
P35031 salmo salar
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canis famil
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                                                                                                         February 12, 2003, 10:04:45; Search time 2.68657 Seconds (without alignments) 308.768 Million cell updates/sec
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            GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                             112892 seqs, 41476328 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.000 + 1.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.000 + 0.00
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                                                                                                           Run on:
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Digestion; Pancreas; Zymogen; Signal;

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Serine protease;
                                                                                                                                                                                                                                                                            241 AA;
                                                                                                                                                                                                                                                                                                                                  Similarity
                   family
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TRY1_SALSA
ID _TRY1_SALSA
AC P35031;
Hydrolase;
                 Multigene
                                                                                        ACT_SITE
ACT_SITE
DISULFID
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Best Local
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                                                                                                                                                                                                                      REQUIRED FOR SPECIFICITY (BY SIMILARITY)

E -> Q (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDLINE=94039130; PubMed=8223632;
Gudmundsdottir A., Gudmundsdottir E., Oskarsson S., Bjarnason J.B.,
Gudmundsdottir A., Gudmundsdottir E., Oskarsson S., Bjarnason J.B.,
Eakin A.E., Craik C.S.;
"Isolation and characterization of cDNAs from Atlantic cod encoding
two different forms of trypsinogen.";
Eur. J. Biochem. 21.1091-1093;
Eur. J. Biochem. 21.1091-1093;
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                     SIMILARITY).
SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                 Score 90; DB 1; Length 241; Pred. No. 1.5e-09; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                 44EC9A0106AD1A69 CRC64;
                                                     (BY
(BY
(BY
                                                                                                                                                                                                                                                         TK -> EA (IN REF. 2).
F -> Y (IN REF. 2).
VSKD -> IN (IN REF. 2)
                                                                                                                                                                                                                                      (IN REF. 2).
IA (IN REF. 2).
                                TRYPEIN I.
CHARGE RELAY SYSTEM (I
CHARGE RELAY SYSTEM (I
CHARGE RELAY SYSTEM (I
BY SIMILARITY.
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 POTENTIAL.
ACTIVATION PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; SOI.151; -...
InterPro; IRRO1114; Chymotrypsin.
InterPro; IRRO1114; Ser_procease_Try.
Pfam; PP001089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM0020; Tryp_SPC; 1.
PROSITE; PS00124; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trypsin X precursor (EC 3.4.21.4). Gadus morhua (Atlantic cod).
                                                                                                                                                                                                                                                                                                                 25941 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X76887; CAA54215.1; -. HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                     94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                              1 IVGGYXCXXHSQAHQVSLNS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 IVGGYECTKHSQAHQVSLNS 39
                                                                                                                                                                                                                                                                                                                                                                      85.0%;
                                                                                                                                                                                                                                                                                                                                                                                          17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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189
25
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 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8049;
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091041;
                                                                                        ACT_SITE
DISULFID
DISULFID
DISULFID
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                                                     ACT_SITE
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                                                                                                                                                                   DISULFID
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TRYX GADMO
TRYX GADMO
DT 01-NOV-
DT
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                                                                                            103 CHARGE RELAY SYSTEM (BY SIMILARITY).
103 CHARGE RELAY SYSTEM (BY SIMILARITY).
105 CHARGE RELAY SYSTEM (BY SIMILARITY).
105 BY SIMILARITY.
106 BY SIMILARITY.
107 BY SIMILARITY.
108 BY SIMILARITY.
109 BY SIMILARITY.
100 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Proteins 20:149-16(1994).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULIAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.82 ANGSTROMS).
MEDLINE-95146588; PubMed=7846025;
Smalas A.O., Heimstad S.S., Hordvik A., Willassen N.P., Male R.;
"Cold adaption of enzymes: structural comparison between salmon and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Protacanthopterygii, Salmoniformes, Salmonidae, Salmo.
NCBI_TaxID=8030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure determination and refinement of benzamidine-inhibited trypsin from the North Atlantic salmon (Salmo salar) at 1.82-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Male R., Lorens J.B., Smals A.O., Torrissen K.R.; "Molecular cloning and Characterization of anionic and cationic variants of tryppia from Atlantic salmon."; Eur. J. Biochem. 232:677-685(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 90; DB 1; I
Pred. No. 1.5e-09;
0; Mismatches 3;
                                 ACTIVATION PEPTIDE. TRYPSIN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FUN-2002 (Rel. 41, Last annotation update)
Trypsin I precursor (EC 3.4.21.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smalas A.O., Hordvik A.; "Structure determination and refinement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.82 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acta Crystallogr. D 49:318-330(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE*Pancreas;
MEDLINE*96035908; PubMed=7556223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmo salar (Atlantic salmon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.7%;
85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 IVGGYECTRHSQAHQVSLNS 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Conservative
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13
19
241
241
193
195
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201
180
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J. Biol. Chem. 259:14255-14264 (1984)
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                                                                                                                                                                                                                                                                      24823 MW;
                                        EMBL, X70073, CAA49678.1, -.
PIR, S31778, S31778,
HSSP, P35031, 1BIT.
MEROPS, S01.258, -.
                                                                                                                                                                                                                                                                                                                       1 IVGGYXCXXHSQAHQVSLNS 20
                                                                                                                                                                                                                                                                                                                                       10 IVGGYECKAYSQPHQVSLNS 29
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
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93
185
145
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218
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170
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                         REQUIRED FOR SPECIFICITY (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
PRIMTS; PR00722; CHYMOTRPEIN.
SMART; SM002020; Tryp. SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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                                                                                                                                                                                                                                                                                                           Score 80; DB 1; Length 242;
Pred. No. 1.1e-07;
1; Mismatches 4; Indels
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25958 MW; 43F5642498067E5A CRC64;
                                                                                                                                                                                             CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                   POTENTIAL.
ACTIVATION PEPTIDE.
TRYPSIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Trypsin II precursor (EC 3.4.21.4) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypsin II precursor (EC 3.4.2 Salmo salar (Atlantic salmon).
EMBL; X70075; CAA49680.1; -.
EMBL; X70071; CAA49676.1; -.
EMBL; X70072; CAA49677.1; -.
                                                                                                                                                                                                                                                                                                                                            1 IVGGYXCXXHSQAHQVSLNS 20
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                                                                                                                                                                                                                                                                                                             84.2%;
                                                                                                                                                                                                                                                                                                                     75.0%;
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.03
Matches 15, Conservative
                     PIR; S3,
PIR; S31776; S2,
PIR; S31777; S31777;
R PDB; 2TBS; 30.4PR-94,
PDB; 1BIT; 01-NOV-94,
S01.151; --
                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                           242
242
60
104
196
1156
61
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216
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242 AA;
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104
196
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ID TRY2_SALSA
AC P35032;
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ACT_SITE
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ACT_SITE
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CS4AlCAFE74FAE18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X.TAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE-87292123; PubMed=1112942;
Sprang S., Standing T., Fletterick R.J., Stroud R.M., Finer-Moore J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Sprague-Dawley,
MEDLINE=82265624; PubMed=6896710,
MCDOnald R.J., Stary S.J., Swift G.H.,
"Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide
sequences of the cloned cDNAs.",
J. Biol. Chem. 257:9724-9732(1982).
                                                                                                                                                                     (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsin I, anionic precursor (EC 3.4.21.4) (Pretrypsinogen I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-85054880; PubMed=6094547;
Craik C.S., Choo Q.L., Swift G.H., Quinto C., McDonald R.J.,
Rutter W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
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ACTIVATION PEPTIDE.
TRYPSIN II.
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75.0%; Pred. No. 1.7e-07;
iive 1; Mismatches 4;
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MEROPS; S01.094; -.
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                             ASPIO2 in serine protease catalysis.";
Science 23::905-909 (1987).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- MISCELLABOUS: THIS SEQUENCE REPRESENTS THE PRECURSOR OF THE MAJOR FORM OF TRYPSIN PRODUCED BY THE ADULT PANCREAS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 Xuong N.-H., Hamlin R., Rutter W.J., Craik C.S.; #The three-dimensional structure of Asn102 mutant of trypsin: role of
                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR00134; Chymotrypsin.
Interpro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00122; CHYMOTRYPSIN.
SWART; SM00020; Tryp. SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SRR; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal; Multigene family; 3D-structure.
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CHARGE RELAY SYSTEM.
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EMBL; J00778; AAA98518.1; -.
PIR; A00948; TRRT1.
PDB; 1TRM; 15-UUL-93.
PDB; ZTRM; 16-UUL-88.
PDB; 1RRA; 30-ARR-94.
PDB; 1BRC; 31-UUL-94.
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                              Gaps
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TISSUE-Pancreas;
WEDLINE-95251611; PubMed=7733885;
WANG K., Lee I., Hood L.E.;
"Isolation and characterization of the chicken trypsinogen gene
                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                          74.7%; Score 71; DB 1; Length 246; 70.0%; Pred. No. 5.6e-06; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                             25959 MW; 6AFA0DAD11943FB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
17-Ppsin II-P29 precursor (EC 3.4.21.4)
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 AA
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Interpro; IPR001214; Ser protesse_Try.
Pfam; PF00089; trypsin; I
RRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; TRYPSIN DOM; I
PROSITE; PS00134; TRYPSIN DOM; I
PROSITE; PS00134; TRYPSIN DOM; I.
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HSSP; P00763; 1DPO.
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Best Local Similarity 70.04
Matches 14; Conservative
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 246 AA;
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                                                                                                                                                                                                                                                                                                                                           REQUIRED FOR SPECIFICITY (BY SIMILARITY) : E5E16B07622B588E CRC64;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                               BY SIMILARITY.
ACTIVATION PEPTIDE (BY SIMILARITY).
TRYPEIN II - P29.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
PS00135; TRYPSIN_SER; 1.
e; Serine protease; Digestion; Pancreas; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Pancreas;
MEDLINE=92165057; PubMed=1537555;
Kang J., Wiegand U., Mueller-Hill B.;
"Identification of CDNAs encoding two novel rat pancreatic serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Prim; PR00029; CHYMOTRYPSIN.
SMART; SMO02020; Tryp. SPC; 1.
PROSITE; PS00210; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SER; FALSE NEG.
Multigene family.
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Pred. No. 5.6e-06;
1; Mismatches 5; Indels
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10-CCT-1993 (Rel. 27, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Trypsin V-A precursor (EC 3.4.21.4).
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                                                                                                                                                                                                                                                                                                                                                                                                          74.78;
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Matches 14; Conservative
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                          Hydrolase, Serine
Multigene family
SIGNAL
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                                                                                                                                                                                           REQUIRED FOR SPECIFICITY (BY SIMILARITY) 1EBE59D88BAB1715 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Mētazoa, Chordata, Craniata, Vertebrata, Buteleoscomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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-!- CRATATYTC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                              (BY SIMILARITY).
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(BY SIMILARITY).
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MEDLINE=92165057; PubMed=1537555;
Kang J., Wiegand U., Mueller-Hill B.;
"Identification of cDNAs encoding two novel rat pancreatic serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine protease; Digestion; Pancreas; Zymogen; Signal;
                                                                                                                                                                                                                                               Length 246
                                                                                                                                                                                                                                         72.6%; Score 69; DB 1; Length 246
65.0%; Pred. No. 1.3e-05;
ive 2; Mismatches 5; Indels
                          TRYPSIN V-A.
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                ACTIVATION PEPTIDE
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TRYPSIN V-B.
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1-OCT-1993 (Rel. 27, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Trypsin V-B precursor (EC 3.4.21.4).
                                                                                                                                                                                                                                                                                                                                                                                                                              246 AA
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InterPro; IPR001254; Ser_protease_Try.
Plan, PF00089; trypsin; PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PR03ITE; PS00240; TRYPSIN DOM; 1.
PR03ITE; PS00135; TRYPSIN HIS; 1.
PR0SITE; PS00135; TRYPSIN HIS; 1.
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les 13; Conservative
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HSSP; P00763; 1DPO.
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Multigene family.
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64 CHARGE RELAY SYSTEM (BY SIMILARITY).
108 CHARGE RELAY SYSTEM (BY SIMILARITY).
200 CHARGE RELAY SYSTEM (BY SIMILARITY).
160 BY SIMILARITY.
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233 BY SIMILARITY.
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MEDLINE=92201369; PubMed=1551419;
Huang Q., Liu S., Tang Y., Zeng F., Qian R.;
Hamino acid sequencing of a trypsin inhibitor by refined 1.6 A X-ray
crystal structure of its complex with porcine beta-trypsin.";
PEBS Lett. 297:143-146(1992).
                                                                                                                                                                                                        Gaps
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Huber R., Piechottka G.P., Matschiner G., Sommerhoff C.P., Fritz H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDDINES-95035057; bubmeda-7947985;
Huang Q., Wang Z., Li Y., Liu S., Tang Y.;
"Refined 1.8-A resolution crystal structure of the porcine epsilon-
                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
1rypsin precursor (EC 3.4.21.4).
Sus scrola (Pig)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OP 9-231.
MEDLINE=72358692; PubMed=4738933;
Hermodson M.A., Exicsson L.H., Neurath H., Walsh K.A.;
"Determination of the amino acid sequence of porcine trypsin by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH LDII
MEDLINE=97390427; PubMed=9242660;
                                                                                                                                                                         Score 69; DB 1; Length 246;
Pred. No. 1.3e-05;
2; Mismatches 5; Indels
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Challes M., Rovery M., Guidoni A.A., Desnuelle P., "Orbarles M., Rovery M., Guidoni A.A., Desnuelle P., "On trypsingen and trypsin of pig.";
Biochim. Biophys. Acta 69:115-129(1963).
                                                                                                                                                                                                                                                                                                                                      231 AA
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Biochim. Biophys. Acta 1209:77-82(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complex.";
J. Mol. Biol. 229:1022-1030(1993).
                                                                                                                                                                                                                                                                                                    RESULT 9

TRYP PIG

TRYP PIG

TO TRYP PIG

AC P00761;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequen)
DT 21-JUL-1986 (Rel. 01, Last sequen)
DT 21-JUL-2002 (Rel. 41, Last sequen
DT 21-JUL-2002 (Rel. 41, Last sequen
DE Trypsin precursor (EC 3.4.21.4).
OC Sus scrofa (Pig).
OC WARMALIS BUTHERIA; Cetartiodacty
OX NCBI_TAXID=9823;
RN

[1] RP SEQUENCE OF 1-10.
RA Charles M., Rovery M., Guidoni A., Rolarles M., Rovery M., Guidoni A., Rolarles M., Rovery M., Guidoni A., Rolarles M., Rovery M., Guidoni A., R. Charles M., Extesson L.H., Ne Fortendiation of the amino acid sequentor analysis.";
RN K. Hands Q., Liu S., Tang Y., Engis R. MEDLINE=93187998; PubMed=8445634; R. Medlined 1.6-A resolution crystal structure of the comparise complex.";
Complex.";
U. Mol. Biol. 229:1022-1030(1993)
RN K. RAY CRYSTALLOGRAPHY (1.6 ANGSTR RY Amino acid sequencing of a trype crystal structure of its complex RY Refined 1.8-A resolution crystal RY Refined 1.8-A resolution crystal Blochim. Biophys. Acta 1209:77-87
RN FEBS Lett. 297:143-146(1992).
RN KRELINE=92201369; PubMed=1551419; RN RELINE=92035057; PubMed=1551419; RN Refined 1.8-A resolution crystal Crystal Strubs M. T., Morenweiser R., Stubs M. T., Morenweiser R., Stubs M. R., Rollined M. T., Morenweiser R., Stubs R., Stubs M. T., Morenweiser R., Stubs R., Stubs M. T., Morenweiser R., Stubs R., Ruber R., Piechottka G.P., Ras Charles R., Stubs R., Piechottka G.P., Ras Charles R., Stubs R., Piechottka G.P., Ras Charles R., Stubs M. T., Piechottka G.P., Ras Charles R., Piechottka G.P., V. Laus C., Piechottka G.P., V. Laus C., Piechottka G.P., V. La
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                                                                                                                                                                          ch 72.6%;
l Similarity 65.0%;
13; Conservative 2
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                                                                                                                                                    246 AA;
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SEQUENCE FROM N.A.
MEDLINE-86284658; PubMed=3841794;
Pinsky S.D., Laforge K.S., Scheele G.;
Pinsky S.D., Laforge K.S., Scheele G.;
"Differential regulation of trypsinogen mRNA translation: full-length mRNA sequences encoding two oppositely charged trypsinogen isoenzymes
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Province, irrout234; Ser_protease_Try.
Prints, PR0089; trypsin; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS50134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN ER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal; SIGNAL.
                                                                                                                                                                                                   0;
                                                                                                                                                                           69.5%; Score 66; DB 1; Length 231;
65.0%; Pred. No. 4.5e-05;
iive 2; Mismatches 5; Indels
                                                                                                                                                     24409 MW; A0A125CF7FC138C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATION PEPTIDE.
                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
12-JUN-2002 (Rel. 41, Last annotation update)
Trypsin, cationic precursor (EC 3.4.21.4)
Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                     PRT; 246 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                        1 IVGGYXCXXHSQAHQVSLNS 20
                                                                                                                                                                                                                                          9 IVGGYTCAANSIPYQVSLNS 28
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                                                                                                                                                                           Query Match
Best Local Similarity 65.09
Matches 13; Conservative
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 171
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231 AA;
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MEROPS; S01.151; -.
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ID TRY1_CANFA
AC P06871;
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                                                                                                                                                                         REQUIRED FOR SPECIFICITY (BY SIMILARITY) E9E5A1DE2391BBBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Earnest T., Fauman E., Craik C.S., Stroud R.;
"1.594 structure of trypsin at 120 K: comparison of low temperature and room temperature structures.";
proteins 10.17.187(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dependent geometry.";
Biochemistry 35:5999-6009(1996).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 9-246 FROM N.A.
STRAND-Sprague-Dawley, ITSSUE-Pancreas,
MEDLINE-822664; PubMed-6896710;
MCDonald R.J. Stary S.J., Swift G.H.,
"Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of the cloned cDNAs."
J. Biol. Chem. 257:9724-9732(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96214506; PubMed-8634241;
Brinen L.S., Willett W.S., Craik C.S., Fletterick R.J.;
"X-ray structures of a designed binding site in trypsin show metal-
                  SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
15-UUL-1988 (Rel. 36, Last sequence update)
15-UW-2002 (Rel. 41, Last annotation update)
TYYPsin II, anionic precursor (EC 3.4.21.4) (Pretrypsinogen II).
                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                              Length 246;
                                                                                                                                                                                                  69.5%; Score 66; DB 1; Length 240, 69.5%; Pred. No. 4.8e-05;
                    TRYPSIN, CATIONIC.
CHARGE RELAY SYSTEM (I
CHARGE RELAY SYSTEM (I
BY SIMILARITY.
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MEDLINE=91351998; PubMed=1881877;
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                                                                                                                                                                                        26170 MW;
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                                                                                                                                                                                                                                                              13; Conservative
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 246
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TRY4 HUMAN
TRY4 HUMAN
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DT 01-FEB
DT 15-UM
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001252; CHYMOTRYPSIN.
SMART; SM00020; TryP.SPC; 1.
PROSITE; PS50240; TRYPSIN. DOM; 1.
PROSITE; PS000134; TRYPSIN. MIS; 1.
PROSITE; PS00135; TRYPSIN. MIS; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 7.4e-05;
2; Mismatches 5; Indels
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V -> I (IN REF. 1).
A8D3630809AEE606 CRC64;
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TRYPSIN 11, ANIONIC.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annocation update)
Trypain III precursor (EC 3.4.21.4).
PRSS3 OR TRY3.
Homo sapiens (Human).
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MEDLINE=90221895; PubMed=2326201;
                                                                                                  L00131; AAA98517.1; -. L00130; AAA98517.1; JOINED
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26228 MW;
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65.0%;
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                                                                           EMBL; V01274; CAA24581.1; -.
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Best Local Similaricy
Watches 13, Conservative
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1SLX; 11-JUL-96.
1SLX; 11-JUL-96.
1DPO, 07-JUL-97.
3TG1; 23-DEC-98.
                                                                                                                                                                     1ANB; 01-APR-97.
1ANC; 01-APR-97.
1AND; 01-APR-97.
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246 AA;
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                                                                                                                                               A22657; TRRT2
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P15951;
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TRY3 HUMAN
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AD PTRY3 HU
DT 01-APR
DT 15-APR
DT 15-TUN
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TRYBEIN III.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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REQUIRED FOR SPECIFICITY (BY SIMILARITY).
W, 697DE163PICEEOD6 CRC64;
Gaps
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
PRIMTS; PR00122; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
SMART; SS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_BER; FALSE_NEG.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=94123994; PubMed=8294000;
MEDLINE=94123994; PubMed=8294000;
Miggand U., Corbach S., Minn A., Kang J., Mueller-Hill B.;
"Cloning of the cDNA encoding human brain trypsinogen and characterization of its product.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 1; Length 24;
Pred. No. 7,4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRY4 HUMAN STANDARD; PRT; 304 AA.
P35030; 015665; Q9UQV3;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Trypsin IV precursor (EC 3.4.21.4) (Brain trypsinogen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS A AND B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26776 MW;
                                                                                                                                                                                                                                                                                                                                                                   EMBL, X15505; CAA33527.1; -... PIR; $12764; $12764. HSSP. P00761; 1EFT. MEROPS; $01.174; -... Genew; HGNC:9486; PRSS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.4%;
65.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Mesotrypsinogen).
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Multigene family.
SIGNAL
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PRSS1 OR TRY1 OR TRP1 OR TRYP1.
Homo sapiens (Human).
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VARIANT HPC ILE-29.
                                                                                                                                       SEQUENCE OF 16-43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT HPC ARG-23.
                                                            SEQUENCE FROM N.A.
                                        NCBI_TaxID=9606;
                                                                                          Matsubara K.;
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                                                                                                                                                                                                                                                                                                                                                                            CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
RY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCGPDDRCPARWFGFGRAVKCGKGLAAARPGRVERGGAQRG
GAGLELHPLLGGRTWRAARDADGCEALGT -> MNPFLILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                   InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM0020; Tryp SPC; 1.
PROSITE; PS50134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN "SER; FALSE_NEG.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal; Milligene family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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MISSING (IN REF. 1; CAA50484).

4C4316C31F1D0FFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 1; Length 304;
Pred. No. 9.3e-05;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRY1 HUMAN STANDARD; PRT; 247 AA.
P07477; Q92955; Q9HAN4; Q9HAN5; Q9HAN6; Q9HAN7;
01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsin I precursor (BC 3.4.21.4) (Cationic trypsinogen).
                                                                                                                                                                                                                                                                                                                                                         ACTIVATION PEPTIDE.
TRYPSIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                  SEQUENCE FROM N.A. (ISOFORM C).
                                                                                                                                                                                          EMBL, X72781, CAB58178.1, -.
EMBL, X71345; CAA50484.1, -.
EMBL, D45417; BAA08257.1; -.
PIR, S33496, S33496.
HSSP, P07477; 1TRN.
MEROPS; S01.174, -.
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304 AA; 32499 MW;
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65.0%;
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1120
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1121
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1217
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164
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257
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TRY1 HUMAN
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Ferec C., Raguenes O., Salomon R., Roche C., Bernard J.P., Guillot M.,
Quere I., Faure C., Mercier B., Audrezet M.P., Guillausseau P.J.,
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SEQUENCE OF 68-151 FROM N.A., AND VARIANTS HPC P-104; C-116 AND F-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [4]
SEQUENCE OF 15-67 FROM N.A., AND VARIANT HPC GLY-22.
MEDLINE=2038982; PubMed=10930381;
Teich N., Ockenga J., Hoffmeister A., Manns M., Mossner J., Keim V.,
"Chronic pancreatitis associated with an activation peptide mutation
that faciliteste trypsin activation.";
Gastroenterology 119:461-465(2000)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND PHOSPHORYLATION.
MEDLINE=96566496; PubMed=8683601;
Gaboriaud C., Serre L., Guy-Crotte O., Porest E.,
Fontecilla-Camps J.-C.;
"Crystal structure of human trypsin 1: unexpected phosphorylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (9)
VARIANTS HPC VAL-16 AND HIS-122.
WEDLINE-99315544; PubMed=10381903;
Witt H., Luck W., Becker M.;
"A signal peptide cleavage site mutation in the cationic trypsinogen gene is strongly associated with chronic pancreatitis.";
Gastroenterology 117:7-10(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98295575; PubMed=9633818;
Taich N., Mossner J., Keim V.;
"Mutations of the cationic trypsinogen in hereditary pancreatitis.";
Hum. Mutat. 12:39-43(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WARIANTS HPC ILE-29 AND HIS-122.
MEDLINE-974-63797; PubMed-3322494 W., Gates L.K. Jr., Preston R.A., Gorry M.C., Gabbaizedeh D., Furey W., Gates L.K. Jr., Preston R.A., Aston C.E., Zhang Y., Ulrich C., Ehrlich G.D., Whitcomb D.C., "Muteations in the cationic trypsinogen gene are associated with recurrent acute and chronic pancrealtis."; gastroenterology 113:1063-1068(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 68-151 FROM N.A., AND VARIANT HPC HIS-122.
MEDLINE-96438841; PubMed=8841182;
Whitcomb D.C., Gorry M.C., Preston R.A., Furey W., Sossenheimer M.J Urich C.D., Martin S.P., Gates L.K. Jr., Amann S.T., Toskes P.P., Liddle R., McGrath K., Uomo G., Post J.C., Ehrlich G.D.;
"Hereditary pancreatitis is caused by a mutation in the cationic trypsinogen gene."
Nat. Genet. 14:141-145(1996).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                          "Cloning, characterization and nucleotide sequences of two cDNAs encoding human pancreatic trypsinogens."; Gene 41:305-310 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90091010; PubMed-2598466; Kimland M., Russick C., Marks W.H., Borgstroem A.; "Immunoreactive anionic and cationic trypsin in human serum."; Clin. Chim. Acta 184:31-46(1989).
                                                                                                                                                                                                    MEDLINE-86221712; PubMed=3011602; Mishide T., Mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Teich N., Bauer N., Mossner J., Keim V., Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99219545; PubMed=10204851;
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[7]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REQUIRED FOR SPECIFICITY (BY SIMILARITY).
A -> V (IN HPC; DISRUPTS SIGNAL SEQUENCE
CLEAVAGE SITE).
                                                                                                                                                                                                                       DISEASE: Defects in PRSS1 are a cause of hereditary pancreatitis, (HPC or HP); also known as chronic pancreatitis (CP). HPC is an autosomal dominant disease characterized by the presence of
Dupont C., Munnich A., Bignon J.D., Le Bodic L.; Mutations in the cationic trypsinogen gene and evidence for genetic heterogeneity in hereditary pancreatitis."; J. Med. Genet. 36:228-232(1999).
                                                                     Zymogen; Signal;
Disease mutation.
                                                                                                                                                                                                                                                                 calculi in pancreatic ducts. It causes severe abdominal pain
                                                                                                                                                                    -i- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-
-i- SUBCELLULAR LOCATION: Extracellular.
-i- MASS SPECTROMETRY: MW=24348; MW_ERR=2; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTIG=-VAR 011693.
D -> G (IN HPC; INCREASED RATE OF ACTIVATION).
/FTIG=VAR_011652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R InterPro; IPR001314; Chymotrypsin.
R InterPro; IPR001354; Ser_protease_Try.
Refam; PF00089; trypsin; I.
REART; SM0022; CHYMOTRYESIN.
SMART; SM0020; Tryps SPC; I.
RP03ITE; PS00134; TRYPSIN DOM; I.
RP03ITE; PS00134; TRYPSIN DOM; I.
RP03ITE; PS0135; TRYPSIN SER; I.
Hydrolase; Serine protease; Digestion; Pancreas; Zym Multigene family; Phosphorylation; 3D-structure; Dis
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CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
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EMBL; V70137; AAC50728.1;
EMBL; AF314534; AAG30943.1;
EMBL; AF315309; AAG30947.1;
EMBL; AF315310; AG30948.1;
EMBL; AF315310; AAG30948.1;
EMBL; AF315311; AAG30948.1;
PIR; AZ5852; AZ5852.
PDB; 1TRN; 03-JUN-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; S01.151; -.
Genew; HGNC:9475; PRSS1.
MIM; 276000; -.
MIM; 167800; -.
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                                                                                                                                                                                          FIGAVAR 012713.

R -> H (IN HPC; SUPPRESSES AN AUTOCLEAVAGE SITE WHICH IS PROBABLY PART AUTOCLEAVAGE SITE WHICH IS PROBABLY PART TRYPSIN, WHICH IS ACTIVATED WITHIN THE PANCREAS, MAY BE INACTIVATED; LOSS OF THIS CLEAVAGE SITE WOULD PERMIT AUTOCLESSION RESULTING IN PANCREATITIS).

FILIA-VAR. 006721.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITE 90091011; PubMed=2598466; Kimland M., Russick C., Marks W.H., Borgstroem A.; Kimland M., Russick C., Marks W.H., Borgstroem A.; "Immunoreactive anionic and cationic trypsin in human serum."; Clin. Chim. Acta 184:31-46(1989).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning, characterization and nucleotide sequences of two cDNAs encoding human pancreatic trypsinogens.";
Gene 41:305-310(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86221712; PubMed-3011602;
Emi M., Nakamura Y., Ogawa M., Yamamoto T., Nishide T., Mori T.,
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
    Q.
K -> R (IN HPC; INCREASED RATE ACTIVATION).
                                                                                                                                                                                                                                                                                                                                                                                       Score 64; DB 1; Length 247;
Pred. No. 0.00011;
2; Mismatches 5; Indels
                                                                                                                                                     /FTId=VAR 011655. 
 R -> C (\overline{\rm IN} HPC; SUPPRESSES AN AUTOCLEAVAGE SITE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsin II precursor (EC 3.4.21.4) (Anionic trypsinogen).
PRSS2 OR TRY2 OR TRYP2.
                                                                                                                                                                                                                                                                                                                                                 FTId=VAR_011656,
DD49A487B8062813 CRC64;
                                                                                L -> P (IN HPC).
/FTId=VAR 011/-
                                                             1=VAR 006720
T (IN HPC).
                                                                                                                         1=VAR 011654
C (IN HPC).
                                   /FIId=VAR 011653 I -> I (IN HPC).
                                                                                                                                                                                                                                                                                                                          C -> F (IN HPC)
/FIId=VAR 01165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 AA
                                                                                                                                            R -> C (IN
/FTId=VAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                247 AA; 26558 MW;
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65.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 65.0 Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                         116
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Best Local Similarity
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P07478;
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Best Local Similarity 85.0
Matches 17; Conservative
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Best Local Similarity 85.03
Matches 17; Conservative
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383.393 Million cell updates/sec
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                                                   February 12, 2003, 10:17:50; Search time 5.01493 Seconds
    GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                           283224 seqs, 96134422 residues
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Maximum Match 100%
Listing first 45 summaries
                                  OM protein - protein search, using sw model
                                                                                                  1 IVGGYXCXXHSQAHQVSLNS 20
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S33496
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trypain (EC 3.4.21.4) II precursor - Atlantic salmon (fragment)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: S66658; S31778
R;Malle, R; Lorens, J.B.; Smalas, A.O.; Torrissen, K.R.
Birt, J. Biochem. 232, 677-685, 1995
A;Title: Molecular cloning and characterization of anionic and cationic variants of tryps
A;Reference number: S66657; MUID: 96035908; PMID: 7556223
                                                                                                                                           A,Accession: S6666.
A,Status: translation not shown
A,Rocession: S6666.
A,Status: translation not shown
A,Rolecule type: mRNA
A,Residues: 28-32,'A', 34-242 <MA2>
A,Cross-references: EMBL:X70072; NID:g64383; PIDN:CAA49677.1; PID:g64384
A,Residues: 28-32,'A', 34-242 <MA2>
A,Cross-references: EMBL:X70072; NID:g64383; PIDN:CAA49677.1; PID:g64384
A,Residues: 28-32,'A', 34-242 <mailelic variant
C,Superfamily: trypsin i trypsin homology
C,Reywords: hydrolase; serine proteinase
F;1-15/Domain: scrivation perfeited predicted <SIG>
F;21-247/Product: trypsin I #status predicted <APT>
F;21-247/Product: trypsin I #status predicted <MAT>
F;21-247/Product: trypsin I #status predicted <APT>
F;21-245/Apomain: trypsin I #status predicted <APT>
F;21-245/Apomain: trypsin I #status predicted <APT>
F;21-245/Apomain: trypsin I #status predicted <APT>
F;21-156,45-61,129-229,136-229,136-229,167-181,92-216/Disulfide bonds: #status predicted F;60,104,196/Active site: His, Asp, Ser #status predicted
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A/Molecule type: mRNA
A/Residues: 1-21 - WAL>
A/Residues: 1-21 - WAL>
A/COMBILIANS
A/COMBILIANS
A/COMBILIANS
A/COMBILIANS
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A/COMBILIANS
A/COMBILIANS
A/COMBILIANS
C/SUPERTAINS
C/SUPER
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A;Residues: 1-242 <MAL>
A;Cross-references: EMBL;X70075; NID:g64379; PIDN:CAA49680.1; PID:g64380
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83.2%; Score 79; DB 2; Length 231;
Best Local Similarity 75.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.2%; Score 80; DB 2; Length 242; 75.0%; Pred. No. 8.3e-07; Live 1; Mismatches 4; Indels
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                                                                                                           A; Experimental source: pancreas
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Best Local Similarity 75.0%
Matches 15; Conservative
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S31778
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C;Species: Salmo salar (Atlantic salmon)
C;Date: O3-Mar-1994 #sequence ravision 03-Nug-1995 #text_change 15-Oct-1999
C;Accession: S66660; S66661; S31777
R;Male, R.; Lorens, J.B.; Smalas, A.O.; Torrissen, K.R.
R;Male, R.; Lorens, J.B.; Smalas, A.O.; Torrissen, K.R.
A;Title: Molecular cloning and characterization of anionic and cationic variants of tryp
A;Reference number: S66657; MUID:96035908; PMID:7556223
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C; Species: Salmo salar (Atlantic salmon)
C; Date: 0.3-Mar-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C; Accession: 866659; 831776
R; Male, R.; Lorens, J.B.; Smalas, A.O.; Torrissen, K.R.
R; Male, R.; Lorens, 232, 677-685, 1995
A; Title: Molecular cloning and characterization of anionic and cationic variants of tryp. A; Reference number: 866657; MUID:96035908; PMID:7556223
                                                                                                           trypsin (EC 3.4.21.4) X - Atlantic cod Crypsin (EC 3.4.21.4) X - Atlantic cod Cypate: 20-May-1994 #sequence_revision 03-Aug-1995 #text_change 20-Jun-2000 Cypate: 20-May-1994 #sequence_revision 03-Aug-1995 #text_change 20-Jun-2000 CyAccession: 639048 RyGudmundsdottir, A.; Gudmundsdottir, MulD:94039130; PMID:8223632 A; Gudmundsr, S39048 A; A; Gudmundsdottir, A
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A/Molecule type: MRNA
A/Residues: 1-242 - MALA
A/Residues: EMBL:X70071; NID:g64381; PIDN:CAA49676.1; PID:g64382
C/Superfamily: trypsin; trypsin; homology
C/Reywords: hydrolase; serine proteinase
F/1-15/Domain: signal sequence #status predicted <APT>
F/1-15/Domain: activation peptide #status predicted <APT>
F/1-242/Product: trypsin | A/M #status predicted <APT>
F/1-235/Domain: trypsin homology <ARX-
F/1-135/ACH-11/129-229/136-202/167-181/122-216/Disulfide bonds: #status predicted
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94.7%; Score 90; DB 2; Length 241;
Best Local Similarity 85.0%; Pred. No. 1.3e-08;
Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Superfamily: trypsin; trypsin homology
K.Rywords: hydrollase; serine proteinase
F;20-234/Domain: trypsin homology <ffry>
F;59,103,195/Active site: His, Asp, Ser #status predicted
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hes 16; Conservative
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C.Species: Ratius norvegicus (Norway rat)
C.Species: 1-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
C.Accession: JOH27
C.Accession: JOH27
A.File: Identification of CDNAs encoding two novel rat pancreatic serine proteases.
A.Fecrence number: JOH471; MUID:92165057; PMID:1537555
A.Accession: JOH27
A.Focossion: JOH27
A.Molecule type: mRNA
A.Residues: 1-246 «KAN»
A.Fecsidues: 1-246 «KAN»
A.Fesidues: 1-24/Domain: accivation peptide #status predicted «ACT»
F.J5-246/Product: trypsin homology «TRY»
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R;Kang, J.; Wiegand, U.; Mueller-Hill, B.
A;Tele: 10, 181-187, 1992
A;Tele: Identification of cDNAs encoding two novel rat pancreatic serine proteases. A;Reference number: JQ1471, MUD:92165057; PMID:1537555
A;Accession: JQ1471
A;Molecule type: mRNA
A;Residues: 1-246 «KAN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trypsin (BC 3.4.21.4) V precursor, a-form - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.6%; Score 69; DB 2; Length 242; 70.0%; Pred. No. 8e-05; Live 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.6%; Score 69; DB 2; Length 246;
65.0%; Pred. No. 8.2e-05;
tive 2; Mismatches 5; Indels
trypsin (EC 3.4.21.4) precursor - Paranotothenia magellanica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trypsin (BC 3.4.21.4) V precursor, b-form - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IVGGYXCXXHSQAHQVSLNS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 IVGGKECSPYSQPHQVSLNS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IVGGYXCXXHSQAHQVSLNS 20
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Les 13; Conserv
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Best Local S:
Matches 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
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                                        A)Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
A;Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17
A;Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17
A;Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17
J. Biol. Chem. 257, 974-9712, 1987
A;Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of A;Reference number: A00948; MUID:82265624; PMID:6896710
                                                                                                                                                                                                                                                        A,Accession: A00948
A,Molecule type: mRNA
A,Residues: 1-246 c/MSA
A,Introns: 14/1; 67/2; 152/1; 197/3
A,Introns: 14/1; 67/2; 152/1; 197/3
A,Introns: 14/1; 67/2; 152/1; 197/3
C,Superiamily: trypsin, pencices #status predicted c/SIO
F;1-15/Domain: signal sequence #status predicted c/SIO
F;16-23/Domain: signal sequence #status predicted c/SIO
F;24-219/Domain: trypsin nompology c/RY
F;30-160,48-64.132-233,139-206,177-185/Disulfide bonds: #status predicted
F;51,107,200/Active site: His, Asp, Ser #status predicted
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Date: 23-Aug-1995 #sequence revision 19-Oct-1995 #text_change 22-Jun-1999
C.Bate: 23-Aug-1995 #sequence revision 19-Oct-1995 #text_change 22-Jun-1999
R.Warg, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995
Biochem. J. 307, 471-479, 1995
A.Reference number: S55065; MUD:95251611; PMID:7733885
A.Recession: S55066.
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A.Residues: 1-248 -WANI>
A.Residues: 1-248 -WANI>
A.Residues: 1-248 -WANI>
A.Cross-references: EMBL:U15157; NID:g603906; PIDN:AAA79914.1; PID:g603907
A.Experimental source: clone 2-P29
C.Superfamily: trypsin, trypsin, proclaid digestion, serine proteinase, zymogen
F.1-16/Domain: signal sequence Hstatus predicted <SIG>
F.1-16/Domain: signal sequence Hstatus predicted <APT>
F.26-24B/Product: trypsin II Hstatus predicted <APT>
F.26-24B/Product: trypsin II Hstatus predicted <ART>
F.26-24B/Domain: trypsin iI Hstatus predicted
F.56-202/Active site: His, Asp, Ser Hstatus predicted
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A; Residues: 1-248 <MAN1>
A; Cross-references: EMBL:U15157; NID:g603906; PIDN:AAA79914.1; PID:g603907
A; Experimental source: clone 2-P29
A; Accession: S72347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.7%; Score 71; DB 1; Length 246; 70.0%; Pred. No. 3.6e-05; tive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 248;
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Best Local Similarity 70.01
Matches 14, Conservative
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Best Local Similarity 70.0°
Matches 14; Conservative
                1-246 <CRA>
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A;Accession: A00949
A;Molecule type: mENA
A;Residues: 9-246 <MAC>
C;Comment: The trypsin II mRNA is present in much lower quantities than the trypsin I mRN
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ajaccession: A22657
Ajaccession: DNA
Ajacsolues: 1-246 <CRA>
Rjacobonald, R.J.; Stary, S.J.; Swift, G.H.
Rjacobonald, R.J.; Stary, S.J.; Swift, G.H.
Ajacobonald, Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of
Ajatle: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of
Ajacerence number: A00948; MUID:82265624; PMID:6896710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trypein (EC 3.4.21.4) II precursor - rat
NyAlternate names: trypeinogen II
NyAlternate names: trypeinogen II
Syspecies Rattus norvegicus (Norway rat)
C;Date: 05-Apr-1983 #sequence_revision 30-Sep-1987 #text_change 18-Jul-1997
C;Accession: A22657; A00949
E;Craik, C.S.; Choo, O.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984
A;Title: Structure of two related rat pancreatic trypein genes.
A;Reference number: A22657; MUID:85054880; PMID:6094547
                                            A; Residues: 1-246 <PIN>
A; Residues: 1-246 <PIN>
A; Cross-references: GBI-MI1590; NID: g164096; PIDN:AAA30900.1; PID: g164097
C; Superfamily: trypsin; trypsin; homology
C; Superfamily: trypsin; trypsin; protein digestion; serine proteinase; zymogen
C; Seywords: hydrolase, pancreas; protein digestion; serine proteinase; zymogen
F; 1-15/Domain: activation peptide #status predicted <APT>
F; 24-246/Product: trypsin, cationic #status predicted <APT>
F; 24-236/Domain: trypsin, cationic #status predicted <ARZ>
F; 24-236/Domain: trypsin, homology <TRY>
F; 20-160, 48-64, 132-233, 139-206, 171-185/Disulfide bonds: #status predicted
F; 53, 107, 200/Active site: His, Asp, Ser #status predicted
F; 75, 77, 80, 85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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CjSuperfamily: trypsin homology
CjSuperfamily: trypsin, trypsin homology
CjSuperfamily: trypsin, trypsin homology
CjSuperfamily: trypsin, trypsin petited algorithm serine proteinase; zymogen
Fj16-23/Domain: signal sequence #status predicted algorithm activation peptide #status predicted and and and activation peptide #status predicted and and arguering register algorithm activation peptide #status predicted and and arguering arguering predicted and and arguering arguering arguering arguering arguering arguering predicted Fj31,00/Active site: His, Asp, Ser #status predicted Fj53,107,200/Active site: His, Asp, Ser #status predicted Fj53,107,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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C;Species: Homo sapiens (man)
C;Decesion: Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
C;Accesion: S12764
R;Tani, T.; Kawashima, I.; Mita, K.; Takiguchi, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.4%; Score 65; DB 1; Length 246; ilarity 65.0%; Pred. No. 0.00043; Conservative 2; Mismatches 5; Indels
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69.5%; Score 66; DB 1; Length 246;
Best Local Similarity 65.0%; Pred. No. 0.00028;
Matches 13; Conservative 2; Mismatches 5; Indels
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nes 13; Conserv
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Matches
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N;Contains: trypsinogen
N;Contains: trypsinogen
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Caccession: Apre-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Caccession: Biophys. Acta 69; 115-129, 1963
A;Title: Sulle tryps: protein
A;Reference number: A90641
A;Molecule type: protein
A;Reference number: A90368, MUID: 73256692; PMID: 4738933
A;Title: Determination of the amino acid sequence of porcine trypsin by sequenator analy
A;Reference number: A90368, MUID: 73256692; PMID: 4738933
A;Accession: A90368
A;Molecule type: protein
A;Residues: 2-231 c-4ER.
A;Molecule type: protein
A;Residues: C;Typsin percled #status experimental c-2YM.
C;Superfamily: trypsin homology cTRY.
F;1-271/Froduct: trypsin peptide #status experimental c-2YM.
F;1-271/Froduct: trypsin peptide #status sexperimental c-2YM.
F;1-271/Froduct: trypsin homology cTRY.
F;2-24/Domain: trypsin homology cTRY.
F;2-124/Domain: trypsin homology cTRY.
F;2-126,00,62,65,70/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
F;60,62,65,70/Binding site: calcium (Glu, Asn, Val, Glu)
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C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C;Accession: B26273
R;Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 266-2676, 1985
MyTitle: Differential regulation of trypsinogen mRNA translation: full-length mRNA seque
A;Reference number: A26273; MUD:86284628; PMID:3841794
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A,Cross-references: EMBL:X59012; NID:g57412; PIDN:CAA41751.1; PID:g57413 A;Experimental source: pancreas C;Superfamily: trypsin, trypsin homology C;Superfamily: trypsin, trypsin homology C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen F;16-24/Domain: aignal sequence #status predicted <ACT> F;15-34/Domain: activation peptide #status predicted <ACT> F;25-34/Product: trypsin V, a-form #status predicted <AMT> F;25-23/Domain: trypsin homology TRXP. F;31-160,49-65,133-233,140-206,171-185/Disulfide bonds: #status predicted F;64,108,200/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Title: Nucleotide sequence of the human pancreatic trypsinogen III cDNA.
A;Reference number: S12764; MUD:90221895; PMID:2326201
A;Recession: S12764
A;Mccession: S12764
A;Mccession: S12764
A;Mclecule type: mRNA
A;Residues: 1-27 < rpn.>
A;Cross-references: EMBL:X15505; NID:g37459; PIDN:CAA33527.1; PID:g37460
C;Genetics: GDB:335297
A;Map position: 7g35-7g35
C;Superfamily: trypsin homology
C;Reywords: calcium binding; hydrolase; pancreas; protein digestion; serine proteinase; C;Reywords: calcium binding; hydrolase; predicted <BTS
C;Reywords: calcium binding; hydrolase; predicted <APT>
F;1-15/Domain: activation peptide #steatus predicted <APT>
F;2-247/Product: trypsin III #steatus predicted <APT>
F;2-247/Product: trypsin lomology <RRY>
F;2-247/Product: trypsin homology <RRY>
F;2-247/Product: trypsin homology <RRY>
F;30-160,48-64,139-206,171-185/Disulfide bonds: #steatus predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;63,107,200/Active site: His, Asp, Val, Glu) #status predicted
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trypsin (EC 3.4.21
                                                                                                                 February 12, 2003, 10:17:50; Search time 5.01493 Seconds (without alignments) 383.393 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                          283224 seqs, 96134422 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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S31779
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A61331
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Maximum DB seq length: 2000000000
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107
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1: pir1:*
2: pir2:*
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Perfect score:
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~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	RESULT 1 TRBOTR () CONTAINS: () Species: E C, Species: E C, Accession R, Mikes, O., A Title: Bichen A, Roleoule to A, Reference A, Residues: R, Hartley, R, Hartley, R, Hartley, R, A, Content Rs; B, Content Rs; B, Content Rs; A, Content Rs; A, A, A, Title: AM, A, Reference	A,Note: 7. Mol. A,Title A,Title A,Conter C,Commer C,Comme
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Query Match 100.0%; Score 107; DB 1; Length 229; Best Local Similarity 100.0%; Pred. No. 6.4e-09; Matches 20; Conservative 0; Mismatches 0; Indels (

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CjAccession: 813813
R;le Huerou, I.; Micker, C.; Guilloteau, P.; Toullec, R.; Puigserver, A.
Ex. J. Blochem. 193, 767-773, 1990
A;fitle: Isolation and nucleotide sequence of cDNA clone for bovine pancreatic anionic to A;Reference number: 813813; MUID:91065383; PMID:1701147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trypaln (EC 3.4.21.4) II precursor - rat
NAlternate names: trypsinogen II
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A22657; A00949
R;Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. (Chem. 259, 14255-14264, 1984
A;Title: Structure of two related rat pancreatic trypsin genes.
A;Reference number: A22657; MUID:85054880; PMID:6094547
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CjSuperfamily: trypsin; trypsin homology
CjSuperfamily: trypsin; trypsin homology
CjSuperfamily: trypsin; trypsin proficed cSIG>
Fj16-23/Domain: signal sequence #status predicted cAPT>
Fj16-23/Domain: activation peptide #status predicted cAPT>
Fj24-23/Domain: trypsin II #status predicted cENZ>
Fj24-23/Domain: trypsin II #status predicted cENZ>
Fj30-160, 40-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
Fj31,177,200/Active site: His, Asp, Ser #status predicted
Fj35,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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C;Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
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K;Keywords: hydrolase; protein digestion; serine proteinase
F;24-239/Domain: trypsin homology <TRY>
F;63,107,200/Active site: His, Asp, Ser #status predicted
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A;Molecule type: mRNA
A;Residues: 1-247 <HUE>
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NyAlternate names: cationic trypsingen
C;Species: Canis lupus familiaris (dog)
C;Date: 30-20-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C;Date: 30-20-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C;Accession: B26273
R;Pinsky, S.D.; LaForge, K.S.; Scheele, G.
MOI Cell. B101. 5, 2669-2676, 1985
MATICLe: Differential regulation of trypsinogen mRNA translation: full-length mRNA seque
A;Reference number: A26273; MUID:86284628; PMID:3841794
A;Reference number: A26273; MUID:86284628; PMID:3841794
A;Residues: 1-246 *PINA
A;Residues: 1-246 *PINA
A;Residues: 1-246 *PINA
A;Residues: 1-246 *PINA
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;16-23/Domain: aignal sequence #status predicted *APINA
F;24-236/Domain: activation peptide #status predicted *APINA
F;24-239/Domain: activation peptide #status predicted *APINA
F;24-239/Domain: cationic #status predicted *APINA
F;30-160,48-64,132-233;139-206,171-185/Disulfide bonds: #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A90641
A;Molecule type: protein
B;Residues: 1-10 cCHA>
B;Residues: 1-10 cCHA>
B;Residues: 1-10 beta-mination of the amino acid sequence of porcine trypsin by sequenator analy
A;Reference number: A90368; MUID:73258692; PMID:4738933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Molecule type: protein
A, Residues: 9-21 cHER>
A, Residues: 9-21 cHER>
C, Superfamily: trypsin; trypsin homology
C, Superfamily: trypsin; trypsin homology
C, Keywords: hydrolase; pancreas; polymorphism; protein digestion; serine proteinase; zym
C, Keywords: hydrolase; pancreas; polymorphism; protein digestion; serine proteinase; zym
F, 1-231/Product: trypsinogen #status experimental cARP>
F, 9-231/Product: trypsin #status experimental cARP>
F, 9-234/Domain: activation peptide #status experimental cARP>
F, 9-234/Domain: trypsin homology cARP>
F, 9-244/Domain: trypsin homology cARP>
F, 9-244/Domain: trypsin homology cARP>
F, 9-244/Domain: trypsin homology cARP>
F, 9-245/Domain: trypsin homology cARP>
F, 9-245/Domain: trypsin homology cARP>
F, 9-245/Domain: trypsin homology cARP>
F, 9-25/Domain: trypsin homology cARP>
F, 9-25
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                                                Nicontains: trypainogen
Cispecies: Sus acrofa domestica (domestic pig)
Cispecies: Sus acrofa domestica (domestic pig)
Cipaces: 24-Apr-1984 #sequestica (acrofa consistence at the consistence acrofa domestica acrofa domestica acrofa ac
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Best Local Similarity 85.0%; Pred. No. 1.4e-06;
Matches 17; Conservative 1; Mismatches 2; Indels
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85.0%; Pred. No. 3.1e-07;
tive 2; Mismatches 1; Indels
trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)
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hes 17; Conservative
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A;Residues: 1-246 <CRA>
A;Residues: 1-246 <CRA>
A;Cross-references: 08:100778; NID:9206507; PIDN:AAA98518.1; PID:9206508
A;Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17(
R;MacDonald, R.J.; Stary, S.J.; Swift, G.H.
J. Bill. Chem. 257, 9724-9737, 1982
J. Bill. Chem. 257, 9724-9737, 1982
J. Bill. Chem. 257, 9724-9737, 1982
A;Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of A;Reference number: A00948; MUID:92265624; PMID:6896710
                                                                                                                                   C;Accession: 533496
Swithsgand, U.; Corbach, S.; Minn, A.; Kang, J.; Mueller-Hill, B.
Submitted to the EMBL Data Library, March 1993
A;Description: Identification, cloning and characterization of a cDNA encoding a human b
A;Reference number: S33496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nyblernate names: trypsinogen I
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 24-Sep-1999
C;Accession: B22657; A00948
B;Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984
A;Telte: Structure of two related rat pancreatic trypsin genes.
A;Reference number: A22657; MUID:85054880; PMID:6094547
A;Accession: B22657
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C; Superfamily: trypsin, trypsin, homology
C; Superfamily: trypsin, trypsin, protein digestion; serine proteinase; zymogen
C; Superfamily: trypsin, pancreas; protein digestion; serine proteinase; zymogen
F; 1-15/Domain: signal sequence #status predicted <SIG>
F; 1-25/Domain: scrivation peptide #status predicted <APT>
F; 24-246/Product: trypsin I #status predicted <ENZ>
F; 24-239/Domain: trypsin homology <TRY>
F; 24-239/Domain: trypsin homology <TRY>
F; 24-239/Domain: trypsin homology <TRY>
F; 26, 200/Active site: His, Asp, Ser #status predicted
F; 37-77, 80, 85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
trypsin (EC 3.4.21.4) IV form a - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Aug-1995 #text_change 15-Aug-1997
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A; Residues: 1.246 <MAC>
A; Cross-lues: 0.246 <MAC>
Cross-lues: 0.246 <MAC>
C; Genetics: 0.206508
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Pred. No. 9.7e-06;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: GDB:335300
A,Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolass: serine proteinase
P;81-296/Domain: trypsin homology <TRY>
F;81-296/Domain: trypsin homology <TRY>
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80.0%;
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-304 <WIE>
A,Cross-references: EMBL:X72781
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Best Local Similarity
Matches 16; Conserva
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Best Local S
Matches 16
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A;Map position: 7435-7455
C;Superfamily: trypsin; trypsin; trypsin homology
C;Superfamily: trypsin; trypsin
                                                                                                                                                                                                                                                                       C,Accession: A26273
R;Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
A;Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA seque A;Title: Difference number: A26273; MUID:86284628; PMID:3841794
A;Accession: A26273
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A; Residues: 1-247 & PID.
A; Residues: 1-247 & PID.
C; Superfamily: trypsin; trypsin; bomology
C; Superfamily: trypsin; trypsin; bomology
C; Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
C; Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
C; Keywords: hydrolase; pancreas; protein disease predicted (ADT)
F; 1-15, Domain: activation peptide #status predicted (ANT)
F; 1-27) Domain: activation peptide #status predicted (ANZ)
F; 1-17, Product: trypsin, anionic #status predicted (ANZ)
                                                                                                                                                  N.Alternate names: carionic trypsinogen
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
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F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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R;Tani, T.; Kawashima, I.; Mita, K.; Takiguchi, Y.
Nucleic Acids Res. 19, 1631, 1990
A;Title: Nucleotide sequence of the human pancreatic trypsinogen III cDNA.
A;Reference number: $12764; MUID:90221895; PMID:2326201
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F;24-239/Domain: trypsin homology <TRY>
F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
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A;Residues: 1-247 <TAN>
A;Cross-references: EMBL:X15505; NID:g37459; PIDN:CAA33527.1; PID:g37460
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80.0%; Pred. No. 7.9e-06;
tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 247;
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Pred. No. 7.9e-06;
2; Mismatches 2; Indels
                                                                                                      trypsin (EC 3.4.21.4) precursor, anionic - dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trypsin (EC 3.4.21.4) III precursor - human C;Species: Homo sapiene 'mrm'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.3%; Scc.
80.0%; Pred
2; h
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S12764
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Riples, W.; Zwilling, R.; Woodbury, R.G.; Neurath, H.
FEBS Lett. 109, 45-49, 1980
A;Title: Amino-terminal amino acid sequences and the evolution of frog (Rana esculenta) t
A;Reference number: A61333; MUID:80113255; PMID:6965480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liypsin (EC 3.4.21.4) II precursor [validated] - human NyAlternate names: trypsin 2; trypsin, anionic; trypsinogen II C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 03.Mar-1994 #sequence revision 03.Mar-1994 #text_change 08-Dec-2000 C;Accession: B25852; A61066; B43988 R;Emi, M; Nakamura, Y; Ogawa, M; Yamamoto, T; Nishide, T; Mori, T; Matsubara, K. A;Title: Cloning, characterization and nucleotide sequences of two cDNAs encoding human particle: Cloning, characterization and nucleotide sequences of two cDNAs encoding human particles number: A;Reference number: Ap1544; MUID:86221712; PMID:3011602
                                                                                                                                                                                                                                                                                                  A Experimental source: clone 2-P29

(Superfamily: trypsin, trypsin homology
C; Superfamily: trypsin, trypsin homology
C; Keywords: hydrolase, pancrass; proteins predicted <81G>
F; 1-16/Domain: signal sequence #status predicted <81G>
F; 2-25/Domain: activation peptide #status predicted <APT>
F; 2-248/Product: trypsin I mattus predicted <APT>
F; 6-241/Domain: trypsin Informatory TRY>
F; 6-31/Domain: trypsin homology TRY>
F; 6-31/Domain: trypsin homology TRY>
F; 6-31/Domain: trypsin homology Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trypsin (EC 3.4.21.4) - edible frog (fragment)
C;Species: Rana esculenta (edible frog)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C;Accession: A61333
                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-248 <WAN2>
A;Cross-references: EMBL:UI5157; NID:g603906; PIDN:AAA79914.1; PID:g603907
                                                    Cross-references: EMBL:U15157; NID:g603906; PIDN:AAA79914.1; PID:g603907; Experimental gource: clone 2-P29
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A.Residues: 1-247 <EMI>
A.Residues: 1-247 <EMI>
A.Cross-references: GB.M27602; NID:g521217; PIDN:AAA61232.1; PID:g521218
R.Kimland, M.; Ruesick, C.; Marks, W.H.; Borgstroem, A.
G.In. Chim. Acta 184, 31-46, 1989
A.Title: Immunocactive anionic and cationic trypsin in human serum.
A.Reference number: A61066; MUID:90091010; PMID:2598466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.4%; Score 85; DB 2; Length 248; 80.0%; Pred. No. 1.6e-05; 1.ve 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 1-30 <PIE>
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 78.5%; Score 84; DB 2;
Best Local Similarity 75.0%; Pred. No. 3e-06;
Matches 15; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 16-39, 'X',41-42, 'XXXX',47-49 <KIM>
R;Koivunen, E.; Huhtala, M.L.; Stenman, U.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 IVGGYTCPEHSVPYQVSLNS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IVGGYTCGANTVPYQVSLNS 20
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Matches 16; Conservative
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                     A;Residues: 1-248 <WAN1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: B25852
                                                                                                         A; Experimental
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                                                                                                                                                                                                                                                                   trypein (EC 3.4.21.4) I precursor [validated] - human
NiAlternate names: trypsin, cationic; trypsinogen I
C;Species: Home sapiens (man)
C;Date: O3-Mar-1994 #sequence tevision 03-Mar-1994 #text_change 08-Dec-2000
C;Accession: A25852; B61066; A43988
R;EMI, M.; Nakamura, Y.; Ogawa, M.; Yamamoto, T.; Nishide, T.; Mori, T.; Matsubara, K.
Gene 41, 305-310, 1986
A;Title: Cloning, characterization and nucleotide sequences of two cDNAs encoding human
A;Recence number: A91544; MUID:86221712; PMID:3011602
A;Recession: A25852
A;Molecule type: mRNA
A;References: GB:M25612; NID:8521712; PMID:3011602
A;Recession: A25852
A;Molecule type: mRNA
A;References: GB:M25612; NID:9521215; PIDN:AA61231.1; PID:9521216
Cin: Chim. Acta 184, 31-46, 1989
A;Title: Imunoreactive anionic and cationic trypsin in human serum.
A;Reference number: A61066; MUID:90091010; PMID:2598466
A;Molecule type: procein
A;Residues: 16-43 ackIM>
A;Residues: 1
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A,Cross-references: GDB:119620; OMIM:276000
A;Map position: 7q35-7q35
A;Note: The human genome contains at least ten trypsin genes or pseudogenes, at least the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; phosphoprotein; protein digestion; serine proteinase;
C;T-15,Domain: signal sequence #status predicted <SIG>
F;16-246/Product: trypsingen I #status experimental <APT>
F;16-23/Domain: activation peptide #status experimental <APT>
F;16-23/Domain: activation peptide #status experimental <APT>
F;12-236/Product: trypsin I #status predicted <ENZ>
F;24-239/Domain: trypsin I #status predicted <ENZ>
F;24-239/Domain: trypsin homology <TRY>
F;30-160,48-64,139-266,171-185,196-220/Disulfide bonds: #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
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$55066

Lrypain (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
NyAlternate names: trypsinogen II
C;Species: Gallus gallus (chicken)
C;Accession: S55066; $723.47

Biochem. J. 307, 471-479, 1995
Biochem. J. 307, 471-479, 1995
A;Reference number: $55065; MUID:95251611; PMID:7733885
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A, Molecule type: protein
A, Residues: 16-54 < KOI>
A, Experimental source: mucinous ovarian tumor cyst fluid
                                                                                       43
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1 IVGGYTCGANTVPYQVSLNS
                                                24 IVGGYTCPEHSVPYQVSLNS
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Matches 16, Conservative
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Length 246;

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A)Residues: 1.246 <STE>
A)Residues: 1.246 <STE>
A)Cross-references: GBN.04574; NID:954918; PIDN:CAA28243.1; PID:954919
A)Cross-references: GBN.04574; NID:954918; PIDN:CAA28243.1; PID:954919
C;Superfamily: trypsin, trypsin homology
C;Reywords: calcium binding; hydrolase; protein digestion; serine proteinase
F)1-23 Domain: signal sequence #sterus predicted <SGS-
F;24-246/Froduct: trypsin #sterus predicted <AMT>
F;24-236/Domain: trypsin #sterus predicted <AMT>
F;24-239/Domain: trypsin homology *TRY>
F;24-239/Domain: trypsin homology *TRY>
F;30-160,486-64,132-233,199-206,171-185/Disulfide bonds: #status predicted
F;63,107,200/Active site: Hs. Asp, Asp, Rest #status predicted
F;63,107,200/Active site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.6%; Score 82; DB 2; Length 246
75.0%; Pred. No. 4.6e-05;
tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          February 12, 2003, 10:28:47
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Best Local Similarity
Matches 15; Conserv
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Job time : 6.01493 secs
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                                                                                                                               A; Recession: B43988
A; Molecule type: protein
A; Residues: 16.49 exCl>
A; Repertantics:
A; Gene: GDB:RSS2; TRY2
A; Cross-references: GDB:335289; CMIM:601564
A; Map position: 7435-7482
A; Note: the human genome contains at least ten trypsin genes or pseudogenes, at least tw.
C; Superdamily: trypsin; trypsin; homology
C; Keywords: Hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F; 1-15/Domain: signal sequence #status predicted <SIG>
F; 16-23/Domain: activation peptide #status experimental <APT>
F; 24-23/Domain: activation peptide #status experimental <APT>
F; 24-23/Domain: trypsin II #status predicted <BCS>
F; 24-246/Product: trypsin II #status predicted <BCS>
F; 24-246/Product: trypsin in monology <TRY>
F; 24-23/Domain: trypsin in monology <TRY>
F; 24-23/Domain: trypsin in monology <TRY>
F; 24-23/Domain: trypsin in monology <TRY>
F; 24-246/Product: trypsin in #status predicted <BCS>
F; 24-246/Product: trypsin in monology <TRY>
F; 24-246/Product: trypsin in #status predicted <BCS>
F; 24-246/Product: trypsin in #status predicted <BCS>
F; 24-246/Product: trypsin in monology <TRY>
F; 24-246/Product: trypsin in #status predicted <BCS>
F; 24-246/Product: trypsin in #status predicted <BCS>
F; 24-246/Product: trypsin in #status predicted <BCS>
F; 24-246/Product: trypsin in monology <TRY>
F; 24-246/Produc
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C;Species: Mus musculus (house mouse)
C;Jate: 30-Uni-1988 #sequence_revision 30-Jun-1988 #text_change 22-Jun-1999
C;Accession: B2528
R;Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A;Title: Sequence organisation and transcriptional regulation of the mouse elastase II
A;Reference number: A93646; WUID:87066713; PMID:3641189
J. Biol. Chem. 264, 14095-14099, 1989
A,Title: Human ovarian tumor-associated trypsin. Its purification and characterization
A,Reference number: A43988, MUID:89340515, PMID:2503510
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R;Fletcher, T.S.; Alhadeff, M.; Craix, C.S.; Largman, C.
Biochemistry 26, 3081-3086, 1987
A,Title: Isolation and characterization of a cDNA encoding rat cationic trypsinogen. A;Reference number: A27547; MUID:87271609; PMID:3607011
A,Accession: A27547
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A; Residues: 1-247 <FEES
A; Cross references: GB:M16624; NID:g206498; PIDN:AAA41985.1; PID:g206499
A; Cross references: GB:M16624; NID:g206498; PIDN:AAA41985.1; PID:g206499
C; Superfamily: trypsin; trypsin homology
C; Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F;25-240/Domain: trypsin homology <TRY>
F;31-161,49-65,133-234,140-207,172-186/Disulfide bonds: #status predicted
F;64,108,201/Active site: His, Asp, Ser #status predicted
F;64,108,201/Active site: His, Asp, Ser #status predicted
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C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 22-Jun-1999
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos tautus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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"Homologies in serine proteinases.";
Philos. Trans. R. Soc. Lond., B, Biol. Sci. 257:77-87(1970).
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Okajima T., Maniwa M., Nagao S., Fujikawa H., Goto S.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=77112431; PubMed=556951;
Sossiakoff A.A., Chambers J.L., Kay L.M., Stroud R.M.;
"Structure of bovine trypsinogen at 1.9-A resolution.";
Biochemistry 16:654-664(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-75146445; PubMed=1092332;
Titani K., Ericsson L.H., Neurath H., Walsh K.A.;
"Amino acid sequence of dogfish trypsin.";
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SEQUENCE OF 15-243, AND DISULFIDE BONDS.
MEDLINE=67168848; Pubmed=5967094;
Mixes O., Holeysovsky V., Tomasek V., Sorm F.;
"Covalent structure of bovine trypsinogen. The I
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Biochem. Biophys. Res. Commun. 24:346-352(1966)
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsinogen, cationic precursor (EC 3.4.21.4)
(Fragment)
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                                                              KLK1_MOUSE
TRYE_DROBE
TRYE_DROME
KLK8_MOUSE
KLK9_MOUSE
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REVISIONS.
MEDLINE=72035053; PubMed=4399051;
TRYP
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R FINCETTO; IFFOOLSON; SEL PROCESSES, ITY.

R PROSITE; PROGOGO; Trypein; 1.

R PROSITE; PSOOL34; TRYPEIN_DOM; 1.

R PROSITE; PSOOL34; TRYPEIN_BER; 1.

R PROSITE; PSOOL35; TRYPSIN_BER; 1.

R PROSITE; PSOOL35; TRYPSIN_BER; 1.

R WHYDCOLAGE; Serine procease; Digestion; Pancreas; Zymogen; Signal; 3.

T SIGNAL <1 14 ACTIVATION PEPTIDE.

T SIGNAL <1 14 ACTIVATION PEPTIDE.

T CHAIN 21 243 ALPHA-TRYPSIN CHAIN 1.

T CHAIN 146 243 ALPHA-TRYPSIN CHAIN 2.

T CHAIN 12 23 SUBSTRATE.

T BINING 191 192 SUBSTRATE.
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PDB; 1TAW; 24-JUN-97.
PDB; 1AQ7; 25-FEB-98.
PDB; 1TIO; 23-SEP-98.
PDB; 2TIO; 30-SEP-98.
PDB; 1XUF; 16-DEC-98.
PDB; 1XUF; 16-DEC-98.
PDB; 1XUF; 11-NOV-98.
PDB; 1XUF; 11-NOV-98.
PDB; 1XUF; 11-NOV-98.
PDB; 1AUJ; 11-NOV-98.
PDB; 1AUJ; 11-NOV-98.
PDB; 1AUJ; 13-JAN-99.
PDB; 1BJV; 13-JAN-99.
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
T "The disulphide bridges of trypsin.";

J. Mol. Bidl. 12:929-932(1965).

- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa. 1-1 CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa. 1-1 SUBCELULIAR LOCATION: EXtracellular.

- I-SUBCELULIAR LOCATION: EXTRACELED IN THE ACINAR CELLS OF THE PANCERAS.

- PTM: AUTOCATALYTIC CLEAVAGE AFTER LYS-20 LEADS TO BETA-TRYPSIN BY RELEASING A TERMINAL HEXAPETIDE. SUBSEQUENT CLEAVAGE AFTER LYS-190

- PTM: AUTOCATALYTIC CLEAVAGE APTER LYS-20 CCUR AFTER LYS-190

- YIELDS PSEUDOTRYESIN. A CLEAVAGE MAY ALSO OCCUR AFTER ARG-119.

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

- HWW*-"http://www.worthington-biochem.com/manual/T/TRY.html".
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1TGB 14-MAR-85.

1TGC 00-APR-85.

1TGN 22-OCT-84.

2TGP 14-MAR-85.

1TGT 15-OCT-90.

2TLD 15-OCT-92.

2TLD 16-OCT-92.

2TLD 16-OCT-92.

2TLD 16-OCT-92.

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1TPA: 14-MAR-85.

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1URT;
1MAX;
1MAY;
1MTS;
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L Structure 5:1465-1474(1997).

C -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.

-!- SUBCELLUTAR LOCATION: Extracellular.

C -!- SIMILARIY: BELONGS TO PEPTIDASE FAMILY S1.

R PDB; HCT; 31-JAN-94.

R PDB; 1AKS; 12-FBS-97.

R PDB; 1EPT; 07-FBS-95.

R PDB; 1LDT; 20-MAY-98.

R PDB; 1LDT; 20-MAY-98.

R PDB; 1AN1; 01-JUL-98.

R PDB; 1AN1; 01-JUL-98.
                                                                                                                                                                                                                                                                                                                                                             REQUIRED FOR SPECIFICITY (BY SIMILARITY). I -> V.
                                                                                                                                           InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser protease_Try.
Pfam. PF001099; trypsin; 1
PR01059; trypsin; 1
PR01059; trypsin; 1
PR01072; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PR051TE; PS50240; TRYPSIN LIS.
PR051TE; PS00134; TRYPSIN LIS.; 1.
PR051TE; PS00135; TRYPSIN LIS.; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; 3D-structure. 1
PR05EP
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CHARGE RELAY SYSTEM.
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MEDLINE=92201369; PubMed=1551419;
Huang Q., Liu S., Tang Y., Zeng F., Qian R.;
Amino acid sequencing of a trypsin inhibitor by refined 1.6 A X-ray
crystal structure of its complex with porcine beta-trypsin.";
FEBS Lett, 297:143-146(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH LDTI.
MEDLINE=97390427; PubMed=9242660;
Stubbs M.T., Morenweiser R., Sturzebecher J., Bauer M., Bode W.,
Huber R., Piechottka G.P., Matschiner G., Sommerhoff C.P., Fritz H.,
Auerswald E.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.03 ANGSTROMS) OF COMPLEX WITH LDTI. MEDLINE-98046095; PubMed-9384562; Addi Marco S., Priestle J.P.; Structure of the complex of leech-derived tryptase inhibitor (LDTI) with trypsin and modeling of the LDTI-tryptase system.";
                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
MEDLINE=93187998; PubMed=8445634;
Huang Q., Liu S., Tang Y.;
Hrefined 1.6-A resolution crystal structure of the complex formed
between porcine beta-trypsin and MCTL-A, a trypsin inhibitor of the
squash family. Detailed comparison with bovine beta-trypsin and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE=58035057; PubMed=7947985;
Hang Q., Wang Z., Li Y., Liu S., Tang Y.;
"Refined 1.8-A resolution crystal structure of the porcine epsilon-
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The three-dimensional structure of recombinant leech-derived tryptase inhibitor in complex with trypsin. Implications for the structure of human mast cell tryptase and its inhibition."; J. Biol. Chem. 272:19931-19937(1997).
                                                                                                                                                                                                                                                                           [2]
SEQUENCE OF 9-231.
MEDLINE=73258692; PubMed=4738933;
Hermodson M.A., Ericsson L.H., Neurath H., Walsh K.A.;
"Determination of the amino acid sequence of porcine trypsin by
                                ô
             Length 243;
                               0; Indels
                                                                                                                                                                                                                                              Charles M., Rovery M., Guidoni A.A., Desnuelle P.; "On trypsinogen and trypsin of pig."; Biochim. Biophys. Acta 69:115-129(1963).
           ch 100.0%; Score 107; DB 1; Similarity 100.0%; Pred. No. 1.4e-09; 20; Conservative 0; Mismatches 0;
                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-2002 (Rel. 41, Last annotation update)
Trypsin precursor (EC 3.4.21.4).
                                                                                                                        231 AA.
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Biochim. Biophys. Acta 1209:77-82(1994).
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                         complex.";
J. Mol. Biol. 229:1022-1030(1993);
                                                                                                                                                                                                                                                                                                                                        Biochemistry 12:3146-3153(1973).
                                                   1 IVGGYTCGANTVPYOVSLNS 20
                                                                21 IVGGYTCGANTVPYQVSLNS 40
                                                                                                                        STANDARD;
        Ouery Match
Best Local Similarity
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ID TRYP PIG
AC P00761;
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Length 246;

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246 AA; 26170 MW; E9E5AlDE2391BBBB CRC64;
                                   Query Match
Best Local Similarity 85.0°
Matches 17; Conservative
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SEQUENCE
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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RY SIMILARITY.
REQUIRED FOR SPECIFICITY (BY SIMILARITY).
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MEDLINE=86284628; PubMed=3841794;

Pinsky S.D., Laforge K.S., Scheele G.;

Differential regulation of trypsinogen mRNA translation: full-length mRNA sequences encoding two oppositely charged trypsinogen isoenzymes in the dog pancreas.";

Mol. Cell. Biol. 5:2669-2676(1985).

Mol. Cell. Biol. 5:2669-2676(1985).

-!- CATALYIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lyg-|-Xaa.

-!- SUBCELLULAR LOCATION: Extracellular.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M1559; AAA30900.1; -.

R HSSP; P00761; LEPT.

R MROPS; P00761; LEPT.

R InterPro; IPR001314; Chymotrypsin.

R InterPro; IPR001324; Ser protease_Try.

R Pfam, PP00089; trypsin; I.

R PRONTZ; SM00020; Tryp_SPC; 1.

R PROSITE; PS50240; TRYPSIN_DOW; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.

R Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;

M Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;

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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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                                                                                                  Score 96; DB 1; Length 231;
Pred. No. 7e-08;
                                                                                                                                            1; Indels
212 216
217 219
221 230
231 AA; 24409 MW; AOA125CF7FC138C2 CRC64;
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15-JUN-2002 (Rel. 41, Last annotation update)
1rypsin, cationic precursor (EC 3.4.21.4).
Canis familiaris (Dog).
                                                                                 89.7%; Scor.
85.0%; Pred. No. ...
2; Mismatches
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                                                                                                                                                                                 1 IVGGYTCGANTVPYQVSLNS 20
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                                                                                                                                       Matches 17; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Earnest T., Fauman B., Craik C.S., Stroud R.;
"1.59-A structure of trypsin at 120 K: comparison of low temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dependent geometry.";
Biochemietry 35:5999-6009(1996).
-!- CATALYTY ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lyg-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1996 (Rel. 01, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsin II, anionic precursor (EC 3.4.21.4) (Pretrypsinogen II)
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MEDLINE=85054880; PubMed=6034547;
Craik C.S., Choo Q.L., Swift G.H., Quinto C., McDonald R.J.,
Ruteer W.J.;
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86.0%; Score 92; DB 1; Length 246
85.0%; Pred. No. 3.2e-07;
ive 1; Mismatches 2; Indels
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MEDLINE=96214506; PubMed=8634241;
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Proteins 10:171-187(1991).
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PIR; A22657; TRRT2.
PDB; LANB; 01-APR-97.
PDB; LANC; 01-APR-97.
PDB; LAND; 01-APR-97.
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MEDLINE≈86284628; PubMed≈3841794;
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hes 16; Conservative
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194 1
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Eur. 7. Biochem. 193.767-773(1990).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SUBLORGS TO PEPTIDASE PAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Holstein-Friesian, TISSUB-Pancreas, MEDINE-91053181, Pubmed=1701147, MEDINE-91053181, Pubmed=1701147, Hicker C., Guilloteau P., Toullec R., Puigserver A., "Isolation and nucleotide sequence of cDNA clone for bovine pancreatic amionic trypsinogen. Structural identity within the
                                                                               InterPro; IPR001114; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam, PF00092; CHYMOTRYPSIN.
SMART; SM00020; THYP.SPC; 1.
PROSITE; PS50240; THYPSIN DOM; 1.
PROSITE; PS00134; THYPSIN DOM; 1.
PROSITE; PS00134; THYPSIN SIN; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal; Multigene family; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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85.0%; Pred. No. 6.5e-07;
ive 1; Mismatches 2; Indels
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ABD3630809AEE606 CRC64;
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TRYPSIN 11, ANIONIC.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last annotation update)
Trypsin, anionic precursor (EC 3.4.21.4).
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 247 AA
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107
107
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246
PDB; 1AMH; 24-DEC-97.
PDB; 1SLU; 11-UTL-96.
PDB; 1SLW; 11-UTL-96.
PDB; 1SLW; 11-UTL-96.
PDB; 1SLX; 11-UTL-96.
PDB; 1SLX; 11-UTL-96.
PDB; 1SLX; 12-UTC-96.
PDB; 1TGI; 23-DEC-98.
PDB; 1TGI; 23-DEC-98.
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                           DR InterPro; IRRO1258; -..
DR InterPro; IRRO1314; Chymotrypsin.
DR Fian; PR001254; Ser_protease_Try.
DR PEAM; PR00129; CHYMOTRYPSIN.
DR PRONTE; PR00120; CHYMOTRYPSIN.
DR PROSTTE; PS00134; TRYPSIN DM; 1.
DR PROSTTE; PS00135; TRYPSIN DM; 1.
DR PROSTTE; PS00135; TRYPSIN DM; 1.
DR PROSTTE; PS00135; TRYPSIN DM; 1.
DR HYDROJASE; Sarie protease; Digestion; Pancreas; Zymogen; Signal.
FT GTAIN 24 247 TRYPSIN, ANIONIC.
FT ACT SITE 63 63 CCTANGE RELAY SYSTEM.
FT ACT SITE 107 107 CHARGE RELAY SYSTEM.
FT ACT SITE 107 107 CHARGE RELAY SYSTEM.
FT ACT SITE 107 160 CHARGE RELAY SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mol. Cell. Biol. 5:3669-2676(1965).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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Mammalia; Butheria; Carnivora; Pissipedia; Canidae; Canis.
NCBI_TaxID=9615;
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
REQUIRED FOR SPECIFICITY.
W, 50A070495A7731DB CRC64;
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ID TRY2_CANFA

STANDARD; PRT; 247 AA.

OF 06872;
DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DT TSPSIN, anionic precursor (EC 3.4.21.4).
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HSSP; P00761; 1EPT.
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MEDLINE=90221895; PubMed=2326201;
Tani T., Kawashima I., Mita K., Takiguchi Y.;
"Nucleotide sequence of the human pancreatic trypsinogen III cDNA.";
Nucleic Acids Res. 18.1631.1631(1990).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELIUIAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                        HSSP, P00763; 1DPO.
MEROPS; S01.258; -.
InterPro: PR001214; Chymotrypsin.
InterPro: PR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PR0072; CHYMOTRYPSIN.
SWART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_ESE; 1.
Hydrolase; Serinis; TRYPSIN_ESE; 1.
Hydrolase; Serinis; Protease; Digestion; Pancreas; Zymogen; Signal; Multigene family.
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(BY SIMILARITY).
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80.0%; Pred. No. 1.9e-06;
cive 2; Mismatches 2; Indels
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TRYPEIN, ANIONIC.
CHARGE RELAY SYSTEM (ECHARGE RELAY SYSTEM (FCHARGE RELAY SYSTEM (BY SIMILARITY.
BY SIMILARITY.
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01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsin III precursor (EC 3.4.21.4).
PRSS3 OR TRY3.
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                        EMBL; M11589; AAA30899.1;
PIR; A26273; TRDG.
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247
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247 AA;
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es 16; Conserv
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P15951;
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TRY3 HUMAN
TD 7482 HUMAN
DT 01-APR.
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DT 15-JUN
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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REQUIRED FOR SPECIFICITY (BY SIMILARITY).
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Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-!- CATIVITC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- ALTERNATIVE PRODUCTS: 3 isoforms; A (shown here), B and C; seem to be produced by alternative splicing.
-!- TISSUE SPECIFICITY: PRUCREAS AND BRAIN.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
MEROPS; SO1.174; -...
Genew; HGNC:9466; PRSS3.
Genew; HGNC:9466; PRSS3.
InterPro; IPRO01214; Chymotrypsin.
InterPro; IPRO01214; Ser_protease_Try.
Pfam; PF00069; trypsin; I
PRO0125; CHYMOTRYPSIN.
SWART; SMO0020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS500134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
Hydrolase; Serind; Protease; Digestion; Pancreas; Zymogen; Signal; Multigene family.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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(BY SIMILARITY).
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Pred. No. 1.9e-06;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1815030; Q15665; Q9UQV3; O1-FEB-1994 (Rel. 28, Created) O1-FEB-1994 (Rel. 28, Last sequence update) O1-FEB-1994 (Rel. 41, Last annotation update) Trypain IV precursor (EC 3.4.21.4) (Brain trypsinogen)
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TRYPSIN III.
CHARGE RELAY SYSTEM
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MEDLINE=94123994; PubMed=8294000;
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80.0%;
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Best Local Similarity 80.0 Matches 16; Conservative
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247 AA;
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TRY4_HUMAN
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or send an email to license@isb-sib.ch).
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28 SIMILARITY.
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Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus,
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague Dawley,
MEDLINE=22265624, PubMed=6896710,
MCDOLAID R.J., Stary S.J., Swift G.H.,
"Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of the cloned cDNAs.",
                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                     InterPro; JPR001314; Chymotrypsin.
InterPro; IPR001354; Ser_protease_Try.
Pfam; PR00099; trypsin; 1.
SMART; SM00020; Tryp_SPC; 1.
PR0STIE; PS50240; TRYPSIN DOM; 1.
PROSTIE; PS50134; TRYPSIN DOM; 1.
PROSTIE; PS00135; TRYPSIN SER; FALSE NEG.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal; SIGNAL.
1 ? POTENTIAL.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsin I, anionic precursor (EC 3.4.21.4) (Pretrypsinogen I)
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Craik C.S., Choo Q.L., Swift G.H., Quinto C., McDonald R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 87; DB 1; Length 304;
Pred. No. 2.3e-06;
2; Mismatches 2; Indels
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ACTIVATION PEPTIDE.
TRYPEIN IV.
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                                           EMBL; X72781; CABSB178.1;
EMBL; X71345; CAASO484.1;
EMBL; D45417; BAA08257.1;
PIR: S33496, S33496,
HSCP; PO7477; 1TRN
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80.0%;
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1es 16; Conservative
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AC P00762;
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MEDLINE=20389982; PubMed=10930381;
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MEDLINE=96438847; PubMed=8841182;
Whitcomb D.C., Gorry M.C., Preston R.A., Furey W., Sossenheimer M.J.,
Ulrich C.D., Martin S.P., Gates L.K. Jr., Amann S.T., Toskes P.P.,
Liddle R., McGrath K., Unomo G., Post J.C., Ehrlich G.D.;
"Hereditary pancreatitis is caused by a mutation in the cationic
                                                                                                                                         Gaps
                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                   MEDLINE-66221712; PubMed-3011602;
Emi M., Nakamura Y., Ogawa M., Yamamoto T., Nishide T., Mori T.,
                                                                                                                                                                                                                                                                 TWO CDNAB
                                                                                                                                                                                                                                                                                        MEDLINE=90091010; PubMed=2598466; Kimland M., Russick C., Marks W.H., Borgstroem A.; "Immunoreactive anionic and cationic trypsin in human serum."; Clin. Chim. Acta 184:31-46(1989).
                                                                                                                                         ö
                                                                                                                                                                        Score 85; DB 1; Length 246;
Pred. No. 3.9e-06;
2; Mismatches 2; Indels
                                                                                                                     25959 MW; 6AFA0DAD11943FB5 CRC64;
                                                                                                                                          2; Mismatches
                                                                                                                                                    IVGGYTCGANTVPYQVSLNS 20
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                                                                                                                                    80.08
                                                                                                                                          16; Conservative
   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bernard J.P., Guillot M.
                                                                                                                                                                                              SEQUENCE OF 68-151 FROM N.A., AND VARIANTS HPC P-104; C-116 AND F-139.
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Rerec C., Raguenes O., Salomon R., Roche C., Bernard J.P., Guillot M. Quere I., Faure C., Marcider B., Audrezet M.P., Guillausseau P.J., Quere I., Faure C., Mercider B., Audrezet M.P., Guillausseau P.J., Dupont C., Munnich A., Bignon J.D., Le Bodic L.;

"Mutations in the cationic trypsinogen gene and evidence for genetic in the rereditary pancreatitis.";

Heterogeneity in hereditary pancreatitis.";

J. Med. Genet. 36:228-232(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98295575; PubMed-96313818;
Teich N., Mossner J., Keim V.;
"Mutations of the cationic trypsinogen in hereditary pancreatitis.";
Hum. Mutat. 12:39-43(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS HPC VAL-16 AND HIS-122.
MEDLINE=99315544; PubMed=10381903;
Witt H., Luck W., Becker M.;
"A signal peptide cleavage site mutation in the cationic trypsinogen gene is strongly associated with chronic pancreatitis.";
Gastroenterology 117:7-10(1999).
Keim V.;
mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gut 50:271-272[2002].
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lyg-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- MASS SPECTROMETRY: MW=24348; MW_ERR=2; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crystal structure of human trypsin 1: unexpected phosphorylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS HPC THR-29 AND CYS-122.
MEDLINE=21648565; PubMed=11788572;
Pfurzer R., Myers E., Applebaum-Shapiro S., Finch R., Ellis I.,
Pfurzer R., Myers U.A., Whitcomb D.C.;
"Novel carionic trypsinogen (PRSS1) N29T and R122C mutations cause autoseomal dominant hereditary pancreatitis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.A.,
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MEDLINE=97463797; PubMed=9322498;
Gorry M.C., Gabbaizedeh D., Furey W., Gates L.K. Jr., Preston R. Aston C.E., Zhang Y., Ulrich C., Ehrlich G.D., Whitcomb D.C.;
"Mutations in the cationic trypsingen gene are associated with recurrent acute and chronic pancreatitis.";
Manns M., Mossner J.,
an activation peptide
                                                                                                                                                                                                                                                                                                                                                               K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND PHOSPHORYLATION
                                                                                                                                                                                                                                                 Teich N., Bauer N., Mossner J., Keim V.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96266496; PubMed-8683601;
Gaboriaud C., Serre L., Guy-Crotte O., Forest E.,
Fontecilla-Camps J.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
    reich N., Ockenga J., Hoffmeister A., Manns M., "Chronic pancreatitis associated with an activat
                                                                                    that facilitates trypsin activation.";
Gastroenterology 119:461-465(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Biol. 259:995-1010(1996)
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TRYPEIN II-P29.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
REQUIRED FOR SPECIFICITY (BY SIMILARITY).
REQUIRED FOR SPECIFICITY (BY SIMILARITY).
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REROPS; SOI.151...
REPROPOS; PRO01254; DEPOCLAGAGE_Try.
PEAM, PRO0008; LYPBAIN; I.
REPRIVES; PRO0009; LYPBAIN; I.
REPROSTE; PSO0144; TRYPEIN_DOM; I.
REPROSITE; PSO0145; TRYPEIN_DOM; I.
REPOSITE; PSO01015; TRYPEIN_LIS; I.
REPOSITE PSO01015; TRYPEIN_
                                                                                                                                                                                                                                                                                                                                                  Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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"Isolation and characterization of the chicken trypsinogen gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
12-JUN-2002 (Rel. 41, Last annotation update)
Trypsin II-P29 precursor (EC 3.4.21.4)
Gallus gallus (Chicken)
                                                                                                                                                                          248 AA.
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MEDLINE=95251611; PubMed=7733885;
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les 16; Conserva
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NCBI_TaxID=9031;
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DT 01-NOV-1
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DE RAPATYOTE
OC GAILURG G
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AUTOCLEANAGE SITE).
/FTIG=VAR_012713.
R -> H (IN HPC; SUPPRESSES AN
AUTOCLEAVAGE SITE).
R -> H (IN HPC; SUPPRESSES AN
AUTOCLEAVAGE SITE WHICH IS PROBABLY PART
OF A FAIL-SAFE MECHANISM BY WHICH
TRYBEIN, WHICH IS ACTIVATED WITHIN THE
PANCREAS, MAY BE INACTIVATED; LOSS OF
THIS CLEAVAGE SITE WOULD PERMIT
AUTODIGESTION RESULTING IN PANCREATITIS).
                                                                                                                                                                                                                                                                                                                               InterPro: IPR001314; Chymotrypsin.

R InterPro: IPR001254; Ser_protease_Try.

R Pan, PP00089; trypabin; 1.

R RRINTS; PR00722; CHYMOTRYPSIN.

R RRINTS; PR00720; Tryp SPC; 1.

R RROSITE; PS00135; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal; Multigene family; Phosphorylation; 30-structure; Disease mutation.

T SIGNAL

T RROPE

T CHAIN

24 247 TRYPSIN I.
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K -> R (IN HPC; INCREASED RATE ACTIVATION).
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D -> G (IN HPC; INCREASED RATE
ACTIVATION).
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DD49A487B8062813 CRC64;
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N -> I (IN HPC).
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(IN HPC).
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           EMBL; M22612; AAA61231.1; ---
EMBL; U70137; AAC50228.1; --
EMBL; AF314534; AAG30943.1; --
EMBL; AF315309; AAG30947.1; ---
EMBL; AF315309; AAG30947.1; --
EMBL; AF315310; AAG30949.1; --
PIR; AF315311; AAG30949.1; --
PIR; A25652; A25852.
PDB; ITRN; 03-UTN-95.
PDB; IFXY; 17-UTN-98.
MEROPS; SQ1.151; ---
MEROPS; SQ1.151; ---
MEROPS; HONC:9475; PRSSI.
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                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00020; TRYPSIN.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                        "Cloning, characterization and nucleotide sequences of two cDNAs encoding human pancreatic trypsinogens.";
Gene 41:305-310(1986).
                                                                                                                                                                                                                                              MEDLINE-86221712; PubMed-3011602;
Emi M., Nakamura Y., Ogawa M., Yamamoto T., Nishide T., Mori T.,
Matsubara K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.5%; Score 84; DB 1; Length 247; 80.0%; Pred. No. 5.6e-06; ive 1; Mismatches 3; Indels
                   01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Trypsin II precursor (EC 3.4.21.4) (Anionic trypsinogen).
PRSS2 OR TRY2 OR TRYP2.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, M27602, AAA61232.1; -. PIR, B25852, B28852. HSSP, P00763, 1DPO. MRROPS, S01.258; -. Genew; HGNC:9483; PRSS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IVGGYTCGANTVPYQVSLNS 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.08;
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247 AA;
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Best Local Similarity
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                                                                                                                                                                                    NCBI_TaxID=9606;
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C63F29CB3300B323 CRC64;
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Wang K., Iytle L., Gan L., Hood L.E.;

Submitted (SEP-1996) to the BMBL/GenBank/DDBJ databases.

-I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.

-I- SUBCELLULAR LOCATION: Extracellular.

-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
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(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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ACTIVATION PEPTIDE (BY SIMILARITY).
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InterPro; IPR001214; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; TRYP SPC; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serima protease; Digestion; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.5%; Score 84; DB 1; Length 244; 75.0%; Pred. No. 5.5e-06; ive 2; Mismatches 3; Indels
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                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
17-Postin precursor (EC 3.4.21.4).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U72330; AAB17274.1; -. HSSP; P00763; 1DPO.
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26 IVGGYTCPEHSVPYQVSLNS 45
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Best Local Similarity 75.0°
Matches 15, Conservative
                                                                                                                          STANDARD;
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TRY2_HUMAN
ID TRY2_HUMAN
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                                                                                                                                           P70059;
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                                                                                 RESULT 12
TRY2_XENLA
TO TRY2_XENLA
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(BY SIMILARITY).
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PRT;

STANDARD;

(Rel. 07, Created)

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                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                      01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsin II, anionic precursor (EC 3.4.21.4) (Pretrypsinogen II).
                                                                                                                                                                                                                                                              STRAIN=A/J;
MEDLINE=87066713; PubMed=3641189;
                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                  NCBI_TaxID=10090;
TRY2 MOUSE
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CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR MEROPS; SOI 056; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IRR001324; Ser protease_Try.
DR PRINTS; PR00725; CHYMOTRYPSIN.
DR PRINTS; PR00725; CHYMOTRYPSIN.
DR PROSTT; PS0020; TryP.SPC.
DR PROSTT; PS0020; TryP.SPC.
DR PROSTT; PS00134; TRYPSIN_DM; I.
DR PROSTT; PS00135; TRYPSIN_MIS.

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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus,
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 26:3081-3086(1987).
--: CATALYTIC ACTUITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa,
--: SUBCELUMAR LOCATION: Extracellular.
--: SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                        01-AUG-1988 (Rel. 08, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsin III, cationic precursor (EC 3.4.21.4) (Pretrypsinogen III).
                                                                                                                                                                                                                                                                                                                      MEDINE-87271609; Pubmed=3607011;
Fletcher T.S., Alhadeff M., Craik C.S., Largman C.;
"Isolation and characterization of a cDNA encoding rat cationic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.5%; Score 84; DB 1; Length 247; 75.0%; Pred. No. 5.6e-06; ive 3; Mismatches 2; Indels
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                                                               247 AA
                                                                 PRT;
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221 BY
195 RE
26269 MW;
                                                                                                    (Rel. 08, Created)
(Rel. 08, Last seq
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                                                                 STANDARD;
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195
147 AA;
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                                                                                                    01-AUG-1988 (Rel.
01-AUG-1988 (Rel.
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                        RESULT 14
TRY3 RAT
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AC P08426;
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TRYPSIN II, ANIONIC.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
RY SUMILARITY.
RY SUMILARITY.
REQUIRED FOR SPECIFICITY (BY SIMILARITY).
                                                                                        HSSP, P00763, 1DPO.

REROPS, S01.064; -.

RICEPTO; IPRO01314; Chymotrypsin.

InterPro; IPRO01254; Ser_protease_Try.

RERIATS, PR00722; CHYMOTRYPSIN.

RAMAT; SM00020; Tryp_SPC; 1.

RERIATS, PSS0040; TRYPSIN.

REROSITE; PS00134; TRYPSIN.

REROSITE; PS00135; TRYPSIN.

REROSITE; PS00
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EMBL; X04574; CAA28243.1; -. EMBL; X04577; CAA28245.1; -. PIR; B25528; B25528.
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Matches 15; Conserv
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RESULT 15 TRY2 MOUSE

Matches 15; Conservative

Local Similarity

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96ggwa moulli ja

96ggwa moulli ja

96gff gillichthys

991016 gadus morhu

992166 pseudopleur

992046 dissostichu

992056 pseudopleur

992096 gissostichu

99405 dissostichu

99407 artus sp.

99497 rattus sp.

963274 rattus norv

92569 cattus sp.

99496 rattus sp.
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088309 mus musculu
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063275 rattus norv
09xy46 ctenocephal
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Q9u7d2 caenorhabdi
Q962g7 culex pipie
Q24091 drosophila
                                                                                                                                                        002570 culex quing
Q9n5f6 caenorhabdi
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MEDLINE=93305808; PubMed=8318586;
Octonel C.E., Novella M.L., Winnica D.E., Lardy H.A.;
Coronel C.E., Novella M.L., Winnica D.E., Lardy H.A.;
Caltrin, the calcium transport inhibitor protein from seminal vesicles of the rat.";
Etherrat.";
Biol. Reprod. 48:1326-1333(1993).
HSSP; P00760; 1AQ7.
SEQUENCE 24 AA; 2452 MW; DDIA6C82EF25FCIA CRC64;
                                                                                                                                                                                                                                                                                                                                   Rattus sp.

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Local Similarity 94.7%; Pred. No. 1e-07;
es 18; Conservative 0; Mismatches 1; Indels
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Q9Z1R9;
01-MAY-1999 (TYEMBLrel. 10, Created)
01-MAY-1999 (TYEMBLrel. 10, Last sequence update)
01-MAR-2002 (TYEMBLrel. 20, Last annotation update)
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PRT;
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Og1515 fugu rubrip
O42159 petromyzon
O42169 petromyzon
O42169 petromyzon
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Ogw7d5 paralichthy
Ogw7d5 paralichthy
Ogw7d7 paralichthy
Og8t99 engralls j
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Q9zlr9 mus musculu
Q9r0t7 mus musculu
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          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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sp_vertebrate:*
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Trypsinogen 16.
TRYGNIG OR TRYPSINOGEN.
Mus musculus (Mozos).
Musculus (Mozos).
Eukaryots, Metacos, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Kashiwabara S., Baba T.
A homologue of pancreatic trypsin is localized in the acrosome of
mammalian sperm and is released during acrosome reaction.";
J. Biol. Chem. 274:29426-29432(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen F., Rowen L., Hood L., Rothenberg B.V.;

"Differential transcriptional requiation of individual TCR Vbeta "Differential transcriptional requiation of individual TCR Vbeta gegments before gene rearrangement.";

J. Immunol. 166:1771-1780(2001).

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE EMBL; ARIO7342; AAC79093.1;

EMBL; ARE070465; AAB69088.1;

-- EMBL; ARO00665; AAB69088.1;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI TaxID=10090,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD, MGIZ14849; Trygn16.
InterPro; IPR001314; Chymctrypsin.
InterPro; IPR001314; Chymctrypsin.
InterPro; IPR001324; Err_protease_Try.
Pfam; PR00089; trypsin; 1.
RRINTS; PR00722; CHYMCTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN DOW; 1.
RPOSITE; PS00134; TRYPSIN DOW; 1.
RPOSITE; PS00135; TRYPSIN ER; 1.
RHYdrolase; Serine protease.
SEQUENCE 246 AA; 26134 MW; 345173818CA2F463 CRC64;
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U-UON-2002 (TIEMBLrel. 21, Last annotation update)
Pancreatic trypsin (9910001B19RIK protein) (Trypsinogen 8)
TD OR 0910001B19RIK OR TRYPSINOGEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BALB/C;
MEDLINE=21103195; PubMed=11160223;
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1es 17; Conservative
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RA Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Prkunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Prkunishi Y., Konno H., Adachi J., Fukuda S., Alamanka I., Radota K., Izawa M., Nishi K., Kiyosawa T., Saito R., Kadota K., Matsuda H.A., Ashburnar M., Baralov S., Casavant T., Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T., Radota K., Matsuda H., King B., Kochiwa H., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bromnstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Rodone P., Marchionni L., Machima J., Mazzarelli J., Mombaerts P., A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.F., Suzuki H., Toyo-oka K., Mang K.H., Wettz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., R. Phunctonal annotation of a full-length mouse cDNA collection.";
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=129;
MEDLINE-21103195; PubMed=11160223;
Chen F., Rowen L., Hood L., Rothenberg B.V.;
Chifferential transcriptional regulation of individual TCR Vbeta segments before gene rearrangement.";
J. Immunol. 166:1771-1780(2001).
-1- SIMILARITY: BELONGS TO PEFTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN PAMILY.
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85.0%; Pred. No. 2.7e-06;
ive 1; Mismatches 2; Indels
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
TESP4 (0910001B19RIK protein) (Trypsinogen 9).
TC OR 0910001B19RIK OR TRYPSINOGEN.
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InterPro; IPR001234; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
FEam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMARY; SM00202; Tryp. SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOMN_1.
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EMBL; AK003667; BAB25621.1; --
EMBL; AK003064; BAB22542.1; --
EMBL; AE00664; AAB69056.1; --
HSSP; P00763; 1SLU.
MEROPS; S01.057; --
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SEQUENCE 246 AA; 26274 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                        RX STRAIN=CSTBL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai T., Hara A., Pukunishi Y., Kiyosawa H., Kondo S., Yamanaka I.,
RA Azawa T., Hara M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saitor T. Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Gatota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Gatota K., Matsuda H.A., Ashburner M., Batalov S., Cosavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Brownstein M.J., Bull C., Fletcher C., Fluita M., Gariboldi M.,
RA Brownstein M.J., Bull C., Fletcher C., Fluita M., Gariboldi M.,
RA Uyons P., Marchionni I., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriquez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Haseqawa Y., Kawaji H., Kohtsuki S.,
RA Havashizaki Y.
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                                         Ohmura K., Kohno N., Kobayashi Y., Yamagata K., Sato S., Kashiwabara S., Baba T., "A homologue of pancreatic trypsin is localized in the acrosome of mammalian sperm and is released during acrosome reaction."; J. Biol. Chem. 274:29426-29432(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen F., Rowen L., Hood L., Rothenberg E.V.;
"Differential transcriptional regulation of individual TCR Vbeta segments before gene rearrangement.";
J. Immunol. 166:1771-1780(2001).
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
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80.0%; Pred. No. 3.9e-06;
tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERNYS; PR00722; CHYMOTRVESIN.
PRINYS; PR00722; CHYMOTRVESIN.
SMRAT; SM00200; TYPYSES; I.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00134; TRYPSIN_SER; 1.
Hydrolaee; Serine protease.
SEQUENCE 246 AA; 26277 MW; 915C92353EC42809 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 AA.
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
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01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129;
MEDLINE=21103195; Pubmed=11160223;
    TISSUE=TESTIS;
MEDLINE=99436155; PubMed=10506205;
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:685-690(2001).
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.058; -.
                                                                                                                                                                                   SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

SEQUENCE STATE-CFSIL65; INTESTINE, AND PANCREAS;

MATCH-CFSIL65; INDEMEd-12785;

A Arakawa T., Shinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S., A Aizawa T., Status M., Nishi Y., Konono H., Adachi J., Fukuda S., A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Sato T., Okazaki Y., Gojbori T., Bono H., Kasukawa T., Saito R., Kadota K., Marsuda H.A., Ashburner M., Batalov S., Casavant T., Kachim D., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M., Ausonstein M.J., Bull L., Fletcher C., Fujita M., Gariboldi M., Nordone P., Kanig B., Ringwald M., Rodriguez I., Sakamoto N., Asaaki H., Sato K., Schoenboch C., Saya T., Shibata Y., Storch K., Fayaki Hayashizaki Y.,

Nordone P., Storch K., Wang K.H., Weitz C., Whittaker C., Milming L., A Wynnsaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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80.0%; Pred, No. 1.2e-05;
wismatches 3; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) 2210010C04RIK procein (Trypsinogen 7).
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EMBL, AK00773; BAB25246.1; --
EMBL, AK00773; BAB25246.1; --
EMBL, AR007663; AAB69044.1; --
EMBL, PO0763; IDPO
MEROPS; SQ1.151; --
MGD, MGT.1944623; --
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
PEAN; PR00689; trypsin; 1.
PROSITE; PS00020; Tryp.SPC; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN ING; 1.
HYDCOIRE; PS00135; TRYPSIN SER; 1.
HYDCOIRE; PS00135; TRYPSIN SER; 1.
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01-JUN-2001 (TrEMBLrel. 17, Created)
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Best Local Similarity 80.0'
Matches 16; Conservative
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                                                                                                                                      Mus musculus (Mouse)
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MEDLINE-21085660; Pubmed=11217851;

Agwai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Izawa M., Nishi K., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kyosawa H., Kondo S., Yamanaka I.

A Alzawa K., Izawa M., Nishi K., Kyosawa H., Kasukawa T., Saito R.,
A Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
A Radota K., Matsuco Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli P., Suzuki R., Tomita M., Wasner L., Washio T.,
Bakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,
Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fullta M., Gariboli M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Stocch K.-P.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Havashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            segments before gene rearrangement.";
J. Immuno.1 166:1771-1780(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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MGD; MGI:1920876; 1810009J06Rik.
InterPro; IPR001314; Chymotrypsin.
InterPro; IRR001254; Ser protease_Try.
Pfam; PF00089; trypsin; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALB/C;
MEDLINE=21103195; PubMed=11160223;
             STRAIN C57BL/6J; TISSUE PANCREAS;
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                                                                                                                                                                                                    CSTRAINCESTBL/63. TISSUE=STOWACH;

MEDLINE=21085660; PubMed=11217851;

MEDLINE=21085660; PubMed=11217851;

A Mara J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kyosawa H., Kondo S., Yamanaka I.,

A Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

A Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,

A Schriml L. Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Schriml L.M., Staubli F., Suzuki R., Tomitam M., Wagner I., Washio T.,

B Lake J., Boffelll D., Bojunga N., Carninci P., de Bonaldo M.F.,

B Lake J., Boffelll D., Bojunga N., Carninci P., de Bonaldo M.F.,

B Lake J., Boffelll D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

A Brownstein M.J., Hull D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring W., Schoenbach C., Seya T., Shibata Y., Storch K.-P.

Shaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.

A Solzuki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Hynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPE; SOULLI; --
MEROPE; SOLLII; --
MGD, MGI:1914623; 2210010C04Rik.
InterPro; 1PR001214; Chymctrypsin.
InterPro; 1PR001214; Chymctrypsin.
InterPro; 1PR001254; Ser_protease_Try.
PRINTS; R00020; Trypsin; I.
SMRRT; R00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
R PROSITE; PS00134; TRYPSIN_MS; UNKNOWN_I.
R PROSITE; PS00134; TRYPSIN_MS; UNKNOWN_I.
R PROSITE; PS00135; TRYPSIN_MS; UNKNOWN_I.
R PROSITE; PS00135; TRYPSIN_ER; 1.
R Hydrolase; Serine protease.
SEQUENCE 247 AA; 26407 MW; 84D474DB322B3A55 CRC64;
  (TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AK008695; BAB25837.1; -. HSSP; P00763; 1DPO.
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  01-JUN-2001 (TrEMBLrel.
                                        2210010C04Rik protein.
                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                NCBI_TaxID=10090;
                                                                2210010C04RIK
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Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota, Metazoa; Chordata; Cranitata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.7%; Score 81; DB 11; Length 24 78.9%; Pred. No. 7.2e-05; ive 2; Mismatches 2; Indele
                                                                                                                                                                                                                                                                                                                                                                    26503 MW; EDPSF7696833C7BC CRC64;
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Q91515,
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
PRINTS; PRO0722; CHYMOTRYBSIN.
SMART; SM00020; TTYP SPC; 1.
PROSITE; PS50240; TTXPSIN. DOM; 1.
PROSITE; PS00114; TRYPSIN. HIS; UNKNOWN 1.
Hydrolae; Serine procteage.
SEGUENCE 247 AA; 26503 WW; EDPSF76968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IVGGYTCGANTVPYQVSLN 19
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Matches 15, Conservative
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AC 09151
AC 09151
DT 01-W
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Ol-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
1810009J06R1k protein (Trypainogen 4).
1810009J06R1k OR TRYPSINOGEN.
Mus musculus (Mouse).
Eukaryota; Metazos; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090; [1] SEQUENCE FROM N.A.

PRT;

PRELIMINARY;

Q9CPN7 Q9CPN7

RESULT 7

26 VGGYTCQRNALPYQVSLNS 44

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MEROPS; S01.128; -
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                                                              01-JAN-1998 (
01-JAN-1998 (
01-JUN-2002 (
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                                      042160
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Q98TH0
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"The Molecular Evolution of the Vertebrate Trypsinogens.";
"The Molecular Evolution of the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
Wang K., Gan L., Lee I., Roach J., Hood L.;
Submitteed (ARR-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perromyzon marinus (Sea lamprey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.4%; Score 71; DB 13; Length 244; 68.4%; Pred. No. 0.0027; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL <1 12 POTENTIAL.
CHAIN 13 244 TRYPSIN B1.
SEQUENCE 244 AA; 25903 MW; C4582EE07E3B8007 CRC64;
                                                                                                                                                                                                                  237 AA; 25726 MW; 30D2DBAAC39080C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Trypsinogen B1 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001324; Ser protease_Try.
Pfam; PF00089; trypsin; 1
PRNTS; PR00722; CHYMOTRYPSIN.
SMART; SM00720; TRYPSIN.
PROSITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_I.
PKOSITE; PS00135; TRYPSIN_ESR; 1.
Hydrolase; Serine protease; Signal.
                                                                               InterPro: IPR001314; Chymotrypsin.

InterPro: IPR001354; Ser_protease_Try.

PEAM; PR00089; LTYPPSin. 1.

PRINTS; PR00722; CHYMOTRYSIN.

SMART; SM00020; TRYPSIN. 1.

PROSITE; PS00134; TRYPSIN. DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN HIS; UNKNOWN_1.

Hydrolase; Serine protease.

NON HS SEROWER 237 AA, 25726 MW; 30D2DBAAC3908
                                                                                                                                                                                                                                                                                                                                                                                     244 AA.
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EMBL; AF011900; AAB69656.1; -.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                               EMBL, U25747; AAA75001.1; -. HSSP; P35031; 1BIT.
MEROPS; S01.125; -.
                                                                                                                                                                                                                                                                                             1 IVGGYTCGANTVPYQVSLNS 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7757;
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Watabe S., Ansan M.N.,
Watabe S., Ansan M.N.,
Watabe S., Ansan M.N.,
"Anchovy trypsinogen mRNA.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL, ABO41929; BAB40329.1; -.
HSSP, P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **EQUENCE FROM N.A.

Roach J.C.;

"The Molecular Boolution of the Vertebrate Trypsinogens.";

"The Molecular Boolution of the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPEN FAMILY.

EMBL; APO1191; AAB69657.1; --
HSSP; PO0763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Engraulis japonicus (Japanese anchovy).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Clupeomorpha, Engraulidae,
                                                                                                                                                                                                                                                                                    Petromyzon marinus (Sea lamprey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
Petromyzontiformes; Petromyzontidae, Petromyzon.
1018_TaxID=7757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <1 13 POTENTIAL.
14 245 TRYPSIN B2.
245 AA; 26001 MW; 9A932508B896C93E CRC64;</pre>
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                             (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R InterPro; IPR001314; Chymotrypsin.
R InterPro; IPR001314; Ser_protease_Try.
R Pfam; PF00089; trypsin; D.
R PRINTS; RR00722; CHYMOTRYPSIN.
R SMART; SM00020; Tryp SPC; 1.
R PROSITE; PS00134; TRYPSIN DOM; 1.
R PROSITE; PS00134; TRYPSIN MIS; UNKNOWN IPROSITE; PS00135; TRYPSIN SER; 1.
HVOLABSE; Serine procease; Signal.
NON TER.
SIGNAL C. 13 POTENTIAL.
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245 AA.
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Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                 Trypsinogen b2 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IVGGYTCGANTVPYQVSLN 19
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Best Local Similarity 68.4
Matches 13, Conservative
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PRELIMINARY;
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EMBL; AB029751; BAA82363.1; -. HSSP; P00763; 1DPO.
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EMBL, AB041930; BAB40330.1; -.
HSSP, P00763; 1DPO.
MEROPS; S01.258; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IVGGYTCGANTVPYQVSLNS 20
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Best Local Similarity 65.04
Matches 13, Conservative
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TISSUE=PYLORIC CAECA;
                                                                                                           SEQUENCE FROM N.A.
TISSUE=PANCREAS;
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Paralichthys olivaceus (Flounder).

Bukaryota, Metazoga, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomotopa, Acanthopterygii, Percomorpha, Pleuronectiformes,
Pleuronectoidei, Paralichthyidae, Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suzuki T., Srivaetava A.S., Kurokawa T.;
"Japanese flounder mRNA for trypeinogen 3.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-- SIMILARIY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN PAMILY.
EMBL; AB02975; BA82364.2; --
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UJUN-2002 (TrEMBLrel. 21, Last annotation update)
Trypsinogen 2 (Fragment).
Trypsinoden 2 (Fragment).
Paralichthys olivaceus (Flounder).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                       62.6%; Score 67; DB 13; Length 240; 65.0%; Pred. No. 0.011; 1ive 3; Mismatches 4; Indels
Pfam; PF00089; trypsin; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS50240; TRYPSIN DM; 1.

PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Serine processe:

SEQUENCE 240 AA; 26026 MW; 299B119BFF071464 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26948 MW; DC4B647179DDD972 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS, S01.124; -...
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR01254; Ser_protease_Try.
Pfam; PR00089; trypsin; 1.
PRINTS; PR00072; CHYMOTRYPSIN.
SWART; SM00020; Tryp. SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
Hydrolase; Serine protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                         247 AA
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                                                                                                                                                                                                                                                                           1 IVGGYTCGANTVPYQVSLNS 20
                                                                                                                                                                                                                                                                                                20 IVGGYECQAHSQPHTVSLNS 39
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                                                                                                                                                                                                                                13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=PANCREAS;
Suzuki T., Sriva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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09W706
1D Q9W70
D7 01-N0
DT 01-N0
DT 01-N0
DT 01-JU
DE PATAIL
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Gaps
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Engraulis japonicus (Japanese anchovy).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Clupeomorpha, Engraulidae,
                                                                                                                                                                                                                            Suzuki T., Srivastava A.S., Kurokawa T.;
"Japanese flounder mRNA for trypsinogen 2.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watabe S., Ahsan M.N., Funabara D.;
"Anchovy trypsinogen mRNA.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.7%; Score 65; DB 13; Length 238; 65.0%; Pred. No. 0.023; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; S01.125; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001324; Ser protease_Try.
Pfam; PR001029; Lrypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00202; Tryp SPC; I.
PROSITE; PSS0240; TRYPSIN DOM; I.
PROSITE; PS00135; TRYPSIN_ER; I.
Hydrollase; Serine protease.
NOW TER
SEQUENCE 238 AA; 26071 MW; P2B8908085BBD062 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Trypainogen II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13;
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InterPro; IPR001214; Ser_protease_Try.
InterPro; IPR001224; Ser_protease_Try.
PRINTS; PR00089; Lrypain; I
PR0187; SMOR122; CHYMOTRYPSIN.
SMART; SMOR020; TRYP SPC; I.
PROSITE; PS50240; TRYPSIN DOM; I.
PROSITE; PS00134; TRYPSIN DOM; I.
PROSITE; PS00134; TRYPSIN SER; I.
PROGITE; PS00135; TRYPSIN SER; I.
PROGITE; PS00135; TRYPSIN SER; I.
SEQUENCE 241 AA; 26282 MW; FE362D39CAEE!
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                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Trypsinogen 1.
Paralichthys olivaceus (Flounder)
Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Actinoprerygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

TISSUE-PANCREAS;
SUZUKI T., Stivastava A.S., Kurokawa T.;
Suzuki T., Stivastava A.S., Kurokawa T.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE EMBL, ABOSINF PAMILY.

EMBL, ABOST950; BAA82362.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; SO1.125; --
RICEPPO; IPRO01314; Chymotrypsin.
InterPro; IPR001354; Ser_protease_Try.
InterPro; IPR001354; Ser_protease_Try.
REINTS; RR0022; CHYMOTRYPSIN.
RMATT; SM00220; TRYPSIN.
RPOSITE; PS03134; TRYPSIN. DM; 1.
RPOSITE; PS03134; TRYPSIN. MM; INTROMN.
RPOSITE; PS03134; TRYPSIN. SER; 1.
RPOSITE; Serine protease.
Mydrolase; Serine protease.
SEQUENCE 242 AA; 26548 MW; 6DA722C80BC194A2 CRC64;
Best Local Similarity 65.0%; Pred. No. 0.024;
Matches 13; Conservative 2; Mismatches 5; Indels
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                                                                                                                                                                     20 IVGGYECQPYSQPHQVSLNS 39
                                                                                                                     1 IVGGYTCGANTVPYQVSLNS 20
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Best Local Similarity 65.01
Matches 13; Conservative
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Search completed: February 12, 2003, 10:27:18 Job time : 15.1493 secs

21 IVGGYECTPYSQPHQVSLNS 40

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                                                                                                                                                                                                                                                        Sequence 9, Application US/08278091
Patent No. 5506139
GENERAL INFORMATION:
APPLICANT: LOSSNORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONO, Pele
APPLICANT: CHONO, Pele
APPLICANT: KLEIN, Raymond F.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                           Sequence 1
Sequence 1
Sequence 1
                                                                         Sequence 1
Sequence 8
Sequence 8
Sequence 8
Sequence 1
Sequence 1
Sequence 2
Sequence 2
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MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPBRATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: 21-UUL-1994
CLASSIFICATION NOFMER: 24.973
FILING DATE: 21-UUL-1994
CLASSIFICATION NOWBER: 24.973
REFERENCE STEWART: MICHAEL 1038-371
TELEPHONE: (416) 595-1153
INFORMATION POR RED ID NO: 9:
SEQUENCE CHARACTERISTICS:
TENCTH: 223 amino acids
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVGGYTCGANTVPYQVSLNS 20
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-278-091-9
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Best Local Similarity 100.0
  CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
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Sequence 11, Appli
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Seguence 9, Appli
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                                                                     February 12, 2003, 10:18:40 ; Search time 4.29851 Seconds
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Sequence 36,
Sequence 13,
Sequence 5,
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Sequence 9,
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Sequence
Sequence
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Sequence 7
Sequence 7
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-487-167-9
US-08-487-167-9
US-08-487-167-9
US-08-487-167-9
US-08-487-167-9
US-08-615-271-9
US-09-074-660-9
US-09-074-660-9
US-09-106-468-9
US-08-944-483-36
US-08-96-219-13
US-08-978-4183-36
US-08-978-418-44
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Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
                                                                                                            US-10-036-371-2
107
1 IVGGYTCGANTVPYQVSLNS 20
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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                                                                                                                                   Sequence:
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Analog of Haemophilue Hin47 Protein with
Reduced Protease Activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: EV-DUS/MS-LUCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,173
FILING DATE: 07-JUN-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: US 08/278,091
FILING DATE: 26-AUG-1994
ATTONNEY/AGENT IMPORMATION:
APPLICATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REFRENCE/POCKET NUMBER: 24,973
TELEPRANTION OF SEQ 1D NO: 9:
SEQUENCE CHARACTERISTICS:
LENTH: 223 anino acids
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100.0%; Pred. No. 1.5e-08;
tive 0; Mismatches 0;
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NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBURNEY
                                                                                                             B: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                      STREET: Suite 701, 330 University
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUT
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Best Local Similarity 100.0%;
Matches 20; Conservative
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-472-173-9
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                                                                                                                                                                                                                                                          APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: COMEN, Raymond P.
APPLICANT: MAIN, MICHEL H.
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: FORDAY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: FORDAY disk
COMPUTER: EBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARCENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,859
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/296,149
FILING DATE: 26-AUG-1994
APPLICATION NUMBER: US/08/296,149
FILING DATE: 21-JUL-1994
APPLICATION NUMBER: 24,973
REPERBNUEY/AGENT INFORMATION:
AMME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DATION INFORMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 9:
REQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 107; DB 1;
100.0%; Pred. No. 1.5e-08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/08472173;
Patent No. 5665353;
GENERAL INFORMATION:
APPLICANT: LOCSWORE, Sheena M
APPLICANT: YANG, Yan-Ping;
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Raymond P.;
APPLICANT: COMEN, Raymond P.;
TITLE OF INVENTION: Analog of Haem
                                                                                                                                                                       Sequence 9, Application US/08483859
Patent No. 5656436
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IVGGYTCGANTVPYQVSLNS 20
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       1 IVGGYTCGANTVPYQVSLNS 20
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US-08-472-173-9
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US-08-483-859-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-296-149-9
) Sequence 9, Application US/08296149
) Sequence 9, Application US/08296149
) GENERAL INFORMATION:
APPLICANT: LOCSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Raymond P.
APPLICANT: KLEIN, MACHAEL H.

TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDERS DARRESS: 23
CORRESPONDERS ADDRESS: 23
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                                                                                                                                                                                                                                                     100.0%; Score 107; DB 2; Length 223; 100.0%; Pred. No. 1.5e-08; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: OHIGHNO
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 107; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Scewart, Michael 1
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-390
TELECOMMUNICATION:
                  (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                   1 IVGGYTCGANTVPYQVSLNS 20
                                                                                                                                                                                                                                                                                                                                                                                                1 IVGGYTCGANTVPYQVSLNS 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IVGGYTCGANTVPYQVSLNS 20
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                                                                                                        LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
             TELEPHONE: (416) 595-115
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                    TOPOLOGY: linear 82-816-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sim
STREET: Suite
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                         US-08-482-816-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-296-149-9
                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: LOCSMORE,
APPLICANT: CANG, Van-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CANGN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease Act
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 107; DB 2; Length 223; Best Local Similarity 100.0%; Pred. No. 1.5e-08; Matches 20; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Suite 701, 330 University Avenue
CITY: Toronto
CITY: Toronto
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.25
CURBRYT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,816
FILING DATE: O7-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
FILING DATE: 26-AUG-1994
FILING DATE: 21-UUL-1994
                                       APPLICATION NUMBER: US/08/487,167
CLASSIFICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26.AUG-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21.JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: SCEWART, MICHAELI I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-508 MIS:VG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
STANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REPERENCE/DOCKET NUMBER: 1038-494 MIS:vg
TELECOMMUNICATION INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,167
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-482-816-9; Sequence 9, Application US/08482816; Patent No. 5935573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IVGGYTCGANTVPYQVSLNS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-487-167-9
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APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: VANG, Yan-Ping
APPLICANT: VANG, Yan-Ping
APPLICANT: MICHAL H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Accided Protease Activity
NUMBER OF SEQUENCES: 23
CARRESPONDENCE ADDRESS:
CONTRY: Canada
ZIP: M5G 1R7
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/074,660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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                             STREET: 6th Floor, 330 Universely
CITY: Toronto
CITY: Toronto
CITY: Toronto
CITY: Canada
ZIP: M50 LR7
COMPUTRY: Canada
ZIP: M50 LR7
COMPUTRY: TBM PC Compatible
COMPUTER: Ploppy disk
COMPUTER: PERDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PERCHIN PC-DOS/MS-DOS
SOFTWARE: PRECHIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,271
FILING DATE: 20-UN-196
CLASSIFICATION: 514
ATTORNEY/ACGNT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 1038-580
TELEFORMINICATION INFORMATION:
TELEPHONE: (416) 595-1163
TELEFORMINICATION INFORMATION:
TELEPHONE: (416) 595-1163
TELEFORMINICATION INFORMATION:
TELEFRA: 23 amino acid
STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 107; DB 2;
Pred. No. 1.5e-08;
                          B: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,167
FILING DATE: 07-UNN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-074-660-9; Sequence 9, Application US/09074660; Patent No. 6020183
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Best Local Similarity 100.0%;
Matches 20; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IVGGYTCGANTVPYQVSLNS 20
CORRESPONDENCE ADDRESS:
                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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                                                                     GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: LOOSMORE, Sheena M
APPLICANT: ANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease Act
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08615271

Sequence 9, Application US/08615271

Sequence 9, Application US/08615271

Sequence 9, Application

Patent No. 5981503

APPLICANT: LOOSMORE, Sheena M.

APPLICANT: CHONG, Yan-Ping

APPLICANT: CHONG, Raymond P.

APPLICANT: CHONG, Raymond P.

TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED

TITLE OF INVENTION: PROTEASE ACTIVITY

NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 223; 1.5e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/801,499 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 07-UNA-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA: 18 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA: 1994
ATONNEN'AGART INFORMATION:
FILING DATE: 21-JUL-1994
ATONNEN'AGART INFORMATION:
FEGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 1038-671 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LELEPAX: 416) 595-1163
TTELEPAX: 416) 595-1163
TTYPE: amino acid
TTYPE: amino acid
TTYPE: amino acid
TTYPE: amino acid
                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sim & McBurney
STREET: 6th Ploor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 107; 100.0%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                   STATE: Ontario
COUNTRY: Canada
ZIP. MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                     Sequence 9, Application US/08801499
Patent No. 5962430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IVGGYTCGANTVPYQVSLNS 20
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Best Local Similarity 100.
Matches 20; Conservative
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US-08-801-499-9
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sim & McBurney
STREET: 6th Ploor, 330 University Avenue
CITY: Toronto
STATE: Ontario
CCUNTRY: Canada
ZIP: MSG 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/615,271
FILING DATE: 20-UNN-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 9, Application US/09106468; Patent No. 6114125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IVGGYTCGANTVPYQVSLNS 20
         TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 223 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                1 IVGGYTCGANTVPYQVSLNS 20
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TYPE: amino acid
STRANDEDNESS: single
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US-09-106-468-9
                                                                                                                                            TOPOLOGY: linear
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US-09-106-468-9
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APPLICANT: LOSSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 107; DB 3; Length 223;
Pred. No. 1.5e-08;
; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/09/074,659
FILING DATE: US/09/074,659
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NOMBER: US 08/487,167
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NOMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NOMBER: US 08/296,149
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INPORMATION:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWARC, MICHARD I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
RELEPAN: (416) 595-1163
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
STRANDEDRESS: single
STRANDEDRESS: single
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-730 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09074659
Patent No. 6025342
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Best Local Similarity 100.0%;
Matches 20; Conservative 0;
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CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG INT
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCB
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APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: GHONG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: RALGO OF HAEMOPHILUS HIN47 WITH REDUCED
TITLE OF INVENTION: PROTEASE ACTIVITY
NUMBER OF SEQUENCES: 23
AND APPLICANT: ADDRESS:
Ouery Match 100.0%; Score 107; DB 3; Length 223; Best Local Similarity 100.0%; Pred. No. 1.5e-08; Matches 20; Conservative 0; Mismatches 0; Indels 0
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Sequence 2, Application US/09120582
Patent No. 6087558
FACENT INFORMATION:
APPLICANT: Howard, John A.
APPLICANT: Hood, Elizabeth
TITLE OF INVENTION: COMMERCIAL PRODUCTION OF PROTEASES IN PLANTS
FILE REFERENCE: 10014
CURRENT APPLICATION NUMBER: US/09/120,582
CURRENT FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                  STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1FF
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 107; DB 3;
100.0%; Pred. No. 1.5e-09;
ive 0; Mismatches 0;
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100.0%; Pred. No. 1.5e-08;
iive 0; Mismatches 0;
                       6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/615,271
FILING DATE: 20-JUN-1996
CLASSIFICATION:
ATTORNEY/AGENT INORWATION:
NAME: Stewart, Michael I
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-824
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IVGGYTCGANTVPYQVSLNS 20
Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQ ID NO 2
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-120-582-2
                     STREET: 6th ri
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-120-582-2
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                                                            Sequence 9, Application US/09106466A
| Sequence 9, Application US/09106466A
| Sequence 9, Application US/09106466A
| Patent No. 6147057
| GENERAL INFORMATION:
| APPLICANT: LOCKORE Sheena M. APPLICANT: CONG. Nan-Ping APPLICANT: CONG. Nan-Ping APPLICANT: CONG. Nan-Ping APPLICANT: CONG. Nan-Ping APPLICANT: CALAN: NALOG OF HAEMOPHILUS HIN47 WITH REDUCED INTERTION: PROTESEE ACTIVITY
| WINDERS OF SEQUENCES: 23 CONGRESPORDENCE ADDRESS: 23 CONGRESPORDENCE ADDRESS: 24 CONGRESSE: Sim & MCBHICAN: CALAGA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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100.0%; Score 107; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IVGGYTCGANTVPYQVSLNS 20
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TOPOLOGY:
US-09-106-466A-9
                                                  RESULT 12
US-09-106-466A-9
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7 IVGGYTCGANTVPYQVSLNS 26

RESULT 15 US-08-956-267A-2

1 IVGGYTCGANTVPYQVSLNS 20

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Sequence 2, Application US/08956267A
Parent No.539104.
GARRAN. INCOMATION:
GARRAN. INCOMATION:
TITLE OF INVESTIGNED. Thomas Brogium
TITLE OF INVESTIGNED. Thomas Brogium
TITLE OF INVESTIGNED.
CORRESSORES.
CARRESSORES.
ADDRESSER.
ADD
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Sequence 14, Application US/09910071
Sequence 14, Application US/09910071
Sequence 10. US20202016146A1
GENERAL INFORMATION:
APPLICANT: Tomikawa, Mayumi
APPLICANT: Aikawa, Seiichi
APPLICANT: Aikawa, Seiichi
APPLICANT: Mayumi Macusawa, Fumiko
TITLE OF INVENTION: Mechod and Apparatus for Extracting and Evaluating Mutually Simil,
TITLE OF INVENTION: Portions in One-Dimensional Sequences in Molecules and/or Three-I
                                                                                                                                                                                                                                                           RESULT 1
US-10-036-371-2
US-10-036-371-2
Sequence 2, Application US/10036371
Parent No. US20020141987A1
GENERAL INFORMATION:
1 IVGGYTCGANTVPYQVSLNS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IVGGYTCGANTVPYQVSLNS
; ORGANISM: Bovine sp.
US-10-036-371-2
US-09-910-071-14
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Appl Sequence 15, Appl Sequence 7, Appl Sequence 9, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 15, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 5, Appl Sequence 5, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appli Sequence 2, Appli
                                                                 (without alignments)
167.821 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                        February 12, 2003, 10:22:36; Search time 3.04478 Seconds
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14: /cgn2_6/ptodata/1/pubpaa/USOF_PUBCOMB.pep:*
      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                 140259 seqs, 25548876 residues
                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
                                                                                                         1 IVGGYTCGANTVPYQVSLNS 20
                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                        US-10-036-371-2
107
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                                                                                        Title:
Perfect score:
                                                                                                                        Scoring table:
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Sequence 10, Appl Sequence 11, Appl Sequence 1, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 617, Appl Sequence 617, Appl Sequence 617, Appl Sequence 617, Appl Sequence 978, Appl Sequence 978, Appl Sequence 978, Appl Sequence 978, Appl Sequence 947, Appl Sequence 11, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BJARNARGON, JON B.
TITLE OF INVENTION: FISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND TITLE OF INVENTION: COSMETIC USE FILE OF INVENTION: COSMETIC USE FILE REFERENCE: 81691/28460 CURRENT APPLICATION NUMBER: US/10/036,371 CURRENT FILING DATE: 2002-01-07 PRIOR APPLICATION NUMBER: 09/411,689 PRIOR PLICATION NUMBER: 5086/99 PRIOR PLICATION NUMBER: 5086/99 PRIOR FILING DATE: 1999-06-18 SOFTWARE: PARCHING NOS: 8 SOFTWARE: PARCHING NOS: 8
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US-09-864-761-33875
US-10-067-761-19
US-09-796-294-10

US-09-96.3 89-66

US-09-907-402-1

US-09-907-402-1

US-09-907-402-1

US-09-925-297-7-45

US-09-925-297-7-45

US-09-925-297-7-45

US-09-895-793-617

US-09-895-793-617

US-09-895-814-617

US-09-895-814-617

US-09-895-814-617

US-09-895-793-998

US-09-895-793-998

US-09-822-827-978

US-09-895-793-982

US-09-895-793-982

US-09-895-793-982

US-09-895-793-947

US-09-895-793-947

US-09-895-793-947

US-09-895-793-947
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STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 281 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                             Query Match 91.6%; Score 98; DB 10; Length 223; Best Local Similarity 95.0%; Pred. No. 1.6e-07; Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pyle, Ruth A.
APPLICANT: Yele, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Xalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT PILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.5%; Score 84; DB 10; Length 24
80.0%; Pred. No. 2.2e-05;
tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: amino acid sequence of trypsin
US-09-910-071-14
Structures of Molecules
             FILE REFERENCE: 522.192102
CURRENT APPLICATION NUMBER: US/09/910,071
CURRENT FILING DATE: 2001-07-23
FRIOR APPLICATION NUMBER: US 08/014,867
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn vergion 3.1
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENČE ADDRESS:
ADDRESSEE: Fish & Richardso
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 154, Application US/09923779; Patent No. US20020076721A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/10021368
Patent No. US200201016367A1
GENERAL INFORMATION:
APPLICANT: Band, Vimla
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IVGGYTCGANTVPYQVSLNS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IVGGYTCCANTVPYOVSLNS 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.5
Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-923-779-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
TITLE OF INVENTION:
                                                                                                                                                                                                           TYPE: PRT
ORGANISM: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-09-923-779-154
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LENGTH: 247
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US-10-021-368-7
                                                                                                                                                                                                                                                            FEATURE:
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Gaps
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US-10-021-368-9
US-10-021-368-9; Sequence 9, Application US/10021368
; Patent No. US2002010567A1
; GENERAL INFORMATION:
; APPLICANT: Band, Vimla
; TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 281;
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COUNTRY: USA

ZIP: 0210-2804

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/021,368

FILING DATE: 12-Dec-2001

CLASSIFICATION: CURNOWN>
PRIOR APPLICATION CURNOWN>
PRIOR APPLICATION NUMBER: 09/201,038

FILING DATE: CURNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, Paul T
REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 30,162

TELECOMMUNICATION INFORMATION:
TELEFAK: 617/542-5070
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/021,368
FILING DATE: 12-Dec-2001
CLASSIFCATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/201,038
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T
REGISTATION NUMBER: 30,162
REGISTATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/100002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1816 & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-10-021-368-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IVGGY-----TCGANTVPYQVSLNS 20
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1 IVGGY-----TCGANTVPYQVSLNS 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 299 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/10036371; Patent No. US20020141987A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                    1 IVGGYTCGANTVPYQVSLNS 20
                                                   1 IVGGYQCEAHSQAHQVSLNS 20
                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.6%; Score 67; DB 9; Length 25; 70.0%; Pred. No. 0.00067; Live 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-00-938-269-17
US-00-938-269-17
Sequence 17, Application US/09938269
Publication No. US20030007951A1
GENERAL INFORMATION:
APPLICANT: Franklin, Richard L.
APPLICANT: Cowling, Didier S.P.
APPLICANT: Hubbel, Jeffrey A.
APPLICANT: Hubbel, Jeffrey A.
APPLICANT: Hubbel, Jeffrey A.
APPLICANT: Hubbel, Jeffrey A.
CURRENT FILING PRETAINON Treatment of Trauma
FILIE REFERENCE: 314572-105
CURRENT APPLICATION NUMBER: US/09/938, 269
CURRENT FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-938-269-14

Sequence 14, Application US/09938269

Publication No. US20030007951A1

GENERAL INFORMATION:
APPLICANT: Franklin Richard L.
APPLICANT: Cowling, Didier S.P.
APPLICANT: Hubbel, Jeffrey A.
ANTHE OF INVENTION: Treatment of Trauma FILLE REFERENCE: 314572-105
CURRENT APPLICATION NUMBER: US/09/938, 269
CURRENT FILING DATE: 2001-08-23

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 14

SEQ ID NO 14

MENTH: 25

MENTH: 25

MENTH: 25
                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                   25 IVGGYRNTRYPVBTCQEHSVPYQVSLNA 52
                                                                                                                                                                                                                                                                                                                                      1 IVGGY-----TCGANTVPYQVSLNS 20
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHRACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IVGGYECKAYSQAYQVSLNS 20
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Best Local Similarity 70.09
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT; ORGANISM: Salmon enzyme
US-09-938-269-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Atlantic cod US-09-938-269-17
                                                                                                                                                                                          US-10-021-368-9
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TITLE OF INVENTION: FISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND TITLE OF INVENTION: COSMETIC USE
FILE REPERENCE: 81691/284901
CURRENT APPLICATION NUMBER: US/310/036,371
CURRENT PILING DATE: 200-01-07
PROR APPLICATION NUMBER: 09/411,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Facetic 8, Application US/10021368

| Sequence 8, Application US/10021368
| Patent No. US20020106367A1
| GENERAL INFORMATION:
| APPLICANT: Band, Vimla | POLYPEPTIDES, DNA, AND RELATED |
| TITLE OF INVENTION: NBS-1 POLYPEPTIDES, DNA, AND RELATED |
| NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESSE: 11 CORRESPONDENCE ADDRESSE: Fish & Richardson P.C. |
| STREET: 222 Franklin Street |
                                                                                                                                                                                                                                                                                                                                                                  COMPUTRY: USA
ZIP: 02110-2804

ZIP: 02110-2804:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NAMBRE: US/10/021,368
FILING DATE: 12-Dec-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 00398/100002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ), MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ 1D NO: 8:
US-10-021-368-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/201,038
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Query Match 57.0%; Score 61; DB 12; Length 225; Best Local Similarity 60.0%; Pred. No. 0.05; Matches 12; Conservative 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-318-269-15
Squence 15, Application US/09938269
Publication No. US20030007951A1
GENERAL INPORMATION:
APPLICANT: Franklin, Richard L.
APPLICANT: Cowling, Didier S.P.
APPLICANT: Hubbel, Jeffrey A.
TITLE OF INVENTION: Treatment of Trauma
FILE REFERENCE: 314572-105
CURRENT PEDLICATION NUMBER: US/09/938,269
CURRENT FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 17
SGOTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 25
LENGTH: 25
                                                                       OTHER INFORMATION: I or unknown FEATURE: NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
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OTHER INFORMATION: M, V or C FEATURE:
NAME/KEY: MOD_RES
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NAME/KEY: MOD RES
LOCATION: (204)
OTHER INFORMATION: H OF N
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Best Local Similarity 60.01
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD RES
LOCATION: (136)
OTHER INFORMATION: V or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (224)
; OTHER INFORMATION: N OF S
US-10-036-371-8
                                                                                                                                   LOCATION: (82)
OTHER INFORMATION: N OF
                                                                                                                                                                                                                     LOCATION: (92)
OTHER INFORMATION: K or
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ORGANISM: Atlantic cod
US-09-938-269-15
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LOCATION: (129)
OTHER INFORMATION: A
                                                                                                                                                                                               NAME/KEY: MOD RES
LOCATION: (92)
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LOCATION: (138)
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LOCATION: (212)
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| Patent No. US20020141987A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: PISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND TITLE OF INVENTION: POSMETIC USE
| PRIOR APPLICATION NUMBER: US/10/07
| PRIOR APPLICATION NUMBER: 09/411,688
| PRIOR FILING DATE: 1999-10-12
| PRIOR FILING DATE: 1999-06-18
| NUMBER: OS SEQ ID NOS: 8
| SOFTWARE: PATENTIN VET: 2.1
| SEQ ID NO 8
| LENGTH: 2.25
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PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION WUMBER: 5086/99
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IVGGYTCGANTVPYQVSLNS 20
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NAME/KEY: MOD RES
LOCATION: (32)
OTHER INFORMATION: K or E
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD_RES

LOCATION: (9)

OTHER INFORMATION: K or R

US-10-036-371-1
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LOCATION: (33)
OTHER INFORMATION: D or Q
                                                                                                                                                                                                        NAME/KEY: MOD_RES
LOCATION: (6)
OTHER INFORMATION: Q or
                                                                                                                                                                                                                                                                                                           LOCATION: (8) OTHER INFORMATION: B or
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LOCATION: (24)
OTHER INFORMATION: Y or
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LOCATION: (64)
OTHER INFORMATION: Y or
                                                                                                                                            TYPE: PRT
ORGANISM: Gadus sp.
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ORGANISM: Gadus sp
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NAME/KEY: MOD_RES
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NAME/KEY: MOD_RES
LOCATION: (9)
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APPLICANT: Craig Rosen; APPLICANT: Steve Ruben; TITLE OF INVENTION: Nacleic Acids, Proteins and Antibodies; FILE REPRENCE: PAIO1
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT APPLICATION NUMBER: CPC/US00/05988
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR PILING DATE: 1090-03-10
PRIOR PILING DATE: 1099-03-12
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 1093
LENGHIA: 235
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46.7%; Score 50; DB 10; Length 1128;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 9; Conservative 4; Mismatches 5; Indels (
                                                                                                                                                            / Match S4.2%; Score 58; DB 12; Length 271; Local Similarity 50.0%; Pred. No. 0.17; les 14; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 97, Application US/0988615
Patent No. US2002064856A1
GENERAL INFORMATION:
APPLICANT: PLOWNAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CARREPEL, SEAN
APPLICANT: CARREPEL, SEAN
APPLICANT: MANNING, GERARD
APPLICANT: WANNING, GERARD
APPLICANT: SUDARSAMA, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038662/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT APPLICATION NUMBER: 05.26
NUMBER OF SEQ ID NOS: 150
SEQ ID NO 97
LENGTH: 1128
LENGTH: 1128
LENGTH: 1128
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                10 IVGGYSSTRYPIIECKAYSQPHQVSLNS 37
                                                                                                                                                                                                                                                              1 IVGGYT-----CGANTVPYQVSLNS 20
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US-09-888-615-97
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US-09-925-300-1093
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US-09-925-300-1093
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US-10-021-368-10
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US-09-888-615-97
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Patent No. US20020106367A1
GENERAL INFORMATION:
APPLICANT: Band, Vimla
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: WA

COUNTRY: USA

ZID: 02110-2804

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/10/021,368

FILING DATE: 12-Dec-2001

CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 56.1%; Score 60; DB 9; Length 25; Best Local Similarity 60.0%; Pred. No. 0.0073; Matches 12; Conservative 3; Mismatches 5; Indels
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REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/100002
TELECHANICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8006
                                                                                          US-09-938-269-16
US-09-938-269-16
Sequence 16, Application US/09938269
Publication No. US20030007951A1
GENERAL INFORMATION:
APPLICANT: Franklin, Richard L.
APPLICANT: Cowling, Didier S.P.
APPLICANT: van de Wetering, Petra
TITLE OP INVENTION: Treatment of Trauma
FILE REFERENCE: 314572-105
CURRENT APPLICATION NUMBER: US/09/938,269
CURRENT FILING DATE: 2011-08-23
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 16
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION UNBER: 09/201,038
FILING DATE: «URKnown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 271 amino acids
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INFORMATION FOR SEQ ID NO: 10:
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       1 IVGGYECTKHSQAHQVSLNS 20
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US-09-938-269-16
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US-10-021-368-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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ö 0; Gaps Query Match 45.8%; Score 49; DB 10; Length 235; Best Local Similarity 45.0%; Pred. No. 3.1; Matches 9; Conservative 6; Mismatches 5; Indels

1 IVGGYTCGANTVPYQVSLNS 20 |||||| : |:||||| | 87 IVGGWECERHSQPWQVAVYS 106 8 &

Search completed: February 12, 2003, 10:31:04 Job time : 4.04478 secs

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Human PRO243
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AAB01312
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AAY50212
AAY64742
ABP03011
AAU61671
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AAE03738
AAY01711
AAU81956
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AAE03736
AAU75168
AAW48978
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AAG60976
 AAR12936
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ABP09202
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Misc-difference 3
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     (first entry)
   Misc-difference
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| SIDSZ/gcgdata/geneseq/geneseqp_embl/AA1980.DAT:*
| SIDSZ/gcgdata/geneseq/geneseqp_embl/AA1981.DAT:*
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                  GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100*
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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The specification describes a fish serine proteinase. The proteinases are useful as medicaments, for treating and preventing a disease in a human or an animal such as pain, acute inflammation, chronic think and inflamed joints, bursitis, ostcoarthritis, checoarthritis, inflamed joints, bursitis, septic arthritis, cheumatoid arthritis, septic arthritis, rheumatoid arthritis, septic arthritis, rheumatoid arthritis, septic arthritis, consorvantalis, acne, eczema, facial sebornaic eczema of the hands, face or neck, foreskin infections, athlete's foot, fistulae infections, infections, arthlete's foot, fistulae infections, infections, wrinkles, scars, chelloids, boils, warts and allergic itch, hemorrhoids, wounds to infections, wounds from burns, fungal infections and immunological and autoimmune diseases. They are also useful for removing dead or peeling skin from otherwise healthy skin, and for treating or preventing a disease in which pathogenesis is caused by bacteria, virus, fungus, parasite or a protozoan or a receptor mediated binding is involved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell activation; pancreas; treatment; cardiovascular disease; trauma; inflammatory disease; autoimmune disease; arthritis; diabetes; stroke; organ reflection; ischemia; Alzheimer's disease; myocardial infarction; haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina; trauma; protease inhibitor; hypertension; sepsis.
                                                                                                                                                                                                     Fish serine proteinase, useful as a cosmetic, medicament for treating eczema, psoriaais, arthritis, and in the manufacture of the medicament for treating, preventing pathogenic diseases involving receptor mediated binding
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                                                                                                                                                                                                                                                                                       Disclosure, Page 5; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY50209 standard; Peptide; 13 AA
                                 15-JUN-2000; 2000WO-IS00005
                                                                   991S-0005086
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Beet Local Similarity 100...
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                                                                                                   (BJAR/) BJARNASON J B.
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                                                                                                                                                                     WPI; 2001-091493/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 AA;
                                                                                                                                     Bjarnason JB;
                                                                   18-JUN-1999;
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28-DEC-2000.
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This invaling compositions which involves preparing a cell activating composition compositions which involves preparing a cell activating composition compositions which involves preparing a cell activating composition compositions which involves because to be removal composition compositions with particulates removed, with a protease; and compositions that carticulates from the homogenate and selecting fractions that exhibit complication activaty. The methods can be used for improving traction activity. The methods can be used for improving congan rejection, diabetes and diabetic complications atrock, ischemia, congan rejection, diabetes and diabetic complications; atrock, ischemia, congan rejection, diabetes and diabetic complications; atrock, ischemia, altabetment of a non-human subject.

Conference in the veterinary treatment of a non-human subject.

Conference diseases and deficiencies. The detection of an elevated level of these diseases and deficiencies. The detection of an elevated level of presence of superoxide dismutase (SOD) indicates leukocyte up completion, e.g. indicative of the onset of an acute cardiovascular confiscence of superoxide dismutase (SOD) indicates leukocyte up condition, a disorders, such as disease onset of implant or immune compromised condition e.g. hypertenation of an planma or whole blood and a low level in the presence of SOD is indicative of a chronic or immune compromised condition e.g. hypertenation or sepals. ANYSOZOI-YSO334 represent peptides
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                                                                                                                                                                                                                                                                                                                                    This invention describes a novel method for the use and preparation of
                                                                                                                                                                                                           diagnosis and treatment of e.g. cardiovascular, inflammatory, autoimmune or Alzheimer's disease, trauma, arthritis, organ rejection,
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                                                                                                      Kistler
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                                                                                                                                                                                   cell activating compositions in developing
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                                                                                                      Hugli TE,
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58.3%; Pred. No. 1;
                                                                                                    Schmid-Schonbein GW,
                                                                                                                                                                                                                                                                                            Example 9; Page 182; 184pp; English.
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                                                                                                                                                                                                                                                   diabetes, stroke or ischemia
                 (CELL-) CELL ACTIVATION INC.
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                                     (REGC ) UNIV CALIFORNIA. (SCRI ) SCRIPPS RES INST.
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                                                                                                    Stoughton RB,
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                                                                                                                                                                                     Use of
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11-MAR-1999;
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The specification describes a fish serine proteinase. The proteinases are useful as medicaments, for treating and preventing a disease in a human or an animal such as pain, acute inflammation, chronic inflammation, arthritis, inflammation, bursitis, observativis, chemical arthritis, protein arthritis, protein arthritis, protein arthritis, repeint arthritis, repeint arthritis, septic arthritis, repeint arthritis, acon, eczema, facial sebortheic eczema, eczema of the hands. Consort foreskin infections, athlete's foot, fistules infections, infected topical ulcers, navel infections in newborns, wrinkles, scars, confections, boils, warts and allergic itch, hemorrhoids, wounds, wound from burns, fungal infections and immunological and autoimmune diseases. They are also useful for removing dead or peeling skin from otherwise healthy skin, and for treating or preventing a disease in which pathogenesis is caused by bacteria, virus, fungus, parasite or a protozoan or a receptor mediated binding is involved. The present sequence represents the amino terminal of bovine trypsin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell activation; pancreas; treatment; cardiovascular disease; trauma; inflammatory disease; autoimmune diseases; arthritis; diabètes; stroke; organ rejection; ischemia; Alzheimer; disease; myocardial infarction; haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina; trauma; protease inhibitor; hypertension; sepsis.
                                                                                                                                                                                           Fish serine proteinase, useful as a cosmetic, medicament for treating eccema, psoriaasis, arthritis, and in the manufacture of the medicament for treating, preventing pathogenic diseases involving receptor mediated binding
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                                                                                        991S-0005086.
                                                               15-JUN-2000; 2000WO-IS00005.
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nes 7, Conservative
                                                                                                                  BJAR/) BJARNASON J B.
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                                                                                                                                                                   WPI; 2001-091493/10.
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              WO200078332-A2.
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                                                                                        18-JUN-1999;
                                                                                                                                          Bjarnason JB
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This invention describes a novel method for the use and preparation of cell activating compositions which involves preparing a cell activating cell activating composition comprising (a) homogenizing panceatic tisue in buffer at about neutral or higher ph to produce a homogenate; (b) removing particulates from the homogenate; (c) optionally incubating the about neutral or higher ph to produce a homogenate; (d) removing the homogenate and selecting fractions that exhibit complication activity. The methods can be used for improving treatment outcome or reducing risk of treatment of e.g. cardiovascular disease, inflammatory disease, trauma, autoimmune diseases, arthritis, congan rejection, diabetes and diabetic complications, stroke, ischemia, creatment of disease, myocardial infarction, unstable angina or trauma. They can be used in the veterinary treatment of a non-human subject. They can be used to lower cell activation resulting from these diseases and deficiencies. The detection of an elevated level of hydrogen peroxide in plasma or whole blood and in the creatment peroxide dismutase (SOD) indicates leukocyte up to presence of superoxide dismutase (SOD) indicates leukocyte up creatment of a none cardiovascular consultions. An elevated confittion e.g. indicative of the onset of an acute cardiovascular confittion e.g. hyperension or appass and whole blood and in the previous of the presence of SOD is indicative of an acute cardiovascular confittion e.g. hyperension or appass. Anysozol-YSO334 represent peptides condition e.g. hyperension or aspass. Anysozol-YSO334 represent peptides condition e.g. hyperension or aspass. Anysozol-YSO334 represent peptides condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Use of cell activating compositions in developing products for diagnosis and treatment of e.g. cardiovascular, inflammatory, autoimmune or Alzheimer's disease, trauma, arthritis, organ rejection.
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                                                                                                                                                                                                                                                                                       Schmid-Schonbein GW, Hugli TE, Kistler E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetes, stroke or ischemia
99WO-US05247.
                                                                   98US-0038894.
                                                                                                                                       (CELL-) CELL ACTIVATION INC. (REGC ) UNIV CALIFORNIA. (SCRI ) SCRIPPS RES INST.
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Best Local Similarity
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                                                                   11-MAR-1998;
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ABEA466. The human pancreatic cancer antigens, given in AAB54008 to
ABEA466. The human pancreatic cancer antigens have cytostatic,
controlled and pancreatic cancer antigens have cytostatic,
neuroprotective, neocropic, immunomodulatory, ralaxant, contraceptive,
gynaecological, cardiant and antiliflammatory activities, and can be used
in gene therapy. The polynucleotide and proteins can be used for
preventing, treating, or ameliorating a medical condition or in assays
for diagnosing a pathological condition or a susceptibility to one in a
subject. Binding partners to the proteins and the activity of the
proteins can be identified. The pancreatic cancer antigens can be used to
detect, treat or prevent pancreatic disorders, especially cancer.
Agonists and antagonists to the antigens can be used to design nucleic
and diagnostic methods that can be used in chromosome mapping, linkage
and diagnostic methods. The proteins can be used to design nucleic
and diagnostic methods. The proteins can be used to generate antibodies
which are used to purify, detect and target the polypeptides, including
both in vivo and in vitro diagnostic and target the polypeptides, including
brotelins can be used to treat or prevent neural, immune system, muscular,
reproductive, gastrointestinal, pulmonary, cardiovascular, remal or
proliferative disorders. AAC99210 and AAB54467 represent
sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                  New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC98773 to AAC99231 encode the human pancreatic cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 21; Length 146;
Pred. No. 11;
1; Mismatches 4; Indels
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                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
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58.3%;
                                                                                                                              08-MAR-2000; 2000WO-US05989
                                                                                                                                                                     99US-0124270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                               2000-579444/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34
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Best Local Similarity
Matches 7, Conserva
                                                                                                                                                                                                                                            Rosen CA, Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 AA;
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                                                                                                                                                                                                                                                                                                 N-PSDB; AAC98956.
                                                      WO200055320-A1
                     Homo sapiens.
                                                                                                                                                                 12-MAR-1999;
                                                                                           21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2000
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Gaps

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The present sequence is bovine chymotrypsinogen. It was included in a review of sequence homologies of several plasminogen activators. Plasminogen is the principal serine procease symogen in the extracellular fluids of vertebrates. Its active form, plasmin, is implicated in pericellular proteolysis associated with a wide range of physiological and pathological processes. Plasminogen expression is physiological and pathological processes. Plasminogen expression is physiological processes. Plasminogen expression is physiological processes. Plasminogen expression is plasminogen to convert it to plasmin or form tight binding complexes with plasminogen to spontaneously convert it to plasmin. The sequence homology analysis has identified a six amino acid peptide involved in plasminogen activation. This peptide is particularly useful when inserted between amino acid residues 644 and 645 of full length human plasminogen activation/recognition site of plasminogen binding proteins. The polypeptides are useful in preparing thrombolytic agents for treating blood clotting disorders such as heart attack.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, protease, cancer, immune-related disorder, cardiovascular disease, neuronal-associated disease, metabolic disorder; inflammatory disorder; neuronal-associated disorder, metabolic disorder; mod disorder; hypertension, psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.
                                                                                                                                                                                                                                                     Polypeptide with plasminogen activator activity useful as thrombolytic agent for treating blood clot disorders e.g. heart attack, comprises 10 amino acid peptide fragment for recognition or activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 21; Length 245;
Pred. No. 19;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of novel human protesse #37.
                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 35-36; 41pp; English.
                                                                                                                                             (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU82738 standard; Protein; 263 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.8%;
58.3%;
                                                                                                                                                                               Zhang XC, Tang JJN;
                                                                        99WO-US09991.
                                                                                                          98US-0110588.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 58.3
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGXPAIXPXXTG 12
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                                                                                                                                                                                                                   WPI; 2000-422975/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 AA;
WO200032759-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200200860-A2.
                                                                    06-MAY-1999;
                                                                                                          02-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                  08-JUN-2000.
                                                                                                                                                                                                                                                                                                               plasminogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Matches
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(CELL-) CELL ACTIVATION INC. (REGC ) UNIV CALIFORNIA. (SCRI ) SCRIPPS RES INST.
                                                                        WPI; 1999-580234/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY50210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY50210
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                                                                                                                                                                                                                   The present invention relates to the isolation of novel human proceases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. thelamatory diseases and asthma), cardiovascular diseases and disorders (e.g. restenosis and coronary thrombosis), brain or neuronal-associated disorders (e.g. theumatory thrombosis), brain or neuronal-associated disorders (e.g. theumatory and coronary thrombosis), central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, migraines, pain, sexual dysfunction, confidencion, psychotic disorders, neurobogical disorders, hypotension, psychotic disorders, neurobogical disorders, municalisated for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as coular disease (e.g. glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel human proteases of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell activation; pancreas; treatment; cardiovascular disease; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.8%; Score 40; DB 23; Length 263; 58.3%; Pred. No. 20; tive 1; Mismatches 4; Indels
                                                              Caenepeel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neutrophil-activating pancreatic derived peptide 8.
                                                              Sudarsanam S, Manning G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY50208 standard; Peptide; 15 AA
                                                                                                                                                                                                   Claim 6; Fig 2M; 313pp; English.
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                 26-JUN-2000; 2000US-214047P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 58.3
ses 7, Conservative
                                                             Plowman G, Whyte D,
Charydczak G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGXPAIXPXXTG 12
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                                                                                                  2002-139913/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 AA;
                                        (SUGE-) SUGEN INC.
                                                                                                             N-PSDB; ABK31780
                                                                                                                                                                                                                                                                                                                                                                                                                           the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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This invention describes a novel method for the use and preparation of cell activating compositions which involves preparing a cell activating composition composition comprising d in homogenizing pancratic tissue in buffer at about neutral or higher pH to preduce a homogenate; (b) removing particulates from the homogenate; (c) optionally incubating the about neutral or higher pH to preduce a homogenate; (d) removing the homogenate and selecting fractions that exhibit construction activity. The methods can be used for improving treatment outcome or reducing risk of treatment of e.g. cardiovascular clisease, inflammatory disease, trauma, autoimmune diseases, arthritis, congan rejection, diabetes and diabetic complications, stroke, ischemia, Alzheimer's disease, whouse insufficiency, unstable angina or trauma. Congan rejection, diabetes, whouse insufficiency, unstable angina or trauma. Conflex on be used in the veterinary treatment of a non-human subject. Protease inhibitors can be used to lower cell activation resulting from these diseases and deficiencies. The detection of an elevated level of hydrogen peroxide in plasma or whole blood and in the cegulation, e.g. indicative of the onset of an acute cardiovascular cegulation, e.g. indicative of the onset of an acute cardiovascular cegulation, e.g. indicative of the onset of an acute cardiovascular cegulation e.g. hyperesence of a chronic or immune compromised condition e.g. hyperesion or a chronic or immune compromised condition e.g. hyperesion or a chronic or immune compromised condition e.g. hyperesion or sepsis. ANY50201-Y50334 represent peptides
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                                                                                                                                                           Use of cell activating compositions in developing products for diagnosis and treatment of e.g. cardiovascular, inflammatory, autoimmune or Alzheimer's disease, trauma, arthritis, organ rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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    Kistler E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
Stoughton RB, Schmid-Schonbein GW, Hugli TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                       Example 9; Page 182; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAYS0210 standard; Peptide; 15 AA
                                                                                                                                                                                                                                                                                            diabetes, stroke or ischemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.1%;
58.3%;
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Best Local Similarity 58.3
"ham 7; Conservative
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WO9109118-A.

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           This protein is a plasminogen mutant cleavable by thrombin. Activation is localised to the thrombus because cleavage to plasmin is by an enzyme of the blood clotting pathway. Compositions comprising the mutant plasminogen are used for treatment or prevention of thrombosis, etc.
                                                                                                                                                                                                                                                                                                                  Activatable fibrinolytic and antithrombic proteins - activated by e.g. factor Xa, thrombin or activated protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activatable fibrinolytic and antithrombic proteins - activated by e.g. factor Xa_{\rm s} , thrombin or activated protein C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39, DB 12; Length 811;
Pred. No. 92;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasminogen mutein X5 with factor Xa cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protease; fibrinolysis; blood clotting; thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
578..583
/label= Factor Xa cleavage site
                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                     Forman JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dawson KM, Edwards RM, Forman JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR12936 standard, Protein, 813 AA
                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Fig 2 and Fig 5; 73pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.1%;
46.2%;
                                                                                                                                      90WO-GB01911.
                                                                                                                 89GB-0027722.
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                                                                                                                                                                         (BRBI-) BRIT BIO-TECHN LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                   Edwards RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
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Best Local Similarity
Local 6; Conserv?
                                                                                                                                                                                                                                                        WPI; 1991-208145/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                See AAQ12542-Q12558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        811 AA;
                                                                                                                                                                                                                                                                             N-PSDB; AAQ12553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ12545
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                                                                        07-DEC-1990;
                                                                                                                                      07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-1990;
                                                                                                                 07-DEC-1989;
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                                     27-JUN-1991
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                                                                                                                                                                                                                 Dawson KM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel method for the use and preparation of cell activating compositions which involves preparing a cell activating compositions which involves preparing a cell activating composition composition (a) homogenizing pancreatic tissue in buffer at about neutral or higher pH to produce a homogenate; (b) removing cabout neutral or higher pH to produce a homogenate; (b) removing the forticulates from the homogenate; (c) optionally incubating the creating the protease; and cell activation activity. The methods can be used for improving treatment outcome or reducing risk of treatment of e.g. cardiovascular congans rejection, diabetes and diabetic complications, stroke, ischemia, altahemer's disease, inflammatory disease, trauma, autoimmune diseases, attritis, organ rejection, diabetes and diabetic complications, stroke, ischemia, altahemer's disease, annowable infarction, hemorrhagic shock, diabetic retinopathy, diabetes, venous insufficiency, unstable angina or trauma. They can be used in the veterinary treatment of a non-human subject. They can be used in the veterinary treatment of an on-human subject. They can be used to lower cell activation resulting from these diseases and deficiencies. The detection of an elevated level of hydrogen peroxide in plasma or whole blood and in the presence of superoxide diamutase (SOD) indicates leukocyte up regulation, e.g. indicative of the onset of an acute cardiovascular disorders, such as disease onset or ischemic complications. An elevated clevel of hydrogen peroxide in plasma or whole blood and a low level in the presence of SOD is indicative of a chronic or immune compromised condition e.g. hypertension or sepsie. ANYSO201-YSO334 represent peptides used in the method of the invention or sepsie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                              Use of cell activating compositions in developing products for diagnosis and treatment of e.g. cardiovascular, inflammatory, autoimmune or Alzheimer's disease, trauma, arthritis, organ rejection,
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                                                                                                                                                                       Kistler E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 20; Length 15;
Pred. No. 1.8;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasminogen mutein T14 with thrombin cleavage site.
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                                                                                                                                                                       Schmid-Schonbein GW, Hugli TE,
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579..583
/note= "recognised by
                                                                                                                                                                                                                                                                                                                                               Example 9; Page 182; 184pp; English.
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                                                                                                                                                                                                                                                                                                            diabetes, stroke or ischemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.1%;
58.3%;
            99WO-US05247.
                                               98US-0038894.
                                                                                      ACTIVATION INC
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                                                                                                       (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                          WPI; 1999-580234/49.
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es 7; Conserva
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                                                                                                                                                                   Stoughton RB,
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Cleavage-site
          11-MAR-1999;
                                               11-MAR-1998;
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Sequence

Query Match Best Loca Matches

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AAR12944;

AAR1294.
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IID A

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X 8 X C C C C C C X 8 8

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Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 10242.
                                                                                                                                                                                                                                                                                                                                    Myers EW;
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                                                       ABB61150 standard; Protein; 626
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                                                                                                                                                                                                                                                                                                                                    Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.48;
                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US09231.
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                                                                                                     (first entry)
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les 5; Conservative
                                                                                                                                                                                  Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       626 AA;
567 CGKPQVEPKKCGY
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                                                                                                                                                                                                        WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                  interactions
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                                                                                                   26-MAR-2002
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Best Local S
Matches 5
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                                                                              ABB61150;
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                                RESULT 13
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                               This protein is a plasminogen mutant cleavable by Factor Xa. Activation is localised to the thrombus because cleavage to plasmin is by an enzyme of the blood clotting pathway. Compositions comprising the mutant plasminogen are used for treatment or prevention of thrombosis, etc.

See AAQ12542-Q12558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Activatable fibrinolytic and antithrombic proteins - activated by e.g. factor Xa, thrombin or activated protein C
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See AAQ12542-012558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.1%; Score 39; DB 12; Length 813; 46.2%; Pred. No. 92; ative 1; Mismatches 6; Indels
                                                                                                                                   Score 39; DB 12; Length 813;
Pred. No. 92;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                        Plasminogen mutein X6 with factor Xa cleavage site.
                                                                                                                                                                                                                                                                                                                                                            protease; fibrinolysis; blood clotting; thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
578..583
/label= Factor Xa cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Fig 2 and Fig 4; 73pp; English
            Claim 7; Fig 2 and Fig 4; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Forman JM;
                                                                                                                                                                                                                                                                    AAR12937 standard; Protein; 813 AA
                                                                                                                                     66.1%;
nilarity 46.2%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89GB-0027722
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Best Local Similarity 46.23
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dawson KM, Edwards RM,
                                                                                                                                                                                                           S67 CGKPQVEPKKCGY 579
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N-PSDB; AAQ12546.
                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                  813 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Cleavage-site
                                                                                                                                                                                                                                                                                                                 23-SEP-1991
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New isolated nucleic acid detection reagent for detecting 1003 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA (ABBS7737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                  Disclosure; SEQ ID NO 10242; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 22; Length 626;
Pred. No. 1.16+02;
3; Mismatches 4; Indels
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a cones. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthamitis. For acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies can be used to downregulate expression and activity of P. acnes polypeptides and codownregulate expression and activity of P. acnes polypeptides and determining P. acnes infections. The antibodies can be used to downregulate expression and activity of P. acnes polypeptides and carginated immunosorbent assay (ELISA).

Codownregulate can determining P. acnes presence, for example, by conzyme linked immunosorbent assay (ELISA).

Codownregulate and of this patent did not form part of the printed construction of the printed form in the involved in the printed form in the involved in the printed form in the production of the printed form in the form and patent did not form at the printed form in the form and patent did not form at the printed form and patent did not form at the printed form and patent did not form at the printed form and patent did not form at the printed form and patent did not form at the printed form and patent did not form at the printed form and patent did not form at the printed form and patent did not form at the form and patent did not form at the form and the patent did not form at the form and the patent did not form at the patent did not form and did not form and pate
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SAPHO syndrome, synovitis, acne, pustulosis, hypertosis, osteomyelitis, uveitis, endophthalmitis, bone, joint, central nervous system; BLISA, inflammatory lesion, acne vulgaris, enzyme linked immunosorbent assay; dermatological, osteopathic, neuroprotectent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitcham JL, Wang SS,
Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID No 15553; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                          21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                           20-APR-2001; 2001WO-US12865.
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e J, Zhang Y,
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                                                                                                                               Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-616774/71.
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Les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 AA;
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                                                                                                                                                                                 WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky YAW,
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Sequence
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                                                                                                                                                                      Human ORFX protein sequence SEQ ID NO:18386.
                                                                               ABP09202 standard; Protein; 106 AA.
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                                                                                                                                         24-JUN-2002
                                                                                                            ABP09202;
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ABP09202
ID ABP0
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AC ABP0
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DT 24-J
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DE Huma

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Treferred to as open reading frame. ORFX, where X is 1-11491 for in the specification). ABN15762 to ABN2722 encode the human ORFX in the specification). ABN15762 to ABN2722 encode the human ORFX proteins are useful for reating or preventing a pathology associated with an ORFX-associated disorder. ORFX polynucleotide syndrome associated with ORFX associated disorder. ORFX polynucleotide syndrome associated with ORFX-associated disorder. ORFX polynucleotide squences can be used in the manufacture of a medicament for treating a squences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, haemorrhage, osteoarthitis, beingn tumours, keloid, degenerative disorders, haemorrhage, cransplantation, cardiovascular diseases, diabetes mellitus, systemic transplantation, various immune disorders, disorders infectious diseases, autoimmune disorders auchine solver infectious diseases, autoimmune thyroiditis, myasthenia gravis, rheumatoid arthitis, autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, inclaining, olders, for treating osteoporosis, bene degenerative disorders, or periodontal disease, and for gut protection or regenerative or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from a systemic cytokine damage.
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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperporliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hyperensison; hypertension; hypertension; hypertension; cholesterol ester storage disease; immune desticiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes substantially purified human proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID 18386; 1037pp; English.
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29-AUG-2000; 2000US-228716P.
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54.5%;
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Best Local Similarity 54...
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N-PSDB; ABN24954.
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7 GKPAVSPAHTG 17
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H55545
C90035
B72498
C28985
T289865
T289865
T289865
A7108
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A92648
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Matches 9; Conservative
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      GenCore version 5.1.3
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S47537
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Claccesion: S7219
Rileth-Larsen, R.; Aggeirsson, B.; Thorolfsson, M.; Norregaard-Madsen, M.; Hojrup, Biochim. Biophys. Acta 1297, 49-56, 1996
Biochim. Biophys. Acta 1297, 49-56, 1996
A;Title: Structure of chymotrypsin variant B from Atlantic cod, Gadus morhua. A;Reference number: S72219; MUID:96439045; PMID:8841380
A;Accession: S72219; MUID:96439045; PMID:8841380
A;Accession: S72219
A;Rolecule type: protein
A;Residues: 1-4;15-244 <LET>
C;Superfamily: trypsin homology
F;15-237/Domain: trypsin homology <TRY>
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R;Gudmundsdottir, A.; Oskarsson, S.; Eakin, A.E.; Craik, C.S.; Bjarnason, J.B. Biochim. Biophys. Act 1219; 211-214, 1994
A;Title: Atlantic cod cDNA encoding a psychorphilic chymotrypsinogen.
A;Reference number: S47537; MUD:9436886; PMID:8086467
A;Accession: S47537
A;Molecule type: MRNA
A;Residues: 1-263 «GUD>
A;Cross-references RRNE:X78490; NID:9468750; PIDN:CAA55242.1; PID:9468751
C;Superfamily: trypsin; trypsin; homology
C;Superfamily: trypsin; trypsin; homology
C;Superfamily: trypsin; degentoe #status predicted <81G>
F;19-263/Product: chymotrypsin #status predicted <AMT>
F;34-256/Domain: trypsin; homology <RRN>
F;34-256/Domain: trypsin; homology <RRN>
F;75,120,213/Active site: His, Asp, Ser #status predicted
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C;Species: Gadus morhua (Atlantic cod)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Aug-1998
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Pred. No. 0.011;
0; Mismatches 4; Indels
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Aymotecule type: protein
A;Residues: 1-245 <SMI>
C;Comment: Chymotrypsinogen B is synthesized, along with chymotrypsinogen A, in the acinc
C;Comment: The first activation cleavage, leading to pi-chymotrypsin B, occurs in the san
C;Comment: The first activation cleavage, leading to pi-chymotrypsin B, occurs in the san
C;Comment: propertain; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;16-245/Product: chymotrypsin B #status experimental <MAT>
F;16-245/Product: chymotrypsin homology <TRX>
F;16-228/Domain: trypsin homology <TRX>
F;16-228/Domain: trypsin homology <TRX>
F;1122,42-58,136-201,168-182,191-220/Disulfide bonds: #status experimental
F;57,102,195/Active site: His, Asp, Ser #status experimental
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NiAlternate names: chymotrypsinogen A
C;Species Bos primigenius taurus (cattle)
C;Date: 07-May-1981 #sequence revision 07-May-1981 #text_change 07-May-1999
C;Accession: A90235; A93158; $29650; A00952
C;Accession: A90235; A93158; $29650; A00952
Biochem. J. 101, 214-229, 19.6
A;Title: Location of disulphide bridges by diagonal paper electrophoresis. The disulphide
A;Reference number: A90235; MUID:67181721; PMID:5971783
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B; Cutruzzola, F:; Ascenzi, P:; Barra, D:; Bolognesi, M.; Menegatti, E.; Sarti, P.; Schnet
B; Cutruzzola, F:; Ascenzi, P.; Barra, D:; Bolognesi, M.; Menegatti, E.; Sarti, P.; Schnet
B; Cutruzzola, F:; Ascenzi, P.; Barra, D:; Bolognesi, M.; Menegatti, E.; Sarti, P.; Schnet
B; Cutruzzola, F:; Ascenzi, P.; Barra, D:; Bolognesi, M.; Menegatti, E.; Sarti, P.; Schnet
A; Reference number: S29650, MUD:93160238; PMID:8431470
A; Molecule type: protein
A; Molecule ty
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A)Contents: annotation; X-ray crystallography
C)Contents: annotation; X-ray crystallography
C)Contents: chymotrypsinogens are synthesized in the acinar cells of pancreas.
C)Comment: Tryptic cleavage after Arg-15 results in a fully active enzyme (pi-chymotrypsi delta-chymotrypsin); further chymotryptic cleavage liberates the dipeptide Thr-147 and Ass delta-chymotrypsin; from chymotryptic cleavage liberates the dipeptide Thr-147 and Ass delta-chymotrypsin; trypsin homology, cleavage liberates to the degraded form neochymotrypsic; Superfamily: trypsin; trypsin homology, cleavage liberates proteinase; zymogen
E)1-245/Product: chymotrypsinogen #status experimental <2YM>
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A, Residues: 1-101, N', 103-245 cBRO>
A, Residues: 1-101, N', 103-245 cBRO>
Residues: 1-101, N', 103-245 cBRO>
Rablow, D.M.; Birktoft, J.J.; Hartley, B.S.
Nature 221, 337-340, 1969
A, Title: Role of a buried acid group in the mechanism of action of chymotrypsin.
A, Title: Role of a buried acid group in the mechanism of action of chymotrypsin.
B, Title: Role of a buried acid group in the mechanism of action of chymotrypsin.
B, Title: Role of a buried acid group in the mechanism of action of chymotrypsin.
B, Muh, I.; Kostka, V.; Moravek, L.; Prusik, Z.; Vanacek, J.; Keil, I Biochim. Blophys. Acta 130, 53-546, 1966
A, Title: Covalent structure of bovine chymotrypsinogen A.
B, Reference number: A90572; MUD:67183948; PMID:5972866
A, Recented of the chymotrypsinogen A.
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58.3%; Pred. No. 2.4;
tive 1; Mismatches
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Best Local Similarity 58.2
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chymotrypsin (EC 3.4.21.1) - Atlantic cod (fragments)
cjopedse: Gadus morhua ditantic cod)
cjopedse: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000
cjAccession: A61229
RjAsgairsson, B.; Bjarnason, J.B.
RjAsgairsson, B.; Bjarnason, J.B.
RjAsgairsson, B.; Bjarnason, J.B.
RjAscession: A61229
RjAscession: A61229
AjTitle: Structural and kinetic properties of chymotrypsin from Atlantic cod (Gadus morh A; Reference number: A61529; MUID:92111252; PMID:1764912
AjAccession: A61529
AjAccession: A61529
AjAccession: A61529
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AjAccession: A61529
CjSuperfamily: trypsin homology
CjSuperfamily: trypsin homology
CjSuperfamily: trypsin homology
CjSuperfamily: trypsin homology
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J. Biol. Chem. 274, 1691-1697, 1999
A.Tile: Enzymes in the extracellular matrix of Volvox: an inducible, calcium-dependent A.Reference number: 220772; MUID:99098915; PMID:9880549
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NyAlternate names: chymotrypsinogen B
Syspeciae primigenius taurus (cattle)
C;becies blor primigenius taurus (cattle)
C;bate: 08-0ct-1981 #sequence_revision 08-0ct-1981 #text_change 18-Jul-1997
C;Accession: A00953
R;Sullile, L.B.; Purka, A.; Nagabhushan, N.; Stevenson, K.J.; Parkes, C.O.
A;Title: Structure of chymotrypsinogen B compared with chymotrypsinogen A and trypsinoge
A;Reference number: A00953; MUID:68238908; PMID:5649671
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRMs
A; Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Volvox carteri
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T30198
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58.3%; Pred. No. 0.19;
iive 1; Mismatches 4; Indels
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Matches 7; Conservative
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CGRPAISPVITGY 31
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chymotrypsin (EC 3.4.21.1) - painted turtle (fragment)
c;Species Chrysemys picta (painted turtle)
C;Species 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
C;Dacession: BG1414
R;Bhargava, A.K.; Barnard, E.A.
J, MOL. EVOLI 2, 187-198, 1973
A;Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determ)
A;Reference number: A61414; MUID:76146602; PMID:4807189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cymotrypsin (EC 3.4.21.1) - slider turtle (fragment)
C;Species: Pseudemys scripta (slider)
C;Species: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
C;Accession: C61414 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
B;Bhargava, A.K.; Barnard, E.A.
J. Mol. Evol. 2, 187-198, 1973
A;Filte: Foulution in the pancreatic chymotrypsinogen series: N-terminal sequence determ)
A;Reference number: A61414; MUID:76146602; PMID:4807189
                                                                                                                                                                                                                                                 C,Accession: A31299
R;Tomita, N.; Izumcto, Y.; Horii, A.; Doi, S.; Yokouchi, H.; Ogawa, M.; Mori, T.; Matsubanchemia, Biophys. Res. Commun. 158, 569-575, 1989
A;Title: Molecular cloning and mucleotide sequence of human pancreatic prechymotrypsinogral A;Reference number: A31299, MUID:89134264; PMID:2917002
A;Accession: A31299
                                                                                                                                                                chymotrypsin (EC 3.4.21.1) precursor - human
C:Species: Homo sapiens (man)
C;Date: 08-Jun-1989 #sequence_revision 08-Jun-1989 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mENA
A;Residues: 1-263 «TOM»
A;Cross.references: GB:MZ4400; NID:g181189; PIDN:AAA52128.1; PID:g181190
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.8%; Score 40; DB 2; Length 263; 58.3%; Pred. No. 2.5; ive 1; Mismatches 4; Indels
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Pred. No. 0.27;
1; Mismatches 4; Indels
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A;Molecule type: protein
A;Residuss: 1.16 <4HA>
C;Keywords: hydrolase; protein digestion; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Gene: GDB:CTRB1; CTRB
A)Cores references: GDB:119820; OMIM:118890
A;Cross-references: GDB:119620; OMIM:118890
C;Map position: 16q23.1.
C;Superfamily: trypsin; trypsin; homology
C;Keywords: hydrolase; protein diggestion; serine proteinase
F;34-256/Domain: trypsin; homology cTRV:
F;35,120,213/Active site: His, Asp. Ser #status predicted
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58.3%;
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Matches 7; Conservative
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Matches 7; Conservative
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Query Match
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C61414
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Ripinsky, S.D.; LaForge, K.S.; buc, V.; Scheele, G.
Proc. Natl. Acad. Sci. U.S.A. 80, 7486-7499, 1988
Proc. Natl. Acad. Sci. U.S.A. 80, 7486-7499, 1988
A;Title: Identification of cDNA clones encoding secretory isoenzyme forms: sequence determines to the control of cDNA clones encoding secretory isoenzyme forms: sequence determines a A2195; MUD:84170253; PMID:6584866
A;Reference number: A21195, MUD:84170253; PMID:6584866
A;Retures preliminary
A;Molecule type: mRNA
A;Residues: 1.263, PMIN
A;Cross-references: GB:KO1173; NID:g163345; PIDN:AAA30841.1; PID:g163946
C;Superfamily: trypsin; trypsin homology
C;Superfamily: trypsin homology rRRY
F;34.256/Domain: trypsin homology rRRY
F;75,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                      chymicrypsin (EC 3.4.21.1) B precursor - rat
NyAlernate names: chymotrypsinogen B
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Dec.1987 #sequence_revision 28-Dec.1987 #text_change 18-Jun-1999
C;Accession: A22668
R;Bell, G.I.; Quinto, C.; Quiroga, M.; Valenzuela, P.; Craik, C.S.; Rutter, W.J.
B;Biol. Chem. 259, 14265-14270, 1984
A;Title: Isolation and sequence of a rat chymotrypain B gene.
A;Reference number: A22658; MUID:85054881; PMID:6209274
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C;Species: Canis lupus familiaris (dog)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 22-Jun-1999
        Gaps
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A;Molcoule type: 1048
A;Residues: 1-563 <BEL>
A;Cross-references: GB:K02298; NID:g203653; PIDN:AAA98732.1; PID:g203654
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67.8%; Score 40; DB 1; Length 263;
Best Local Similarity 58.3%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 5; Indels
                                                                                                                                              Score 40; DB 1; Length 245;
Pred. No. 2.4;
1; Mismatches 4; Indels
                                                                                                                                                    67.8%;
58.3%;
                                                                                                                             Query Match
Best Local Similarity 58.3.
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A,Accession: B61414

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two component sensor kinase exsG [imported] - Agrobacterium tumefaciens (strain C58, Dupc C,Species: Agrobacterium tumefaciens (58, Dupc C,Species: Agrobacterium tumefaciens (5,2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 #sequence_revision 11-Jan-2002 #sequence_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lranscription repressor [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Paccession: Al3382
B;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Gollesman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessor Proc. Natl. Acad. Sci. U.S.A. 99, 443,448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi
                                                                                                                                                                                                                                                                                                                                                                                                                   ster, E.W.
A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A.Reference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-350 «KUR»
A;Cross-references: GB:AE008687; PIDN:AAL45778.1; PID:g17743513; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52227.1; PID:g17983011; GSPDB:GN00190
A;Experimental source: strain 16M
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50.0%; Pred. No. 20;
iive 1; Mismatches 5; Indels
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Pred. No. 21;
0; Mismatches
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A.Map position: I
C.Superfamily: hypothetical protein H10753
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Best Local Similarity 50.0%;
Matches 6; Conservative
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C. Species Peededomonas aeruginosa
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C. Species Peededomonas aeruginosa
C. Species Peededomonas aeruginosa
C. Saccession: A82865
R. Scover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br. Stover, C.K.; Pham, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Vuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Alecter and Been and Been aequence of Pseudomonas aeruginosa PA01, an opportunistic pathon A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Residues: 1-542 acstro
A; Residues: 1-542 acstro
A; Residues: 1-542 acstro
A; Residues: 1-542 acstro
A; Reperimental source: strain PA01
C; Genetics:
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C;Species: Solanum tuberosum (potato)
C;Species: 30-apr-1999 #sequence_revision 30-apr-1999 #text_change 11-May-2000
C;Accession: T07043
R;Stapleton, A.; Beetham, J.K.; Pinot, F.; Garbarino, J.E.; Rockhold, D.R.; Friedman, Plant J. 6, 251-258, 1994
A;Ritle: Cloning and expression of soluble epoxide hydrolase from potato.
A;Reference number: Z1S881; MUID:95004665; PMID:7920715
A;Accession: T07043
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-321 <STA>
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Experimental source: cv. Lemhi Russet; wounded tuber
C;Superfamily: tropinesterase
C;Keywords: ether hydrolase
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                                                                                                                                                                                                   Query Match 66.1%; Score 39; DB 2; Length 17; Best Local Similarity 58.3%; Pred. No. 0.29; Matches 7; Conservative 1; Mismatches 4; Indels
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cive 1; Mismatches 6; Indele
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <BHA>
C;Keywords: hydrolase; serine proteinase
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RESULT 14

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1- SUBCELLULAR LOCATION.
1- SIMILARITY: BELONGS TO r.
HSRD: POOT FROOTIS!
2- NEROOTIS: TYPESIN; 1.
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DR PROSTE; PSOO134; TRYPESIN DOW; 1.
DR PROSTE; PSOO135; TRYPESIN DOW; 
                                       P9913 bos tautus

920195 sus scrofa

P01359 sus scrofa

003403 homo sapien

003404 mus musculu

00993 rattus norv

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P57769 rattus norv

012887 candida mal
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MEDLINE=96439045; PubMed=8841380;
Leth-Larsen R., Asgeirsson B., Thorolfsson M., Noerregaard-Madsen M.,
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MEDINE-911125; PubMed-1764912;

MEDINE-911125; PubMed-1764912;

MSTINE-911125; PubMed-1764912;

"Structural and kinetic properties of chymotrypsin from Atlantic cod (Gadus morbua). Comparison with bovine chymotrypsin.";

Comp. Blochem. Physiol. 998:327-335[1991].

-! CARLATIC GATIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Phe-|-Xaa, Leu-|-Xaa, Leu-|-Xa
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoejrup P.; "Structure of chymotrypsin variant B from Atlantic cod,
                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 41, Last annotation update)
Chymotrypsin B (EC 3.4.21.1).
Gadus morhua (Atlantic cod).
                                                                                                                                                                                                                                                                                                         245 AA
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            DPOL_HPBV9
FTSK_ECOLI
FBN1_BOVIN
FBN1_PIG
TFF2_PIG
TFF2_HOG
TFF2_MOUSE
TFF2_RAT
YPX4_CAEEL
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Copyright (c) 1993 - 2003 Compugen Ltd.
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NCBI_TaxID=9913;
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01-FEB-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsin A precureor (BC 3 4.21.1).
Gadus morbhus (Atlantic cod).
Eukaryota; Metazos; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neoperygii; Teleostei; Euteleostei;
Actinopterygii; Neoperygii; Gadiformes; Gadidae; Gadus.
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001324; Ser protease_Try.
InterPro; IPR001324; Ser protease_Try.
InterPro; IPR001324; Ser protease_Try.
PR00125; CHYMOTRYPSIN.
PR00125; PS00240; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Atlantic cod cDNA encoding a psychrophilic chymotrypsinogen.";
Biochim. Biophys. Acta 1219:211-214(1994).
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                                                                    88.1%; Score 52; DB 1; Length 245; 69.2%; Pred. No. 0.0018; ive 0; Mismatches 4; Indels
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MEDLINE-9416886; PubMed-8086467;
Gudmundsdottir A., Oskarsson S., Eakin A.E., Craik C.S.,
                                     74FE0D425517AB02 CRC64;
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Best Local Similarity 69.4.,
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos
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MEDLINE-67181721; PubMed-5971783;
Brown J.R., Hartley B.S.;
"Location of disulphide bridges by diagonal paper electrophoresis.
The disulphide bridges of bovine chymotrypsinogen A.";
Biochem. J. 101:214-228(1966).
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MSDLINES-7183948; PubMed=5972866;
Meloun B., Kluh I., Kostka V., Moravek L., Prusik Z., Vanacek J.,
Keil B., Sorm F.;
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MEDINE=72035052; PubMed=4399050;
Birktoft J.J., Blow D.M., Henderson R., Steitz T.A.;
Birktoft J.S., Blow D.M., Henderson R., Steitz T.A.;
"I. Serine proteinases. The structure of alpha-chymotrypsin.";
Philos. Trans. R. Soc. Lond., B, Biol. Sci. 257:67-76(1970).
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Smillie L.B., Hartley B.S.;
"Histidine sequences in the active centres of some 'serine'
                                                                                                                                                                                                                                                                                              88.1%; Score 52; DB 1; Length 263; 69.2%; Pred. No. 0.0019; 1ive 0; Mismatches 4; Indels
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R -> 5 (IN REF. 2).
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"Role of a buried acid group in the mechanism of action
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Amino-acid sequence of bovine chymotrypsinogen-A."; Nature 201:1284-1287(1964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Covalent structure of bovine chymotrypsinogen A.";
Biochim. Biophys. Acta 130:543-546(1966).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsinogen A (EC 3.4.21.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 AA
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MEDLINE=69106266; PubMed=5764436;
                                                                                                                                                                                                                                          28294 MW;
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                                                                                                                                                                                                                                                                                                                                                   Conservative
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2300
2300
211
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                                                                                                                                                                                                                                          263 AA;
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    1 CGXPAIXPXXTGY
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Local Similarity 58.3%;
es 7; Conservative
                                    \begin{array}{c} 127 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\ 147 \\
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        3D-structure. CHAIN 14 CHAIN 14 CHAIN 14 CHAIN 14 ACT_SITE 19 DISULFID 13 DISULFID 13 DISULFID 19 DISULFID 19 DISULFID 19 HELIX 1 STRAND 2 TURN 2 2 TURN 12 CHAIN 2 2 CHAIN 12 CHAIN 14 CHAIN 14
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Best Local Si
Matches 7;
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TURN
TURN
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HELIX
TURN
           Dp
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MEDLINE-82078042; PubMed=6914398;
Cohen G.H., Silverton E.W., Davies D.R.;
"Refined crystal structure of gamma-chymotrypsin at 1.9-A resolution. Comparison with other pancreatic serine proceases.";
J. Mol. Biol. 148:449-479(1981).
                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.68 ANGSTROMS) OF ALPHA-CHYMOTRYPSIN.
MEDLINE-86011575, Pubmed=4046030;
TSHKAda H., Blow D.M.;
"Structure of alpha-chymotrypsin refined at 1.68-A resolution.";
J. Mol. Biol. 184:703-711(1985).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF CHYMOTRYPSINOGEN.
MEDLINE=70177557; PubMed=5442169;
Freer S.T., Kraut J., Robertus J.D., Wright H.T., Xuong N.H.;
"Chymotrypsinogen: 2.5-A crystal structure, comparison with alpha-
elymotrypsin, and implications for zymogen activation.";
Biochemistry 9:1997-2009(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phe-|-Xaa, Leu-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIOASE FAMILY SI.
-!- DATABASE: NAWH-Worthington enzyme manual;
WWW-"http://www.worthington-biochem.com/manual/C/CHY.html".
PIR; A00952; KYBOA.
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00220; Tryp, SPC; 1.
PROSITE; PSS0134; TRYPSIN_DOM; 1.
PROSITE; PSS0134; TRYPSIN_HIS; 1.
PROSITE; PS0135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser protease Try.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2CGA, 15-ARR-90.
2CHA, 11-MAY-84.
4CHA, 29-0CT-85.
5CHA, 16-0CT-87.
1CHG, 27-JAN-84.
1CHG, 27-JAN-84.
1CHG, 15-0CT-97.
4CCH, 15-0CT-97.
4CCH, 15-0CT-90.
6CGH, 15-0CT-90.
6GCH, 15-0CT-90.
6GCH, 15-0CT-90.
1GCT, 15-0CT-91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHA, 16-0CT-87
CCHA, 16-0CT-87
CCHA, 16-0CT-87
CCH, 13-0CT-92
CCH, 15-0CT-97
CCH, 15-0CT-97
CCH, 15-0CT-91
CCCT, 15-0CT-91
CC
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30-APR-94
22-JUN-94
22-JUN-94
22-JUN-94
30-SEP-94
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PDB, 2CGA, 15-APR
PDB, 2CGA, 15-APR
PDB, 2CGA, 15-APR
PDB, 5CHA, 16-OCT
PDB, 6CHA, 16-OCT
PDB, 1CHC, 16-JUL
PDB, 1CHC, 15-JUL
PDB, 3CCH, 15-OCT
PDB, 6CCH, 15-OCT
PDB, 6CCH, 15-OCT
PDB, 6CCH, 15-OCT
PDB, 6CCH, 15-OCT
PDB, 1CGT, 15-OCT
PDB, 1CCT, 12-NOV
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Gaps
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CHYMOTRYBSIN A, A CHAIN.
CHYMOTRYBSIN A, B CHAIN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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Phe-|-Xaa, Leu-|-Xaa.
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                  PIR; A21195; A21195.
HSSP; P00766; IACB.
MEROPS; S01.152; *.
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DISULFID
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CTRB_HUMAN
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                                                                                     SEQUENCE, DISULFIDE BONDS, AND ACTIVE SITE.
MEDLINE-68238908; Purka A., Nagabushan N., Stevenson K.J., Parkes C.O.;
"Smillie L.B., Furka A., Nagabushan N., Stevenson K.J., Parkes G.O.;
"Skillie L.B., Furka A., Nagabushan B. Schucture of chymotrypsinogen B compared with chymotrypsinogen A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                trypsinogen.";
Nature 218:343-346(1968).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDILINE=84170253; PubMed=6584866; Pinsky S.D., Laforge K.S., Luc V., Scheele G.; Pinsky S.D., Laforge K.S., Luc V., Scheele G.; secretory isoenzyme forms: "Identification of CDNA clones encoding secretory isoenzyme forms: sequence determination of canine pancreatic prechymotrypsinogen 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615;
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                                                                                                                                                                   Phe-|-Xaa, Leu-|-Xaa.
-!-SUMCELULAR LOCATION EXTRACELLULAR.
-!-SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- DATABASE: NAME-Worthington enzyme manual;
WWW-"http://www.worthington-biochem.com/manual/C/CHY.html",
PIR, A00953; KYBOB.
                                                                                                                                                                                                                                 HSSP, P00766, LACB.

MEROPS; S01.152; -.
InterPro; IPR001214; Chymotrypsin.
InterPro; IPR001224; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRNNTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; TRYPSRO; 1.
PROSITE; PS00240; TRYPSIN DOW; 1.
PROSITE; PS00134; TRYPSIN LIS; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
PKOSITE; PS00135; TRYPSIN SER; 1.
PKOSITE; PS00135; TRYPSIN SER; 1.
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                                                                                                                                                                                                                                                                                                                                                          CHYMOTRYPSIN B, A CHAÎN.
CHYMOTRYPSIN B, B CHAIN.
CHYMOTRYPSIN B, C CHAIN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25755 MW; 678016446FF5FEB5 CRC64;
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13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypainogen 2 precursor (EC 3.4.21.1).
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 58.3
es 7; Conservative
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102
122
122
58
201
182
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DISULFID
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DISULPID
SEQUENCE
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                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001314; Chymotrypain.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
SMART; SS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 1; Length 263;
Pred. No. 0.56;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHYMOTRYPSINOGEN 2.
CHYMOTRYPSIN 2, A CHAIN.
CHYMOTRYPSIN 2, B CHAIN.
CHYMOTRYPSIN 2, C CHAIN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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    -!- SUBCELLULAR LOCATION: Extracellular.
    -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Pancreas;
MEDLINE=89134264; PubMed=2917002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTRB HUMAN STANDARD; F
P17538;
01-AUG-1990 (Rel. 15, Created)
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                                                                                                                                                                                                                                                                                                                                            EMBL; K01173; AAA30841.1; -.
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27849 MW;
                                                                                                                                                          EMBL; K02298; AAA98732.1; -.
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263 AA;
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NCBI_TaxID=7650;
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                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
ENkaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
        Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALVIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Phe-|-Xaa, Leu---Xaa, Leu---Xaa.
-!- SUBCELLUTAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                          CHYMOTRYPSIN B, A CHAIN.
CHYMOTRYPSIN B, B CHAIN.
CHYMOTRYPSIN B, C CHAIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                              InterPro: IPR001314; Chymotrypsin.
InterPro: IPR001254; Ser_protease_Try.
Pfam. PP00089; crypsin, 1.
PRNNTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN JER; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-85054881; PubMed-6209274;
Bell G.I., Quinto C., Quiroga M., Valenzuela P., Craik C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 1; Length 263;
Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
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                                                                                                                                                                                                                                                                                                                                    CHYMOTRYPSINOGEN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTRB_RAT STANDARD; PRT; 263 AA. 190738; 01-APR-1988 (Rel. 07, Created) 01-APR-1988 (Rel. 07, Last sequence update) 15-UNA 2002 (Rel. 41, Last annotation update) CTYMotrypsinogen B precursor (BC 3.4.21.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                         EMBL; M24400; AAA52128.1; --
EMBL; BC005388; AAH05385.1; --
PIR; A31299; A31299
HSSP; P00766; 1CHG.
MEROPS; SQL 152; --
GGNEW; HGNC.2521; CTRB1.
MIM; 118890; --
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263 AA;
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Best Local Similarity
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Nomura K., Shimizu T., Kinoh H., Sendai Y., Inomata M., Suzuki N.;
"Sea urchin hatching enzyme (envelysin): cDNA cloning and deprivation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS, SOLISE:

REASP, SOLISE:

REASP, SOLISE:

RICETPO: IPRO01314; Chymotrypsin.

RICETPO: IPRO01314; Chymotrypsin.

RICETPO: IPRO01354; Ser_procease_Try.

REART; PRO0125; CHYMOTRYPSIN.

REART; PRO0125; CHYMOTRYPSIN.

REART; PRO0136; TRYPSIN DOM; 1.

REASTE; PSO0134; TRYPSIN DOM; 1.

REASTE; PSO0135; TRYPSIN DOM; 1.

REASTE; PSO0135; TRYPSIN DOM; 1.

REASTE; PSO0135; TRYPSIN SER; 1.
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Rutter W.J.;
"Isolation and sequence of a rat chymotrypsin B gene.";
J. Biol. Chem. 259:14265-14270(1984).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, TrF-|-Xaa, Phe-|-Xaa, Leu-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHYMOTRYPSIN B, A CHAIN.
CHYMOTRYPSIN B, B CHAIN.
CHYMOTRYPSIN B, C CHAIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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195951, 199551, 169751, 186. Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-GOT-2001 (Rel. 40, Last annocation update)
Hatching enzyme precursor (EC 3 4.24.12) (HE) (HEZ) (Envelysin) (Sea-urchin-hatching proteinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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TISSUE=Blastula;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAFDBACF8C4DA6D CRC64;
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CARBOHYD
CARBOHYD
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CONFLICT
CONFLICT
CONFLICT
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CONFLICT
CONFLICT
CONFLICT
CONFLICT
                           DISULPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                     URCHIN TO SWIM FREELY.

CATALYTIC ACTIVITY: Preferential cleavage: on the amino side of bulky hydropholic residues, -leu, -lee, -be, as well as -Tyr.

SUBUNT: DURING HATCHING, THE 50 kDB MATURE ENZYME IS

AUTOLYTICALLY CLEAVED TO PRODUCE A MAJOR 38 kDB AND A MINOR 15 kDB KDB WHELLY CLEAVED TO PRODUCE A MAJOR 38 kDB AND A MINOR 15 kDB KDB SPECIES YIELDS A 32 kDB NON-SPECIFIC PROTEASE.

DEVELOPMENTAL STACE: BMBRYO, BLASTULA STACE: HIGHEST ACTIVITY AT DOMAIN: THERE ARE TWO DISTINCT DOMAINS IN THER ARE TWO DISTINCT DOMAINS IN THE CATALYTIC N-TERMINAL, AND THE C-TERMINAL WHICH IS INVOLVED IN
                                                                                                                                                                                                                                                                                                 FEBS Lett. 321:84-88(1993).
-!- FUNCTION: ALLOWS THE SEA URCHIN TO DIGEST THE PROTECTIVE ENVELOPE
DERIVED FROM THE EGG EXTRACELLULAR MATRIX THUS ALLOWING THE SEA
                                                                                                                                                                                                          MEDLINE-93223852; PubMed-8467915;
Nommira K., Suzuki N.
Stereo-specific inhibition of sea urchin envelysin (hatching enzyme)
by a synthetic autoinhibitor peptide with a cysteine-switch consensus
                                                                         MEDLINE-91283448; PubMed-1711895; Nomura K., Tanaka H., Kikkawa Y., Yamaguchi M., Suzuki N.; "The specificity of sea urchin hatching enzyme (envelysin) places it in the mammalian matrix metalloproteinase family."; Blochemistry 30:6115-6123(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 KDA HATCHING ENZYME.
32 KDA HATCHING ENZYME.
33 KDA HATCHING ENZYME.
15 KDA HATCHING ENZYME.
15 KDA PEPTIDE.
ASP/GUL-RICH (ACIDIC).
ASP/GUL-RICH (HINGE REGION).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
SINC (CYTALYTIC) (BY SIMILARITY).
CLEAVAGE (AUTOLYTIC DURING HATCHING).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVATION PEPTIDE (BY SIMILARITY)
protein substrate specificity by autolytic degradation.",
ochemistry 36:7225-7238(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001819; Matrixin.

InterPro; IPR001819; Interpress Interpres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYSTEINE SWITCH (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO PEPTIDASE FAMILY MIDA. SIMILARITY: CONTAINS I HEMOPEXIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROBABLE
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                                                                                                                                                                                        STEREO-SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; M10.010;
                                                                                                                                                                                                                                                                                       sequence.";
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RECENTINE-20196006; PubMed=10731132;
RADINE-20196006; PubMed=10731132;
RADINE-1076; ROGERS P. Richards S. Ashburner M., Henderson S.N.,
RADINE R. R., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RADINE R.M., Basu A., Baxendale J., Bayraktaroglu L., Besaley E.M.,
RADINE R.M., Basu A., Barman B.P., Bhandari D., Bolshkov S.,
RADINE R.C., Busam D.A., Butler H., Cadieu E., Center A., Chadra I.,
RADINER R.C., Busam D.A., Butler H., Cadieu E., Center A., Chadra I.,
RADINE R.C., Busam D.A., Butler H., Cadieu E., Center A., Chadra I.,
RADINE R.C., Busam D.A., Dong Z., Mays A.D., Dow I., Dietz S.M.,
RADINE R.C., Evraz C., Ferraz C., Perriera S., Pleischmann W.,
RADINE R.C., Busgelieta C.C., Ferraz C., Perriera S., Pleischmann W.,
RADINE R.C., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
RADINE R.C., Busker D., Helman T.J., Hernandez J.R., Houck J.,
RADINE R.J., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RADINE R.J., Harvey D., Helman T.J., Wei M., Inbeyam C.,
RADINE R.J., Harvey D., Rapen G.H., Re Z., Kennison J.A.,
RADINE R.J., Howlend R.J., Howlend R.J., Ketchum R.A.,
RADINE R.J., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RADINE R.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

BEDLINE-SP6102814, PubMed=8582281;

Nakato H., Futch T.A., Selleck S.B.;

"The division abnormally delayed (dally) gene: a putative integral membrane proteoglycan required for cell division patterning during postembryonic development of the nervous system in Drosophila.";

peyelopment 121:3687-3702(1995).
CLEAVAGE (AUTOLYTIC DURING HATCHING)
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
S -> N (IN REF. 1; AA SEQUENCE).
T -> N (IN REF. 1; AA SEQUENCE).
L -> I (IN REF. 1; AA SEQUENCE).
SL -> GN (IN REF. 1; AA SEQUENCE).
E -> N (IN REF. 1; AA SEQUENCE).
E -> N (IN REF. 1; AA SEQUENCE).
E -> N (IN REF. 1; AA SEQUENCE).
E -> L (IN REF. 1; AA SEQUENCE).
E -> L (IN REF. 1; AA SEQUENCE).
P -> L (IN REF. 1; AA SEQUENCE).
P -> L (IN REF. 1; AA SEQUENCE).
R -> L (IN REF. 1; AA SEQUENCE).
R -> L (IN REF. 1; AA SEQUENCE).
R -> L (IN REF. 1; AA SEQUENCE).
               (AUTOLYTIC DURING HATCHING)
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(POTENTIAL)
(POTENTIAL)
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DALY DROME
TO DALY DROME
TO O24114; O9VSOB;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DF 16-OCT-2001 (Rel. 40, Last annotation update)
DF DALLY OR CG4974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 1; Length 591;
Pred. No. 3.2;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.4%;
58.3%;
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Mus musculus (Mouse)
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264 AA;
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Q9Z0E2;
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ACT SITE
ACT SITE
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CARBOHYD
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Luu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshren I.A.,
Mentkulov G., Milshina N.V., Mobarry C., Morris J., Moshren D.L.,
Menut S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A plazzolo M.P. Mitama G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ra Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Sannders R.D.C., Scheeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Sylrekas R., Tector C., Turner R., Venter E., Mang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Weilliams S.M., Woodage T., Worley K.C., Mu D., Yang S., Yao Q.A.,
Williams S.M., Woodage T.N., Zhong W., Zhou G., Zhao Q., Zhao G.,
A williams S.M., Woodage T.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
A chops R.A., Myers E.W., Rubin G.M., Venter J.C.;
Schone 287.1185-1295(2000).
CELL DIVISION PATTERNING DURING POST-EMBRYONIC DEVELOPMENT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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REMOVED IN MATTRE FORM (POTENTIAL).
N.LINKED (GLCNAC. .) (POTENTIAL).
N.LINKED (GLCNAC. .) (POTENTIAL).
N.LINKED (GLCNAC. .) (POTENTIAL).
O.LINKED (GLCNAC. .) (POTENTIAL).
O.LINKED (GLYCOSAMINOGLYCAN) (POTENTIA.).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=9606;
                                                                                                                                                                                                                                                                  NERVOUS SYSTEM.
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003554; AAF50358.1; --
FlyBase; PEGNOULS77, dally.
InterPro; IRROL01633; Glypican;
Pfam; PF01153; Glypican; 1.
PROSITE; PS01207; GLYPICAN; PALSE_NEG.
Proteoglycan; Heparan sulfate; Glycoprotein; Signal; GPI-anchor.
SIGNAL
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FED-1902 (Rel. 41, Last annotation update)
Chymotrypsin-like protease CTRL-1 precursor (EC 3.4.21.-).
CTRL OR CTRL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.4%; Score 38; DB 1; Length 626; 41.7%; Pred. No. 3.4;
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Matches 5; Conservative
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626 AA;
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CHYMOTRYPSIN-LIKE PROTEASE CTRL-1.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLONAC. . .) (POTENTIAL).
BY SIMILARITY.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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Lu B., Bachiller D., Agius E., Piccolo S., De Robertis B.M.;
"BWb-binding domains in the chordin secreted protein.";
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=94093544; PubMed=8268911;
Larsen F., Solheim J., Kristensen T., Kolsto A.B., Prydz H.;
"A tight cluster of five unrelated human genes on chromosome 16q22.1.";
Hum. Mol. Genet. 2:1589-1595(1993).
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 1; Length 264;
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SIGNAL 1 18
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        948 AA.
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InterPro; IRR001254; Ser protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PR0SITE; PS00134; TRYPSIN LDM; 1.
PR0SITE; PS00134; TRYPSIN HIS; 1.
PR0SITE; PS00135; TRYPSIN SR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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33
264
264
1121
214
1114
141
220
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                                                                                                                                                                                                                                                                                                      Describe 34:401-200.

18 [3]

29 SEQUENCE OF 51-125; 705-762; 784-850 AND 872-932 FROM N.A.

20 Bacchiler D., Agius E., Larrain J., Piccolo S., Nieters A.,

21 Bac Dinding modules in the chordin patterning protein.";

22 Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

23 In EMBL DOSABLISTING factor. Key developmental protein that dorsalizes early vertebrate embryonic tissues by binding to ventralizing TGP-beta family bone morphogenetic proteins (BMPB)

23 In Submitted RoCATION: Secreted (By similarity).

24 SUBCELLULAR LOCATION: Secreted (By similarity).

25 In ALTERNATIVE PRODUCTS: 5 isoforms; 1 (shown here), 2, 3, 4 and 5;

26 In TISSUE SPECIFICITY: Expressed at the highest level in liver.

27 In SIMILARITY: BELONGS TO THE CHORDIN PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . ) (POTENTIAL).
PQ - SP (IN ISOPORM 2).
PQWGRRTRGP -> TGTLRPREMK (IN ISOPORM 3).
MISSING (IN ISOPORM 3).
GLTOVPLALOILHGGOLLBELQA -> DSTPGAATARTGGOCLESPGTRLC (IN ISOPORM 4).
MISSING (IN ISOPORM 4).
MISSING (IN ISOPORM 4).
MISSING (IN ISOPORM 5).
ROLP -> QVAA (IN REF. 2).
                                                                                                                                                                                                                                      "Coding sequence and expression patterns of mouse chordin and mapping of the cognate mouse chrd and human CHRD genes.";
Genomics 52:236-239(1998).
                 Millet C., Lemaire P., Orsetti B., Guglielmi P., Francois V.; "The human chordin gene encodes several differentially expressed spliced variants with distinct BMP opposing activities.";
                                                                                                                                                                                        Pappano W.N., Scott I.C., Clark T.G., Eddy R.L., Shows T.B., Greenspan D.S.,
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SEQUENCE OF 115-955 FROM N.A. (ISOFORM 5)
MEDLINE=99000848; Pubmed=9782094; FAAV
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EMBL, AF209929, AAG3768.1;
EMBL, AF20930, AAG35769.1;
EMBL, AF076612; AAG6895.1;
EMBL, AF283325, AAG35784.1;
EMBL, AF136632, AAF70236.1;
EMBL, AF136633, AAF70237.1;
EMBL, AF136634, AAF70238.1;
                                                                                                 Mech. Dev. 106:85-96(2001).
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N, 4DC2DA01D9BD2147 CRC64;
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Q9H2XO; Q9POZ2; Q9POZ3; Q9POZ4; Q9POZ5; Q9H2W8; Q9H2D3;
O9S2S4;
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                                                                       MEDLINE=99000848; PubMed=9782094;
Pappano W.N., Scott I.C., Clark T.G., Eddy R.L., Shows T.B.,
Greenspan D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 1; Length 948; Pred. No. 21; 1; Mismatches 5; Indels
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
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BOTENTIAL.
CHORDIN.
VWFC 1.
VWFC 2.
VWFC 2.
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CHRD.
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MEDLINE=21366001; PubMed=11472837;
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EMBL, AF069501; AAC68867.1;
MGD, MGI:1313268; Chrd.
InterPro; IPR001007; VWF.C.
FEAN; PF00093; VWC; 4,
PROSITE; PS01208; VWC; 2,
Developmental protein; Repeat; Gl
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877 8
948 AA;
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DOMAIN
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242 GAPAVFSRVTGY 253
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PIR; A3894; A3894.
HSSP; P00761; 1EPT.
MEROPS; S01.UPA; -.
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265 AA;
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DISÜLFID
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                                                                                                                                                                                                                                                                                        RESULT 13
SERI DROME

ID SERI DROME

TO SERI DROME

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TO PAUG-1990 (Rel. 15, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annoctation update)

DT 15-JUN-2002 (Rel. 41, Last annoctation update)

DE Serine proteases 1/2 precursor (EC 3.4.21.-).

GN (SER99DA OR SERI OR CG797) AND (SER99DB OR SER2 OR CG15519).

OS Drosophila melanogaster (Fruit fly).

OC Insecta; Retryocta; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Retryocta; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NO NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-89219053; PubMed=2469005;
Yun Y., Davis R.L.;
"Levels of RNA from a family of putative serine protease genes are
reduced in Drosophila melanogaster dunce mutants and are regulated by
                                                                                                                                                                           Gaps
                                                                                                                                                                        ;
                                                                                                                        DB 1; Length 955;
                                                                                                                                                                        5; Indels
  189 189 V -> A (IN REF. 2).
216 216 S -> P (IN REF. 2).
674 674 T -> P (IN REF. 2).
955 AA; 102013 MM; 12AC030CEACFF3ED CRC64;
                                                                                                                        59.3%; Score 35; DB 50.0%; Pred. No. 22; Ative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cyclic AMP.";
Mol. Cell. Biol. 9:692-700(1989).
                                                                                                                                                     Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                        411 CGADALIPVQTG 422
                                                                                                                                                                                                                           1 CGXPAIXPXXTG 12
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SEQUENCE
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A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., dibbs R.A., Wyers E.W., Rubin G.M., Venter J.C., The grone sequence of Drosophila melanogaster.", Science 28:1218-2195(2000).

L. Science 28:1218-2195(2000).

L. FUNCTION: MAJOR FUNCTION MAY BE TO AID IN DIGESTION.

-! FUNCTION: MAJOR FUNCTION MAY BE TO AID IN THE LARVAL GUT.

-! TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THE LARVAL GUT.

-! DEVELOPMENTAL STAGE: BEGAN TO APPEAR AT LATE EMBRYO STAGE AND CONTINUED TO INCREASE IN ABUNDANCE THROUGHOUT THE LARVAL STAGE.

THEY ARE NOT PRESENT IN PUPAE BUT REAPPEARED IN THE ADULT.

-! MISCELLANDROOS: THE SEQUENCE SHOWN IS THAT OF SER!.

-! SIMILARITY: BELONGS TO PEPPIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable inorganic polyphosphate/ATP-NAD kinase (EC 2.7.1.23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.6%; Score 34; DB 1; Length 265; 50.0%; Pred. No. 9.7;
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A -> T (IN REF. 1; AAB02553).

44848C523F03384B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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EMBL, M27379, AAB02553.1; -.
EMBL, AE003771, AAF56971.1; ALT_SEQ.
EMBL, AAF03771; AAF56972.1; -.
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                                                                                                                                                                                                                                                                                                                              gene model prediction.
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265
78
123
215
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MEDLINE=84169548; PubMed=6324121;
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                 6
                                                                                                                                                                                                              WEDLINE=20504483; PubMed=11016950,
W WEDLINE=20504483; PubMed=11016950,
W WEDLINE=20504483; PubMed=11016950,
W WW., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
W Swartzall S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
M Addocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
M Addocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
A leenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
A lam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
A Bhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
T "Genome sequence of Hallobacterium species NRC-1.";
T "Genome sequence of Hallobacterium species NRC-1.";
T "Genome sequence of Hallobacterium species NRC-1.";
T "Genome sequence of phosphorylation of NAD to NADP. Utilizes
T "Ang and other nucleoside triphosphates as well as inorganic
Dolyphosphate as a source of phosphorus (By similarity).
T "COPACTOR: Requires divalent metal ions for activity (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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McGeoch D.J., Dolan A., Donald S., Rixon F.J.;
"Sequence determination and genetic content of the short unique
region in the genome of herpes simplex virus type 1.";
J. Mol. Biol. 181:1-13(1985).
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Pred. No. 10;
1; Mismatches 5; Indels
                                               Halobacterium sp. (strain NRC-1),
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: BELONGS TO THE NAD KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002504; ATP NADK.
Pfam; PF01513; NAD kinase; 1.
Transferase; Kinase; NAD; NADP; Complete proteome.
SEQUENCE 282 AA; 29120 MW; 5DAIAF25147D7500 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
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01-JAN-1988 (Rel. 06, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Virion protein US10.
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  (Poly(P)/ATP NAD kinase).
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Best Local Similarity
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                       NCBI_TaxID=64091;
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P06486;
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US10 HSV11
AC P06486
DT 01-JAN
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Gaps
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SEQUENCE 312 AA; 34055 MW; 12D01B0E7C920EA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X14112; CAA32275.1; -...
EMBL; X00428; CAA25064.2; -...
EMBL; X00428; CAA25126.1; -...
EMBL; L00036; AAA96678.1; -...
PIR; A05242; QQBG07.
InterPro; IPR000087; Collagen.
InterPro; IPR000014; EHV_Unk.
Pfam; PF02053; Gene66; 1.
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Matches 5; Conservative
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ZN FING
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Search completed: February 12, 2003, 10:23:14 Job time : 3.74627 secs

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Q9dgy8 hepatitis b
Q9e9b4 hepatitis b
Q9e9b4 hepatitis b
Q9dh92 hepatitis b
Q9db57 hepatitis b
Q9e9b2 hepatitis b
Q9e9a8 hepatitis b
Q9e9a9 hepatitis b
Q9e9a9 hepatitis b
Q99b8 hepatitis b
Q99h8 hepatitis b
Q95h8 pytococcus
Q41412 solanum tub
Q8N14 agrobacteri
Q8ygv9 brucella me
Q9xr04 chlamydomon
Q9xr02 chlamydomon
Q9xr02 chloromonas
O65774 chlamydomon
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                                                                                                    O65777 chloromonas
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052046 halobacteri
Q93rx9 streptomyce
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Q9x2j3 ralstonia m
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"Chymotrypsin isoenzymes in Atlantic cod, differences in kinetics and
substrate specificity.",
Comp. Biochem. Physiol. 112B:393-398(1995).
NON TER 23 23
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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01-MAY-2000 (TrEMBLrel. 13, Last sequen
01-DEC-2001 (TrEMBLrel. 19, Last annotat
Chymotrypsin isoenzyme (HT2 (Fragment).
Gadus morhua (Atlantic cod).
                            08YGV9
09XR04
09XR03
065774
065777
08QUV3
09DGY8
                                                                                                                                                                                                                                                                                                         057465
09PSP2
057786
059100
052046
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090092
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096982
096983
096983
096983
099889
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                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
 NCBI TaxID=8049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                 GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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                                                                         OM protein - protein search, using sw model
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Q9PRS1
Q9PWG6
Q9WYQ4
Q9DC86
Q9DBXB
Q9CR35
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Gapop 10.0 , Gapext 0.5
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sp_human:*
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Maximum DB seq length: 200000000
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59
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No.
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A SUZUKI T., Srivastava A.S., Kurokawa T.;

Suzuki T., Srivastava A.S., Kurokawa T.;

"Japanese flounder mRNA for chymotrpsinogen 2.";

Submitted (Jul-1999) to the EMBL/GenBank/DDBJ databases.

"I. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.

REMBL; AB023754; BAA82366.1; -.

REMBL; PRO0755; D0766; 1CHG.

RECORS; S01.152; -.

RECORS: S01.152; -.

RECOR
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidai; Paralichthyidae; Paralichthys.
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyldee; Paralichthys
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Japanses ef flounder mRNA for chymotrypsinogen 1.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
EMBL; AB029753; BAA823455.1; -.
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                                                                                                                                                                                01-NNV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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69.2%; Pred. No. 0.018;
                                                                                                                                         260 AA.
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                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                Chymotrypsinogen 2.
Paralichthys olivaceus (Flounder).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paralichthys Ölivaceus (Flounder).
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                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
          17 CGSPAIQPQVTGY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGXPAIXPXXTGY 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=PANCREAS;
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                                                                                 RESULT 4
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                                                                                                                                                                                                   SEQUENCE.
MEDLINE=56042258; PubMed=7584866;
Raae A.J., Flengsrud R., Sletten K.;
Chymotrypsin isoenzymes in Atlantic cod; differences in kinetics and substrate specificity.";
Comp. Biochem. Physiol. 1128:393-398(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                  Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus. NCBI_TaxID=8049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gadus morhua (Atlantic cod).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryotai, Neoperygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Paracanthopterygii, Gadiformes, Gadidae, Gadus.
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MEDLINE=20464334; PubMed=11011764;
MEDLINE=20464334; PubMed=11011764;
MEDLINE=20464334; PubMed=11011764;
MEDLINE=20464334; PubMed=11011764;
Midled Comp. Gudmundsdottir A. Allantic Cod Chymotrypsinogen B.";
Microb. Comp. Genomics 5:41-50(2000).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPENTY.
TRYPENTY PAJ24521; CAB43766.1; -.
HSSP; P00766; 1CHG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52, DB 13; Length 24;
Pred. No. 0.0011;
0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                      24 AA; 2400 MW; 0A416ACA7B67F68D CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Chymotrypsin isoenzyme CHT1 (Fragment). Gadus morhua (Atlantic cod).
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR00124; Ser protease_Try.
Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNROWN_1.
PROSITE; PS00135; TRYPSIN JSR; 1.
Hydrolase; Serine protease; Signal.
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Best Local Similarity 69.47
9; Conservative
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Best Local Similarity 69.2
Matches 9, Conservative
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RESULT 3
09PW06
10 PW
AC 09PW
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Gaps

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Indels

us-10-036-371-3.rspt

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Hydrolase, Serine protease.
SEQUENCE 263 AA; 27898 N
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es 8; Conservative
                        Query Match 74.6
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                             PRELIMINARY;
                                                                                              1 CGXPAIXPXXTG 12
                                                                                                                              19 CGVPAIQPVLTG 30
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Q9D8X8;
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SEQUENCE FROM N.A.

MEDINE-2108660; DABDE-31217851;

KRAWAI J., Shinagawa A., Fukunishi Y., Konho M., Itoh M., Ishii Y., Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alaxawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Cozaki Y., Gojobori T., Mondo S., Yamanaka I., Saito T., Chazaki Y., Gojobori T., Mandon H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Schriml L.M., Solido T., Fletcher C., Fulita M., Gariboldi M., Sata K., Okido T., Pletcher C., Fulita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P., Nordone P., Ring B., Ringala M., Rodriguez I., Sakamoto N., Saski H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Hardelawa Y., Kawaji H., Kothtsuki S., Hardelawa Y., Kawaji H., 
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
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0
                                                                                                                                                                                                     74.6%; Score 44; DB 13; Length 261; 53.8%; Pred. No. 0.5; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROFS; SOL 152; ---
MGD; MGT:191372; ---
MGD; MGT:191372; ---
MGD; MGT:191372; ---
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; I.
PR00175; PR00722; CHYMOTRYPSIN.
SMART: SM00020; Tryps SPc; 1.
PROSITE; PS00130; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN I.
PROSITE; PS00135; TRYPSIN HIS; UNKNOWN I.
PHYGROLASE; Serine protease.
SEQUENCE 263 AA; 27821 MW; 2620A27AFBASD04D CRC64;
                                                                                                                                                                    28184 MW; D7090A9D65395B7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01.JUN-2001 (TrEMBLrel. 17, Created)
01.JUN-2001 (TrEMBLrel. 17, Last sequence update)
01.JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 263 AA.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser protease_Try.
Pfam; PP00089; trypsin; 1
PRINTS; PR00722; CHYMOTRYPSIN.
SWMRT; SM00200; Tryp. SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 2.
PROSITE; PS0135; TRYPSIN SER; 1.
PKD101364; Serine protease.
SEQUENCE 261 AA, 28184 MM; D7090A9D65395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK003060; BAB22539.1; -. HSSP; P00766; 1GCT.
                                                                                                                                                                                      Query Match
Best Local Similarity 53.87
--hea 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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2200008D09RIK.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-PANCREAS;

KREDLINE-21085660, PubMed-117851;

KRAW1 J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishli Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Anizawa K., Itawa M., Nishi K., Kiyosawa T., Salto R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Nishi R., Tonita M., Wagner L., Washio T.,

Schriml L.M., Staubli F., Sizuki R., Tonnita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Boluga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J. Bult C., Pletcher C., Fujita M., Gariboldi M.,

Mornstein M.J., Bult C., Pletcher C., Fujita M., Gariboldi M.,

Mornstein M.J., Strombach C., Seya T., Sakamoto N.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Satok K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Mynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashisahi V.
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                                                                              Gaps
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Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYESIN PAMILY.
EMBL; ARO07566; BAB25112.1;
HSSP; P00766; IGCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
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74.6%; Score 44; DB 11; Length 263; 66.7%; Pred. No. 0.5; cive 0; Mismatches 4; Indels
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Last annotation update)
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InterPro; IRR001314; Chymotrypsin.
InterPro; IRR001314; Chymotrypsin.
Pfam; PR00099; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                         263 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq)
01-JUN-2002 (TrEMBLrel. 21, Last ann)
2200008009Rik protein.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Alkaline phosphatase precursor (EC 3.1.3.1).
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es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
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Q9JJF2;
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Q966VS
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Q9JJF2
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SECUENCE TRAIN—CSTEL/63; TISSUE=STONACH, SPLEEN, AND PANCREAS;

MEDLINE=21085660; PubMed=11217851;

A RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Nashio T.,

A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Suya T., Shibata Y., Storch K.-F.,

Mynchbaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Mynchbaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS0240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Serine protease.
SEQUENCE 263 AA; 27822 MW; 28C4487AFIA26B27 CRC64;
                                                                                                                                                                           Last sequence update)
Last annotation update)
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66.7%; Pred. No. 0.5;
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                                                                           263 AA
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protesse_Try.
Pfam; PP00089; trypsin; 1.
                                                                                                                                            Created)
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01-MAY-1999 (TrEMBLrel. 10, Created)
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EMBL, AKO03079; BAB25235.1; ...
EMBL, AKO07065; BAB25241.1; ...
EMBL, AKO07015; BAB25280.1; ...
EMBL, AKO08795; BAB2580.1; ...
EMBL, AKO0889; BAB25861.1; ...
EMBL; AKO0889; BAB25954.1; ...
                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21,
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                                                                           PRELIMINARY;
                                                                                                                                                                                                                                         2200008D09Rik protein.
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                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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RESULT 8

109CR35

109CR35

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Q9ZP14
ID Q9ZP
AC Q9ZP
DT 01-M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Enzymes in the extracellular matrix of Volvox: an inducible, calcium-dependent phosphatase with a modular composition.";
J. Biol. Chem. 274:1691-1697(1999).
EMBL, AJ012458; CAA10030.1; -.
Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tauda M., Taumi S., Nakato H.;
Transcriptional and Rostranscriptional Regulation of the dally Gene,
"Transcriptional and Rostranscriptional Regulation of the dally Gene,
a Drosophila Integral Membrane Proteoglycan.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB052367; BAB60703.1;
EMBL, AB052365; BAB60703.1;
FIYBASE; FABGO101577; dally.
InterPro; IPRO10163; Glypican.
Pfam: PF01153; Glypican;
PF01154; Glypican;
PF01155; Glypica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Volvox carteri.
Sukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Volvocaceae, Volvox.
VCBI_TaxID=3067;
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Pred. No. 4.1;
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24 1365 ALKALINE PHOSPHATASE.
1365 AA; 146283 MW; 0290DA5C4A792CC4 CRC64;
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Last annotation update)
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Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
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                                                                                                                                                                                                                                                                                                       STRAIN=HK 10;
MEDLINE=99098915; PubMed=9880549;
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(TrEMBLrel. 1 (TrEMBLrel. 1 (TrEMBLrel. 2
01-JUN-2001 (TrEMBLrel
01-JUN-2001 (TrEMBLrel
01-JUN-2002 (TrEMBLrel
1810004D15Rik protein.
                                         CTRL OR 1810004D15RIK.
                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; S01.256;
                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 CGVPAITP 26
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SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; Pubmed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Garber R.J., Goltry L., Tolentino E., Westbrock-Madman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Hancock R.E. W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                         Gaps
                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Brain cDNA, clone MNCD-0953, similar to Mus musculus SPAG4 protein alternative spliced.
                                       Mus musculus (Mouse).
Eukaryoca, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                 62.7%; Score 37; DB 11; Length 103; 50.0%; Pred. No. 5.3; tive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        opportunistic pathogen.";
Nature 406:995-946 (2000).
Nature 406:995-946 (2000).
InterPro; IPR001296; Glycos transf_1.
InterPro; IPR001396; Glycos transf_1.
Hypotherical proceens. Complete proteome.
SEQUENCE 542 AA, 61018 MW; 537F8A7978804CAB CRC64;
                                                                                                                                                                                                                                                                                                                                       01-MAR.2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein PA5455.
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                                                                                                                                                                                                                                                                                                                       542 AA.
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Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                Local Similarity 50.0
es 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonae aeruginosa
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                                                                                                                                                                                                                                                                   S9 CGEPALSPGMPG 70
                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas.
NCBI_TaxID=287;
                                                                                                          STRAIN=C57BL;
                                                                                                                                                                                                       Query Match
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Q9D960
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SEQUENCE FROM N.A.

STAIN-CS-PIL-65; ITSUE=PANCREAS;

MEDLINE-21085660; PubMed=11217851;

A rakawa T., Shinagawa A., Enkunish; Y., Konno H., Adachi J., Fukuda S., Arakawa T., Shinagawa A., Enkunish; Y., Konno H., Adachi J., Fukuda S., Amarawa M., Nishi Y., Kiyosawa H., Kondo S., Yamanaka I., Antara A., Marburner M., Baralow S., Yamanaka I., Radota K., Marauda H.A., Ashburner M., Batalow S., Casavant T., Raber Peisschmann W., Gasaterland T., Gissi C., King B., Kochiwa H., Rachi P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Ruehl P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Rahi P., Lewis S., Marsuo W., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Mormann M., Hume D.A., Kamiya M., Lee N.H., Lyono P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Norone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Norone P., Ring B., Ringwald M., Rodiquez I., Sakamoco N., Schoenbach C., Seya T., Shibata Y., Stock K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Namina L., Shallakaki Y.,

"Functional annotation of a full-length mouse cDNA collection.";

Nature 409:865-690(2001).

TRYSSIN PANILY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYSSIN PANILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilming L.,
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                                                                                                                                                                                                           Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
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Last annotation update)
17, Created)
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21, Last annotation update)
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InterPro; IRR001314; Chymotrypsin.
InterPro; IRR001314; Chymotrypsin.
InterPro; IRR001314; Chymotrypsin.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00200; Tryp_SPO; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
Hydrolase; Serine protease.
SEQUENCE 264 AA; 28151 MW; 1D979719E07C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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01-UTN-2001 (TrEMBLrel. 17, Created)
01-UTN-2001 (TrEMBLrel. 17, Last sequer
01-UTN-2002 (TrEMBLrel. 21, Last annota
1810004015Rik proceain.
CTRL OR 1810004015RIK.
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SEQUENCE FROM N.A.

STRAIN-C57BJ/6J; TISSUE-TONGUE;

MEDLINE-2108566); Dubmed-11217851;

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., Arakawa T., Hara A., Shibata K., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S., Alaxawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Adota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T., Ruchl P., Lewis S., Matsuo Y., Nikaido I., Resole G., Quackenbush J., Sakani K., Okido T., Furuno M., Aonn H., Baldaralli R., Barsh G., Schriml L., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Buruno M., Aonn H., Baldaralli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoch K., P., Sasaki H., Sato K., Schoch K., Wang K., Wang K., Wang K., Wang K., Kawaji H., Kohtsuki S., Nahahariaki, V., Wang K., Wang K., Kawaji H., Kohtsuki S.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116,
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SOGGME Y., Mitsui S., Kataoka K., Kashima K., Kato M., Sakagami J.,
Sogame Y., Mitsui S., Kataoka K., Kashima K., Kato M., Sakagami J.,
Yamaguchi N.;
"Molecular cloning of rat chymopasin.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
TRYPSIN FAMILY.
EMBL. ABUZO177; BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
EMBL. ABUZO177; BAR20287.1; -.
MESSP; PO0766; 4CHA.
MESSP; 201.256; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL; AK009019; BAB26029.1; --
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MGD; MGI:88558; CCrI.
MGD; MGI:88558; CCrI.
InterPro: IPR001214; Chymotrypsin.
InterPro: IPR001214; Chymotrypsin.
InterPro: IPR001214; Chymotrypsin.
InterPro: IPR00125; CHYMOTRYPSIN.
INTERINTS; PR00122; CHYMOTRYPSIN.
INTERINTS; PR00120; TYPESIN DON; I.
I. PROSITE; PS00134; TRYPSIN DON; I.
I. PROSITE; PS00134; TRYPSIN DON; I.
I. PROSITE; PS00135; TRYPSIN HIS; UNKNOWN_I.
I. PROSITE; PS00135; TRYPSIN SER, I.
I. Hydrolass; Serine protesse.
I. SEQUENCE 264 AA; 28167 MW; ID979469A07056C2 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Chymopasin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGVPAITP 26
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Q9EQZ8,
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Matches
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09 2028
AC 09 2028
AC 09 2021
DT 01-MAD
DT 01-MAD
DT 01-MAD
DT 01-UU
DE Chymer
CC Eukary
OC Eukary
CC TISSUUR
RA SOG BM
RA SOG
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DR InterPro; IPR001314; Chymotrypsin.

DR Pfam; PF00089; trypsin.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PROSTTE; PS00134; TRYPSIN_DOM; 1.

DR PROSTTE; PS00134; TRYPSIN_DOM; 1.

DR PROSTTE; PS00135; TRYPSIN_DOM; 1.

DR PROSTTE; PS00135; TRYPSIN_DOM; 1.

DR PROSTTE; PS00135; TRYPSIN_DOM; 1.

KW Hydrolase; Serine protease.

Query Match

Query Match

Query Match

Gl.0%; Score 36; DB 11; Length 264;

Best Local Similarity 75.0%; Pred. No. 22;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps

Qy 1 CGXPAIXP 8

Qy 1 CGXPAIXP 8

Db 19 CGVPAITP 26

Search completed; February 12, 2003, 10:27:22
Job time: 13.197 secs
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us-10-036-371-3.rai

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26, Appl
26, Appl
26, Appl
5514558
5, Appli
5202417
                                                                                                                                                                                                                                                                                     Sequence 317, App
Sequence 3487, Ap
Sequence 4847, Ap
Sequence 11, Appl
                                                                Sequence 15, Appl
Sequence 19, Appl
Sequence 10, Appl
Patent No. 5202417
Sequence 26, Appl
    Sequence 387, App
Patent No. 5202417
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                               Sequence 26,
Sequence 26,
Sequence 26,
Patent No. 551
                                                                                                                                                                                                                                               Seguence 5,
Patent No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUCHORDIN AND USES THEREOF NUMBERS OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: BAA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: DISA
COUNTR
US-08-469-260A-387
5202417-3
US-08-47-6705A-5
US-08-631-4698-15
US-08-631-4698-19
US-09-056-8688-10
US-09-056-8688-10
US-09-056-8688-10
US-09-105-11-26
US-09-105-11-26
US-09-105-11-26
US-09-105-11-26
US-09-105-11-26
US-09-109-637A-317
US-09-1194-198E-5
US-09-1194-198E-5
US-09-1194-198E-5
US-09-1194-198E-5
US-09-1194-001C-3487
US-09-134-001C-3487
US-09-204-208A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: ISM COMPATIBLE
COMPUTER: ISM COMPATIBLE
OPERATING SYSTEM: Windows95
SOFTWARE: PEASESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,365
FILING DATE: 26-SEP-1997
CLASSIFICATION: 514
PRICR APPLICATION: DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/040001
TELECOMMUNICATION INFORMATION:
TELERBHONE: 617/542-5906
                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08938365; Patent No. 5989909; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
      , MOLECULE TYPE: protein US-08-938-365-3
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Best Local Similarity
Matches 6; Conserv
      RESULT 1
US-08-938-365-3
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Sequence 3, Appli
Sequence 3, Appli
Sequence 4074, Ap
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 1, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 29, Appli
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Sequence 2, 7
Sequence 2, 7
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Sequence 7, P
Sequence 7, P
Sequence 22,
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Sequence
Sequence
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-938-365-2

US-08-949-165-3

US-09-130-012A-3

US-09-130-012A-3

US-09-130-012A-1

US-09-953-163

US-08-416-950-11

US-08-410-976-1

US-08-491-976-1

US-08-491-976-1

US-08-491-976-1

US-08-491-976-1

US-08-491-976-3

US-08-491-976-3

US-08-491-976-3

US-08-491-976-3

US-08-460-45-2

US-08-460-451-2

US-08-460-458-2

US-08-460-458-2

US-08-460-458-2

US-08-460-458-2

US-08-460-458-2

US-08-460-458-2

US-08-360-455-2

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.09-609-161B-22
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                                                                                                                                                                                                                                                                                                                                                                         262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                           US-10-036-371-3
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Perfect score:
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                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                           Searched:
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us-10-036-371-3.rai

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Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEGUENCE 3, Application US/09130032A

Sequence 3, Application US/09130032A

Patent No. 5986056

GENERAL INFORMATION:
APPLICANT: Lavallia, Edward
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Candridge
STATE: Respondence: Tombridge
STREET: Genetics Institute, Inc.
COUNTRY: Cambridge STATE: Massachusetts
COUNTRY: USA
ZIP: O2140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BACHORIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,032A
FILING DATE: Adgust 4, 1998
CLASSIFICATION: Adgust 4, 1998
CLASSIFICATION NUMBER: 32,618
REFERENCE DOCKET NUMBER: GI 5284-DIV
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARATERISTICS:
LENGTH: SAT amino acide
TYPE: amino acid
TYPE: amino acid
TYPE: modein acid
TYPE: modein
MEDLUM ILER: F.L.PLY ALER.

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,169A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: LAZAR, Steven R.
REFERENCE/DOCKET NUMBER: G1 5284
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF $76.95
TELERA (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 amino acids
                                                                                                                                                                                                                                                                                 is 954 amino acids
                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 CGADALIPVQTG 422
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US-09-130-032A-3
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                                         Sequence 3, Application US/08749169A
Patent No. 5846770
GENERAL INFORMATION:
APPLICANT: RACIE, Lisa
APPLICANT: BAYALLIE; Edward
APPLICANT: DAROBERTS, Edward
APPLICANT: DAROBERTS, Edward
APPLICANT: DAROBERTS, BAWAL
APPLICANT: DAROBERTS, BAWAL
APPLICANT: DAROBERTS, BAWAL
TITLE OF INVENTION: CHORDIN COMPOSITIONS
NUMBER OF SEQUENCES:
ADDRESSE: 87 CambridgePark Drive
STATE: MASSACHUSETTS
STATE: MASSACHUSETTS
COUNTRY: USA
COMPUTER READABLE FORM:
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US-08-749-169A-3
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us-10-036-371-3.rai

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Gaps
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Sequence 11, Application US/08416950
Patent No. 578036
GENERAL INFORMATION:
APPLICANT: CHISARI, Francis V.
TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS B VIBUS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.9%; Score 33; DB 4; Length 15; Best Local Similarity 62.5%; Pred, No. 4.7; Matches 5; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.

ZIP: 94105-1492

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,950
CLASSIPICATION DATA:
APPLICATION NUMBER: US
FILING DATE: CANG-1992
FRIOM APPLICATION NUMBER: US 07/935,898
FILING DATE: US ANG-1992
PRIOM APPLICATION DATA:
APPLICATION NUMBER: US 07/935,898
FILING DATE: US ANG-1992
PRIOM APPLICATION DATA:
APPLICATION NUMBER: US 07/749,540
FILING DATE: SEANG-1991
ATTOMNEY/AGENT INFORMATION
NAME: PATENTED PATENTED.
                             REFERENCE/DOCKET NUMBER: 018623-011520US
                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 163;
                                  TELECOMMUNICATION INFORMATION:
TELEPAN: 415-576-0200
TELERAX: 415-576-0300
TELEX: CURNOWN
INFORMATION FOR SEQ ID NO: 163:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 aning acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEBRAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 845 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             // MOLECULE TYPE: peptide
US-08-416-950-11
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                   Sequence 4074, Application US/09134001C

Sequence 4074, Application US/09134001C

GENERAL INFORMATION

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: DEPLOATED AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: DEPLOATED ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: DEPLOATED ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: DEPLOATED ACID ACID SEQUENCES

FILE REFERENCE: GTC-07

CURRENT FILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-11-08

PRIOR FILING DATE: 1999-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NOS: 5674
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                                                                    Gaps
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Query Match 59.3%; Score 35; DB 2; Length 954; Best Local Similarity 50.0%; Pred. No. 1.1e+02; Matches 6; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.6%; Score 34; DB 4; Length 662; 60.0%; Pred. No. 1.1e+02; tive 1; Mismatches 3; Indels
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US-09-009-953-163
US-09-009-953-163
Sequence 163, Application US/09009953
Fatent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
ITILE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94111-3834
COMPUTER READALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPREATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: AUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
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APPLICATION NUMBER: US 60/037,432
FILING DATE: 07.FEB.1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4074
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Best Local Similarity 60.0%;
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411 CGADALIPVQTG 422
                                                                                                    1 CGXPAIXPXXTG 12
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Query Match 55.9
Best Local Similarity 62.5
Matches 5; Conservative
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                          LENGTH: 845
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Sequence 11, Application US/08469830
Sequence 11, Application US/08469830
Sequence 11, Application US/08469830
Sequence 11, Application
SEQUENCE 11 PEPTIDES FOR INDUCING CYTOTOXIC TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS B VIRUS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 1
CORPUTER READABLE FORM: COCOMPATY: COCOMPATY: LANGUAGE FOR COMPATION ADDRESSED COCOMPATY: COCOMPATY: LANGUAGE FOR COMPATION ADDRESSED COCOMPATY: COCOMPATY: LANGUAGE FOR COCOMPATY: 
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APPLICANT: NUTER, WILLIAM J., GOODMAN, HOWARD M.
TILE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

55.9%; Score 33; DB 2; Length 845;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels
   Query Match
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651 CGYPALMP 658
                                                                                                                                                                                                         651 CGYPALMP 658
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                                                                                                                                         1 CGXPAIXP 8
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5196194-17
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us-10-036-371-3.rai

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APPLICANT: POGOLSKY, Daniel K.
TITLE OF INVENTION: INTESTINAL TREFOLL PROTEINS.
FILE REPERENCE: 00786-066005
CURRENT APPLICATION NUMBER: US/09/056,868B
CURRENT FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: US 08/476,705
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1994-02-02
PRIOR FILING DATE: 1994-02-02
PRIOR APPLICATION NUMBER: US 08/037,741
PRIOR FILING DATE: 1993-03-25
PRIOR APPLICATION NUMBER: US 07/837,192
PRIOR FILING DATE: 1992-02-13
PRIOR FILING DATE: 1991-02-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PRECENTION DATE: 1991-02-14
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: synthetically generated peptide US-09-056-8688-15
     APPLICATION NUMBER: US/08/631,469B
FILING DATE: 12-Apr-1996
PRIOR APPLICATION DATE: 12-Apr-1996
APPLICATION NUMBER: 08/631,469
FILING DATE: 12-APR-1996
APPLICATION NUMBER: 08/19,352
FILING DATE: 02-FEB-1994
APPLICATION NUMBER: 08/037,741
FILING DATE: 55-MAR-1993
APPLICATION NUMBER: 07/637,192
FILING DATE: 13-FEB-1992
APPLICATION NUMBER: 07/655,965
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: 07/655,965
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: 07/655,965
ATTORNEY/AGENT INFORMATION: NUMBER: 07/655,965
ATTORNEY/AGENT INFORMATION: AMITA L. NAMIR Melikelbühn, Ph.D., Amita L. NAMIR Melikelbühn, Ph.D., Amita L. NAMIR Melikelbühn, 20-003
                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 35,283
ERERRENCE-DOCKET WINBER: 00786/322001
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-08-631-4698-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-056-868B-15
; Sequence 15, Application US/09056868B
; Patent No. 6316218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 106 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 200107
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 62.5'
Matches 5; Conservative
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                                                                                                                                                                Sequence 7, Application US/08476705A; Patent No. 668375S; Patent No. 668375S; Patent No. 668375S; Patent No. 668375S; Patent INPORMATION: INTESTINAL INFORMATION: INTESTINAL TREFOIL PROTEINS NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSES: Fish & Richardson, P.C. STREET: S.S. Franklin Street.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/08631469B
Patent No. 6221840
GENERAL INFORMATION:
APPLICANT: Daniel K. Podolsky
ITIME OF INVENTION: INTESTINAL TREFOIL PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTE: US

ZIP: 02110-2804

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: TBM Comparible

OPERATING SYSTEM: Windows95

SOFTWARE: PastSEO for Windows Version 2.0

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              CUNTRY: DOSCON

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: TBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,705A
FILING DATE: 07-JUN-1995
CLASSIFICATION: H.D., Anita L.
REGISTRATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meix.e.john, Ph.D., Anita L.
REFERENCE/DOCKET NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 30,784
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-542-5070
INFORMATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 106 amino acids TYPE: amino acid
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Best Local Similarity 62.5°
....hes 5; Conservative
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US-08-476-705A-7
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                                              68 CGYPGISP 75
1 CGXPAIXP 8
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US-08-631-469B-20
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Ouery Match
54.2%; Score 32; DB 4; Length 106;
Best Local Similarity 62.5%; Pred: No. 46;
Matches 5; Conservative 0; Mismatches 3; Indels
Matches 5; Conservative 0; Mismatches
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54.2%; Score 32; DB 2; Length 156; 50.0%; Pred. No. 67; tive 1; Mismatches 4; Indels
                                                                                                       Search completed: February 12, 2003, 10:30:08 Job time : 4.79403 secs
                 ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0
Matches 5; Conservative
CORRESPONDENCE ADDRESS:
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66;
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                                                                                                                                                      Sequence 29, Application US/08330394A

Faquence 29, Application US/08330394A

Facturence 10. 5856201

GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Shoiegl, Itai
APPLICANT: Shoiegl, Itai
APPLICANT: Goldstein, Marc A.
APPLICANT: Doi, Roy H.
TITLE OF INVENTION: METHODS OF DETECTION USING THE
TITLE OF INVENTION: ABLUECS: 33
CORRESPONDED ADDRESS:
ADDRESSEE: PENNIE & EDMONIS
STREET: 1155 AVENUE OF THE AMERICAS
COMPUTRY: U. S.A.
ZITP: 10014
COMPUTRY: U. S.A.
ZITP: 10014
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER TEADABLE FORM:
COMPUTER TEADABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.2%; Score 32; 50.0%; Pred. No.
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amino acid
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Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-330-394A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 PVVNPKVTGY 145
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          CGXPAIXP 8
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                                                                                                                                  RESULT 14
US-08-330-394A-29
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US-08-330-394A-22
; Sequence 22, Application US/08330394A
; Patent No. 5856201
; GENERAL INFORMATION:
 APPLICANT: Shoseyov, Oded
; APPLICANT: Yosef, Karmey
APPLICANT: Sphied!, Itai
APPLICANT: Goldstein, Marc A.
APPLICANT: Doi, Roy H.
; TITLE OF INVENTION: METHODS OF DETECTION USING THE
; TITLE OF INVENTION: CELLULOSE BINDING DOMAIN
; NUMBER OF SEQUENCES: 33

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Gaps

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35 59.3 954 10 US-09-944-396-7 35 59.3 954 10 US-09-944-097-7 35 59.3 954 10 US-09-944-32-7 35 59.3 954 10 US-09-943-762-7	24 35 59.3 954 10 US-09-944-654-7 Sequence 7, App 25 35 59.3 954 10 US-09-943-851A-7 Sequence 7, App 26 35 59.3 955 9 US-10-044-716-8 Sequence 8, Appl 27 35 59.3 955 9 US-09-978-051-8 Sequence 8, Appl 28 34 57.6 200 10 US-09-925-299-817 Sequence 817, App	34 57.6 360 9 US-09-905-291A-213 34 57.6 360 9 US-09-902-851-213 34 57.6 360 9 US-09-907-844-213 34 57.6 360 9 US-09-907-841-213 34 57.6 360 9 US-09-907-841-213	34 57.6 360 9 US-101-174-590-28 34 57.6 360 9 US-10-174-590-28 34 57.6 360 9 US-10-176-758-28 34 57.6 360 9 US-10-175-737-28	34 57.6 360 9 US-101-966-742-213 34 57.6 360 9 US-101-373-706-28 34 57.6 360 9 US-10-175-738-28	34 57.6 360 9 US-10-175-752-28 Sequence 34 57.6 360 9 US-10-176-482-28 Sequence 34 57.6 360 9 US-10-176-482-28 Sequence 34 57.6 360 9 US-10-176-157-28	34 57.6 360 9 US-10-180-552-28 Sequence 28, 34 57.6 360 9 US-10-180-557-28 Sequence 28, 34 57.6 360 9 US-10-180-557-28 Sequence 28,	ALIGNMEN OCH US/10036371 1987A1 N, JON B. FISH SERINE PROTEINAS COSMETIC USE 17/284960 2002-01-07 MUNDER: US/10/036,377 299-10-12 MBER: 5086/99 999-06-18 999-06-18 Sor Q I or V I or V 86.4%; Score 51;	Similarity 100.0%; Pred. No. 0.0005; 3; Conservative 0; Mismatches 0;
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.	OM protein - protein search, using sw model Run on: February 12, 2003, 10:22:36 ; Search time 1.9791 Seconds (without alignments)		table: BLOSUM62 Gapop 10.0 ,	Searched: 140259 segs, 25548876 residues Total number of hits satisfying chosen parameters: 140259		Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries	Database : Published Applications AA:*	9 35 59.3 954 10 US-09-945-015-7

35 59.3 954 10 US-09-944-35 59.3 954 10 US-09-943-35 59.3 954 10 US-09-943-35 59.3 954 10 US-09-943-34 57.6 360 9 US-09-962-34 57.6 360 9 US-09-967-8 34 57.6 360 9 US-09-176-73 34 57.6 360 9 US-10-176-73 34 57.6 360 9 US-10	Sequence 7, Ap. Sequence 8, Ap. Sequence 8, Ap.	817 Sequence 81, Sequence 81, Sequence 2113 Sequence 2113 Sequence 2113 Sequence 218 Sequence 218 Sequence 28, Sequence 28	S AND THEIR PHARMACEUTICAL AND	
15 59.3 954 15 59.	0 US-0 US-0 US-0 US-0 US-0 US-0 US-0 US-	0. US - US	ALIGNMENT 0036371 3. 11NE PROTEINASE; 12 US/10/036,371 11-07 11-07 11-07 12-07 12-07 13-08	
1	E. E		ication US/1(20141987A1 ION: MARSON, JON E ION: COSMETT 10N: COSMETT 110N: UNBER: COSMETT 110N: UNBER: COSMETT 110N: UNBER: COSMETT 110N: UNBER: ST 110N: UNBER: ST	. R or S or .
22222222222222222222222222222222222222		N. ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ Մ. Մ. ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ Մ. Մ. ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ ಈ	0 036 encent LICILI LICIL LICIL LICIL LICIL COR OOR OOR OOR OOR OOR OOR	.aeee

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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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CORGANISM: Homo saptens
US-09-925-297-529
                                                                                                                                                                                                                                                                                1 CGXPAIXPXXTG 12
                                                                                                                                                                                                                                                                                                                     23 CGVPAIHPVLSG 34
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                                                                                                                          RESULT 2
US-10-036-371-5
# Sequence 5, Application US/10036371
# Sequence 5, Application US/10036371
# Patent No. US20020141987A1
# Patent No. US20020141987A1
# TITLE OF INVENTION: FIGH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND TITLE OF INVENTION: COSMETIC USE
# TITLE OF INVENTION: COSMETIC USE
# TITLE OF INVENTION: COSMETIC USE
# PILE REPERENCE: 81691/284960
# CURRENT APPLICATION NUMBER: US/10/036,371
# PRIOR PILING DATE: 1999-10-12
# PRIOR PILING DATE: 1999-10-12
# PRIOR PILING DATE: 1999-10-12
# PRIOR PILING DATE: 1999-06-18
# NUMBER OF SEQ ID NOS: 8
# SOFTWARE: Patentin Ver. 2.1
# LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE
LOCATION: (2)
UNDER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (94)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (126)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (130)
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sequence 643, Application US/09925297

sequence 643, Application US/09925297

sequence 643, Application US/09925297

sequence 643, Application US/09/025, 297

current Filing Date: 2001-08-10

prior Piling Date: 2001-08-10

prior Piling Date: 2000-03-08

prior Piling Date: 1999-03-12

NUMBER OF SEQ ID NOS: 928

software: Patentin Ver. 2.0

seq ID NO 643

LENGTH: 146

TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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Best Local Similarity 58.3
Matches 7; Conservative
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                                       CGXPAIXPXXTGY 13
                                                                              1 CGXPAIXPXXTGY 13
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US-09-925-297-643
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NAME/KEY: SITE
DOCATION: (137)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (143)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-643
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; Beach No. US20020084659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TILLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 529
LENTH: 192
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Pred. No. 1.3;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                          Query Match
67.8%; Score 40; DB 10; Length 146;
Best Local Similarity 58.3%; Pred. No. 0.72;
Matches 7; Conservative 1; Mismatches 4; Indels
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Sequence 96, Application US/0968615

Sequence 96, Application US/0968615

Patent No. US20020064856A1

GENERAL INFORMATION:
APPLICANT: PLOWMAN GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: GENEREL, SEAN
APPLICANT: GENEREL, GENEN
APPLICANT: GENEREL, GENEN
APPLICANT: GENERALMA, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT APPLICATION NUMBER: 00/214,047
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PRETEING BATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PRETEING BATE: 2010
TYPE: PRETEING BATE: 2010
SOFTWARE: 2010
SOFTWARE: PRETEING BATE: 2010
SOFTWARE: 2010
SOFTWARE: 2010
SOFTWA
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58.3%;
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Best Local Similarity 58.3
Matches 7; Conservative
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APPLICANT: Tunas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLCI
CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR PILING DATE: December 3, 1997
PRIOR PILING DATE: December 1, 1997
PRIOR PLING DATE: December 1, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR APPLICATION NUMBER: 60/069335
PRIOR APPLICATION NUMBER: 60/069335
PRIOR APPLICATION NUMBER: 60/069278
                                                                                                                    Gaps
                                                                                                                    0
                                                             Query Match 59.3%; Score 35; DB 10; Length 948; Best Local Similarity 50.0%; Pred. No. 42; Matches 6; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: Docember 3, 1997
PRIOR FILING DATE: Docember 11, 1997
PRIOR PILING DATE: Docember 11, 1997
PRIOR PILING DATE: Docember 11, 1997
PRIOR PELICATION NUMBER: 60/069,234
PRIOR PELICATION NUMBER: 60/069,279
PRIOR PELING DATE: Docember 11, 1997
PRIOR PLING DATE: Docember 11, 1997
PRIOR PLING DATE: Docember 12, 1997
PRIOR PLING DATE: Docember 12, 1997
PRIOR PLING DATE: Docember 16, 1997
PRIOR PLING DATE: Docember 17, 1997
PRIOR PLING DATE: Docember 18, 1997
PRIOR PLING DATE: Sebruary 9, 1998
PRIOR PLING DATE: February 9, 1998
PRIOR PLING DATE: February 25, 1998
PRIOR PLING DATE: Pebruary 25, 1998
PRIOR PLING DATE: Docember 16, 1998
PRIOR PRING DATE: Docember 16, 1998
PRIOR PRING DATE: Pebruary 25, 1998
                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09944413
Patent No. US20020156004A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Godowski, Paul
Grimaldi, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                     Baker, Kevin
Botstein, David
Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen, Mary
Goddard, Audrey
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Hillan, Kenneth
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Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William
                                                                                                                                                                             407 CGADALIPVQTG 418
; ORGANISM: Mus musculus
US-09-897-699-2
                                                                                                                                                 1 CGXPAIXPXXTG 12
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                                                                                                                                                                                                                                                          RESULT 8
US-09-944-413-7
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GENERAL INFORMATION:
GENERAL INFORMATION:
TOTALE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT PELLOR DATE:
CURRENT PELLOR DATE:
CURRENT FILING DATE:
PRIOR APPLICATION NUMBER: US 60/215,179
PRIOR PAPEL ONS:
SOFTWARE: FASE OF MINDOWS Version 4.0
SOFTWARE: FASE OF MINDOWS Version 4.0
SOFTWARE: PASE OF MINDOWS VERSION 4.0
TYPE: PRI
         59.3%; Score 35; DB 10; Length 192; 75.0%; Pred. No. 8.7; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.3%; Score 35; DB 9; Length 867;
50.0%; Pred. No. 38;
tive 1; Mismatches 5; Indels
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Patent No. US20020038468A1
  Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 50.0
Matches 6, Conservative
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US-09-811-088-10
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                                                                                                                                   15 CGIPAIKP 22
                                                                                          1 CGXPAIXP 8
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US-09-897-699-2
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APPLICARY: WOOCA WILLIAM

TITLE OF INVENTION: ACIDS ENCORING THE SAME
CURRENT APPLICATION WINDER: 18/09/944.403
CURRENT APPLICATION WINDER: 2001-05-25
PRIOR PLING DATE: JOOL-05-25
PRIOR PLING DATE: JOOL-05-25
PRIOR APPLICATION WINDER: 60/06/313
PRIOR APPLICATION WINDER: 60/06/314
PRIOR APPLICATION WINDER: 60/06/32
PRIOR PLING DATE: December 12, 1997
PRIOR APPLICATION WINDER: 60/06/303
PRIOR PLING DATE: December 13, 1997
PRIOR PLING DATE: PEDFURCE 10/04/40
PRIOR PLING 
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PRIOR PILING DATE: March 3, 1999
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: March 3, 1999
PRIOR PILING DATE: March 1999
PRIOR PILING DATE: June 22, 1999
PRIOR PILING DATE: June 22, 1999
PRIOR PILING DATE: OWINGER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: NO. US20020165143Anember 30, 1999
PRIOR PILING DATE: No. US20020165143Anember 30, 1999
PRIOR PILING DATE: DECEMBER: PCT/US99/28301
PRIOR PILING DATE: DECEMBER: PCT/US99/28301
PRIOR PILING DATE: DECEMBER: PCT/US99/30095
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 11, 1999
PRIOR PILING DATE: PCT/US99/30095
PRIOR PILING DATE: PCT/US00/0365
PRIOR PILING DATE: PCT/US00/0366
                                                                                                   Tumas, Daniel
Wood, William
                                                                                                              APPLICANT
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Pred. No. 42;
1; Mismatches 5; Indels
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: December 1, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR APPLICATION NUMBER: 09/216,311
PRIOR PILING DATE: December 22, 1998
PRIOR PILING DATE: March 3, 1999
PRIOR PILING DATE: December 12, 1999
PRIOR PILING DATE: September 12, 1999
PRIOR PILING DATE: September 12, 1999
PRIOR PILING DATE: September 12, 1999
PRIOR PILING DATE: NO. US20020156004A1ember 30, 1999
PRIOR PILING DATE: December 1, 2099
PRIOR PILING DATE: December 1, 2090
PRIOR PILING DATE: PEDVILAY 22, 2000
PRIOR PILING DATE: MARCH 30, 2000
PRIOR PILING DATE: PEDVILAY 22, 2000
PRIOR PILING DATE: PEDVILAY 28, 2000
PRIOR PILING DATE: PEDVILAY 28, 2000
PRIOR PILING DATE: PEDVILAY 28, 2001
PRIOR PILING DATE: PEDVILAY 28, 2001
PRIOR PILING DATE: WARCH 30, 2001
PRIOR PILING DATE: PEDVILAY 28, 2001
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Patent No. US20020165143A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Gerriteen, Mary
Goddwaki, Paul
Grimaldi, Christopher
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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Best Local Similarity 50.0
Matches 6; Conservative
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CORGANISM: Homo Sapien
US-09-944-413-7
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APPLICANT:
APPLICANT:
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Gurney, Austin Hillan, Kenneth

APPLICANT: APPLICANT:

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59.3%; Score 35; DB 9; Length 954; 50.0%; Pred. No. 42; 1. Mismatches 5; Indels
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OR APPLICATION NUMBER: 09/216, 021

OR PILING DATE: December 16, 1998

OR PILING DATE: December 22, 1998

OR FILING DATE: December 22, 1998

OR FILING DATE: December 22, 1998

OR PILING DATE: March 3, 1999

OR PILING DATE: March 3, 1999

OR PILING DATE: JUME 22, 1999

OR PILING DATE: JUME 22, 1999

OR PILING DATE: SPETEMBER: PCT/US99/21090

OR FILING DATE: SPETEMBER: PCT/US99/28409

OR FILING DATE: SPETEMBER: PCT/US99/28409

OR PILING DATE: No. US20020168715A1ember 30, 1999

OR PILING DATE: No. US20020168715A1ember 30, 1999

OR PILING DATE: NO. US20020168715A1ember 30, 1999

OR APPLICATION NUMBER: PCT/US99/28331
                                                                         PRIOR FILING DATE: December 14, 139, PRIOR PRIOR FILING DATE: December 18, 1997

PRIOR APPLICATION NUMBER: 60/074, 406

PRIOR PELING DATE: January 5, 1998

PRIOR PELING DATE: Pebruary 9, 1998

PRIOR PILING DATE: February 9, 1998

PRIOR PILING DATE: February 9, 1998

PRIOR PILING DATE: February 25, 1998

PRIOR PILING DATE: Pebruary 25, 1998

PRIOR PILING DATE: Pebruary 25, 1998

PRIOR PILING DATE: Pebruary 25, 1998

PRIOR PILING DATE: December 16, 1998

PRIOR PILING DATE: December 16, 1998

PRIOR PILING DATE: December 17, 1998

PRIOR PILING DATE: December 1, 1999

PRIOR PILING DATE: PEPTION SOUGH 1, 1999

PRIOR PILING DATE: PEPTION SOUGH 1, 1999

PRIOR PILING DATE: NA. US20020168715A1ember 1, 1999

PRIOR PILING DATE: NO. US20020168715A1ember 1, 1999

PRIOR PILING DATE: NO. US20020168715A1ember 1, 1999

PRIOR PILING DATE: NO. US20020168715A1ember 1, 1999

PRIOR PILING DATE: PEPTION YOUNGER: PCT/US99/2819

PRIOR PILING DATE: PEP
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Best Local Similarity 50.0
Matches 6; Conservative
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; ORGANISM: Homo Sapien
US-09-944-896-7
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACTUS ENCODING THE SAME
TITLE OF INVENTION: ACTUS ENCODING THE SAME
TITLE OF INVENTION: ACTUS ENCODING THE SAME
FILE REFERENCE: P25.48Plc1
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 00/069,334
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: Docember 11, 1997
PRIOR PAPLICATION NUMBER: 60/069,334
PRIOR PAPLICATION NUMBER: 60/069,335
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 11, 1997
PRIOR PAPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 16, 1997
PRIOR PAPLICATION NUMBER: 60/069,696
PRIOR PAPLICATION NUMBER: 60/069,696
PRIOR PAPLICATION NUMBER: 60/069,702
PRIOR PLING DATE: December 16, 1997
PRIOR PLING DATE: December 16, 1997
PRIOR FILING DATE: December 17, 1997
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PRIOR FILING DATE: February 22, 2000
FRIOR APPLICATION NUMBER: PCT/USOO/05841
PRIOR PLING DATE: March 2, 2000
FRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR PLING DATE: May 28, 2000
PRIOR PLING DATE: JULY 28, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR PLING DATE: Ebernary 28, 2001
PRIOR APPLICATION NUMBER: PCT/USOI/0520
PRIOR PRIOR PLING DATE: December 1, 2000
PRIOR PLING DATE: February 28, 2001
SEQ ID NO 7.
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Patent No. US20020168715A1
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Goddard, Audrey
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Hillan, Kenneth
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Tumas, Daniel
Wood, William
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Napier, Mary
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; ORGANISM: Homo Sapien
US-09-944-403-7
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APPLICANT:
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PRIOR PILLING DATE: 2001-09-26
PRIOR PILLING DATE: 2001-09-26
PRIOR PILLING DATE: December 3, 1997
PRIOR PILLING DATE: December 1, 1997
PRIOR PILLING DATE: December 11, 1997
PRIOR PILLING DATE: DECEMBER 60/69, 529
PRIOR PILLING DATE: DECEMBER 10, 1999
PRIOR PILLING DATE:
                  Sequence 7, Application US/09944944
Patent No. US20020173463A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              Godowski, Paul
Grimaldi, Christopher
                                                                                                                                                                                                 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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Hillan, Kenneth
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Tumas, Daniel
Wood, William
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US-09-944-944-7
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CURRENT APPLICATION NUMBER: US/09/944,907

CURRENT FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: 09/866,028

PRIOR FILING DATE: 2001-08-25

NUMBER OF SEQ ID NOS: 120
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PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR PILING DATE: No. US20020173463Alember 30, 1999
PRIOR PILING DATE: No. US20020173463Alember 30, 1999
PRIOR PILING DATE: No. US20020173463Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/28095
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: Pebruary 21, 2000
PRIOR FILING DATE: Pebruary 22, 2000
PRIOR PILING DATE: Pebruary 22, 2000
PRIOR PILING DATE: March 2, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: May 28, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR FILING DATE: July 28, 2001
PRIOR FILING DATE: July 28, 2001
PRIOR FILING DATE: Pebruary 28, 2001
PRIOR PILING DATE: PEBRUARY 28, 2001
PRIOR PILING DATE: PEBRUARY 28, 2001
PRIOR FILING DATE: PEBRUARY 28, 2001
PRIOR PILING DATE: PEBRUARY 28, 2001
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Publication No. US20020198147A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William
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Best Local Similarity
Matches 6; Conserv
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Sequence 7, Application US/0994449
Patent No. US20020102647A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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Best Local Similarity 50.0%;
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APPLICANT: Botstein, David
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Hillan, Kenneth
                                                     Kljavin, Ivar
Napier, Mary
Roy, Margaret
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Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William
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ORGANISM: Homo Sapien
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US-09-944-449-7
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFRENCE: P5548PIL
CURRENT APPLICATION NUMBER: US/09/944,929
PRIOR APPLICATION NUMBER: 2001-08-31
PRIOR PRILING DATE: 2001-08-25
NUMBER OF SEQ ID NOS: 120
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Pred. No. 42;
1; Mismatches 5; Indels
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US-09-866-028-7
; Sequence 7, Application US/0966028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Bactein,Dan
; APPLICANT: Estron,Dan
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gertitsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Goddard,Audrey
; APPLICANT: Goddard,Audrey
; APPLICANT: Goddwæki,Paul
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Publication No. US20020197612A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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Hillan, Kenneth
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Napier, Mary
Roy, Margaret
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                                TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-907-7
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; ORGANISM: Homo Sapien
US-09-944-929-7
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Best Local Similarity
Matches 6; Conserv
; SEQ ID NO 7
; LENGTH: 954
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##PILICANI' WOOG, WILLIA AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC FILE REPERRORE: PS444P101

FILE REPERRORE: PS444P101

CURRENT APPLICATION NUMBER: 09/866,028

PRIOR APPLICATION NUMBER: 09/866,028

PRIOR APPLICATION NUMBER: 06/067,411

PRIOR PLILING DATE: 2001-05-25

PRIOR PLILING DATE: December 1, 1997

PRIOR PLILING DATE: December 11, 1997

PRIOR PLILING DATE: 06/069,335

PRIOR PLILING DATE: 06/069,335

PRIOR PLILING DATE: 06/069,279

PRIOR PLILING DATE: 06/069,279

PRIOR PLILING DATE: 06/069,279

PRIOR PLILING DATE: December 11, 1997

PRIOR PLILING DATE: December 12, 1997

PRIOR PLILING DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,636

PRIOR APPLICATION NUMBER: 60/069,636

PRIOR PLILING DATE: December 16, 1997

PRIOR PLILING DATE: December 16, 1997
APPLICANT: ROY-MATGRICAL
APPLICANT: ROY-MATGRICAL
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, WILLIAM
TITLE OF INVENTION: SECRETED AND TRANSMEWBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT APPLICATION NUMBER: US/09/866,028
PRIOR APPLICATION NUMBER: US/09/866,028
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 7
LENGTH: 954
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Score 35; DB 10; Length 954; pred. No. 42; 1; Mismatches 5; Indel8
PRIOR APPLICATION NUMBER: 60/669,870
PRIOR APPLICATION NUMBER: 60/669,871
PRIOR APLICATION NUMBER: 60/66,101
PRIOR APLICATION NUMBER: 60/66,101
PRIOR APLICATION NUMBER: 60/66,101
PRIOR APLICATION NUMBER: 60/66,101
PRIOR PLINING DATE: December 16, 1999
PRIOR PLINING DATE: PED-1994
PRIOR PLINING DATE: PED-1
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Best Local Similarity 50.0%;
Matches 6; Conservative 1
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Search completed: February 12, 2003, 10:31:05 Job time : 2.9791 Becs

411 CGADALIPVQTG 422 CGXPAIXPXXTG 12 Н

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Gaps

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198.395 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                     908470 seqs, 133250620 residues
                                                                       OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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1 IVNGEEAVPHXWXWQVSLQX 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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A Geneseq 101002:*

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| SIDSZ/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDSZ/gcgdata/geneseqfy-emb1/AA1981.DAT:*
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| SIDSZ/gcgdata/geneseqfy-emb1/AA1991.DAT:*
| SIDSZ/gcgdata/geneseqfy-emb2/AA1991.DAT:*
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| SIDSZ/gcgdata/geneseqfy-emeseqfy-emb1/AA1991.DAT:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Amino terminal seq Amino terminal seq PX, porcine pancre Sequence of human Bovine chymotrypsi Porcine pancreatic Bovine chymotrypsi N-terminal of a bo N-terminal of bovi Human pancreatic c Description SUMMARIES AAB31576 AAB31578 AAW02588 AAP60061 AAY99596 AAR29621 AAY33344 AAY93935 AAE07941 ü 13 20 21 22 22 Length DB 245 253 20 20 20 20 146 Query Match Score 922 922 932 933 933 m 4 m 9 r 8 e 0 Result No.

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ALIGNMENTS

Pish, serine proteinase; pain; acute inflammation; chronic inflammation; arthritis; inflamed joint; bursitis; osteoarthritis; septic arthritis; rheumatoid arthritis; juvenile rheumatoid arthritis; fibromyaldia; systemic lupus erythematosus; phlobitis; tendinitis; rash; psoriasis; acne; eczema; facial seborrheic eczema; foreskin infection; athlete's foot; fistulae infection; utcer; navel infection; wrinkle; soar; kelloid; boll; wart; allergic itch; hemorrhoid; wound; fungal infection; autoimmune disease. Amino terminal sequence of cod trypsin B chain. AAB31576 standard; peptide; 20 AA (first entry) 20-APR-2001 AAB31576; RESULT 1 AAB31576

Location/Qualifiers /label= Ser, Thr Misc-difference 13 Misc-difference 13 Gadus callarias.

'label= Ser, Pro, Tyr /label= Asp, Gln Misc-difference 20 WO200078332-A2

28-DEC-2000

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18-JUN-1999; 9918-0005086
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Matches
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                                                                                                                                                                                                  The specification describes a fish serine proteinase. The proteinases are useful as medicaments, for treating and preventing a disease in a human or an animal such as pain, acute inflammation, chronic chronic chronic chronic architis, inchains the medicaments, bursitis, osteoarthritis, inchails remarked arthritis, inchails erythematosus, phlebitis, tendinitis, rash, psoriaais, acne, eczema, facial seborrheic eczema of the hands, face or neck, foreskin infections, athlete's foot, fistulae infections, infected topical ulcers, navel infections in newborns, wrinkles, scars, felicions, wounds from burns, fungal infections and immunological and antecimmune diseases. They are also useful for removing dead or peeling skin from otherwise healthy skin, and for treating or preventing a classes in which pathogenesis is caused by bacteria, virus, fungus, parasite or a protozoan or a receptor mediated binding is involved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fish, serine proteinase; pain; acute inflammation; chronic inflammation; arthritis; inflamed joint; bursitis; osteoarthritis; septic arthritis; theumatoid arthritis; florematoid arthritis; florematoid; systemic lupus erythematosus; phiebitis; tendinitis; trash; psoriasis; acne; eczema; facial seborrheic eczema; foreskin infection; arthere's a foot; fistulae infection; ulcer; navel infection; wrinkle; scar; kelloid; boil; wart; allergic itch; hemorrhoid; wound; kungal infection; autoimmune disease.
                                                                                                          rian serine proteinase, useful as a cosmetic, medicament for treating eczema, psoriasis, arthritis, and in the manufacture of the medicament for treating, preventing pathogenic diseases involving receptor mediated binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                  Disclosure; Page 5; 38pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IVNGEEAVPHXWXWQVSLQ 19
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      15-JUN-2000; 2000WO-IS00005
                              99IS-0005086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Conservative
                                                   (BJAR/) BJARNASON J B
                                                                                                  WPI; 2001-091493/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                             18-JUN-1999;
                                                                            Bjarnason JB;
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AAB31578
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The specification describes a fish serine proteinase. The proteinases are useful as medicaments, for treating and preventing a disease in a human or an animal such as pain, acute inflammation, chronic chronic chronic chronic chronic architis, inflamed joints, bursitis, osteoarthritis, inflamed joints, bursitis, osteoarthritis, cheumatoid arthritis, septic arthritis, resh, cheumatoid arthritis, septic arthritis, rash, cheumatoid arthritis, septic arthritis, rash, cheumatoid arthritis, septic arthritis, rash, chected activates, acceme of the hands, face or neck, foreskin infections, athlete's foot, fistulae infections, infected topical ulcers, navel infections in newborns, wrinkles, scars, infections, wounds from burns, ling infections and immunological and autoimmune diseases. They are also useful for removing dead or peeling stin from otherwise healthy skin, and for treating or preventing a disease in which pathogenesis is caused by bacteria, virus, fungus, parasite or a protozoan or a receptor mediated binding is involved. The present sequence represents the amino terminal of bovine trypsin B
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                                                                                                                                                                                          Fish serine proteinase, useful as a cosmetic, medicament for treating eczema, psoriasis, arthritis, and in the manufacture of the medicament for treating, preventing pathogenic diseases involving receptor mediated binding -
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Paget's disease; fracture repair; bone defect; osteopetrosis;
metastasis; osteoblast; osteoclast.
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84.2%; Pred. No. 1.6e-07;
Mismatches 3; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PX, porcine pancreas-derived factor N-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW02588 standard; peptide; 31 AA.
                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 5, 38pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yoneda T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-US16826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ivnderavpgswpwovsid 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 84.2 es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mundy GR,
(BJAR/) BJARNASON J B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-309523/31.
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                                                                                                                                 WPI; 2001-091493/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-1994;
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                                                                       Bjarnason JB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUN-1996.
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us-10-036-371-4.rag

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                                                                                     AAM02588 is the N-terminal portion of a factor derived from pig pancreatic tissue. The factor was designated PX. PX inhibits the action of otecoclasts and stimulates the action of otecoblasts, hence PX inhibits bone resorption and stimulates bone formation. The new factor also stimulates the proliferation of human MG-63 osteobastcoma calls (osteoblast-like cells). The factor is useful for treating bone loss, e.g. due to osteoporosis or Paget's disease. The factor may also be used to hasten bone fracture repair. Antibodies and antagonists of PX can be used to treat osteopetrosis and
                                                                                                                                                                                                                                                                                                      Gaps
           increatic-derived factor - which inhibits bone increases bone formation, used to develop prods. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The genetically engineered prod. can eliminate the dependency on human pancreas supplies for the elastase, and avoids antibody formation and possibility of anaphylaxis using porcine elastase.
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using hosts modified DNA coding for enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawashima I, Eurukawa H, Ohmine T;
                                                                                                                                                                                                                                                                  85.0%; Score 85; DB 17; Length 31; 73.7%; Pred. No. 2.7e-07; Live 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of human pancreatic elastase IIIB.
           New isolated pancreatic-derived factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzyme; serum lipoprotein metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                      AAP60061 standard; Protein; 242 AA
                                                                 Claim 1; Fig 14; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 8; 45pp; English.
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85JP-0072308.
85JP-0091986.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                 Local Similarity 73.7
hes 14; Conservative
                                                                                                                                                                                                                osteoblastic metastasis
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                                    diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85JP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1986-280300/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 AA;
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                                                                                                                                                                                                                                           31 AA;
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                            resorption and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fakiguchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-1985;
27-APR-1985;
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                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohsumi J;
                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                             Matches
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The present sequence is bovine chymotrypsinogen. It was included in a review of sequence homologies of several plasminogen activators. Plasminogen is the principal serine protease zymogen in the practical interpretates. Its active form, plasmin, is implicated in pericellular proteelysis associated with a wide range of physiological and pathological protecesses. Plasminogen expression is regulated by plasminogen activators which hydrolyse a peptide bond in the plasminogen to convert it to plasmino or form tight binding complexes with plasminogen to spontaneously convert it to plasmin. The sequence plasminogen to spontaneously convert it to plasmin or form tight bunding through analysis has identified a six amino acid peptide involved in plasminogen activation. This peptide is particularly useful when inserted the propriet of plasminogen activation free plasminogen activation/recognition site of plasminogen benden as the properties are useful in preparing thrombolytic agents for treating the plasminogen activation free plasminogen benders such as heart attack.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide with plasminogen activator activity useful as thrombolytic agent for treating blood clot disorders e.g. heart attack, comprises 10 amino acid peptide fragment for recognition or activation of
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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85.0%; Score 85; DB 7; Length 242; 73.7%; Pred. No. 2.7e-06; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine; plasminogen activator; cardiant; thrombolytic; heart attack; stroke; blood clotting disorder.
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                                                                                                                                                                                                                                                                                                                                                                                  AAY99596 standard; protein; 245 AA.
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                                                                                                                                         1 IVNGEEAVPHXWXWQVSLQ 19
                                                                                                                                                                                   1 VVNGEDAVPYSWPWQVSLQ 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovine chymotrypsinogen A.
                                                                            Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-422975/36.
   Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY99596;
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AAY9787
AAY9787
AAY97
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This invention describes a novel method for treating ache and eczema using a krill-derived multifunctional enzyme [1] which comprises 2 or more of the activities of chymotrypsin, trypsin, collagenase, elastase or exopeptidase and is reactive with cell surface receptors such as proteins or glycoproteins. The product of the invention have antisebornheic, anti-ache, dermatological and anti-eczema activity.

[1] removes or inactivates cell surface receptors (proteins and glycoproteins) and adhesion molecules such as ICAM-1 (i.e. CD54), ICAM-2, VCAM-1, CD3, CD28, CD29, CD31, CD44, CD49, CD51, CD102 and the asialo GMI ceramide. This sequence represents the N-terminal fragment of bovine chymotrypsin which is used to describe the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transplantation rejection; hydrolase; graft versus host disease; cell surface adhesion molecule; immune reaction; inflammation; shock; tumour metastasis; autoimmune disease; Krill derived multifunctional enzyme.
                                                                                                                                                                    Treating acne and eczema using a krill-derived multifunctional enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preventing or ameliorating transplantation rejection reactions using hydrolase enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 82, DB 20; Length 20
Pred, No. 5.2e-07;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-terminal of a bovine chymotrpsin hydrolase enzyme.
                                                                                                         De Faire JR
                                                                                                                                                                                                       Disclosure; Column 21-22; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY93935 standard; peptide; 20 AA.
                                                                                                         Lindblom R, Kay J, Franklin RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.0%;
78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PHAI-) PHAIRSON MEDICAL INC
             94US-0388501.
95US-0385540.
95US-0486820.
                                                                           (PHAI-) PHAIRSON MEDICAL INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 78.5
Matches 15; Conservative
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                                                                                                                                           WPI; 1999-561004/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AA;
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                               08-FEB-1995;
07-JUN-1995;
                22-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multifunctional enzyme; treatment; acne; eczema; chymotrypsin; trypsin; collagenase; elastase; exopeptidase; cell surface receptor; anti-acne; antiseozraeic; dermatcologicai; anti-eczema; adhesion molecule; ICAM-1; CD54; ICAM-2; VCAM-1; CD8; CD29; CD31; CD34; CD44; CD49; CD62L; CD102; GM1 ceramide; krill; bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                    pig; swine; bile acid; gall bladder; bile acid secretion promoters;
liver function improvers; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents porcine pancreatic elastase III. It was expressed in E. coli YA21 using the expression vector pELE001. It may be used in bile acid secretion promoters and liver function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pig pancreas elastase protein - used in bile acid secretion promoters and liver function improvers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 85; DB 13; Length 253;
Pred. No. 2.8e-06;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine chymotrypsin N-terminal fragment.
                                                AAR29621 standard; Protein; 253 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 8; 10pp; Japanese.
                                                                                                                                              Porcine pancreatic elastase III.
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                                                                                                                30-APR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 73.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         (SANY ) SANKYO CO LID.
                                                                                                                                                                                                                             Sue scrofa domestica
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-428826/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ31724
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                                                                                                                                                                                                                                                             JP04325090-A.
                                                                                                                                                                                                                                                                                                                             23-APR-1991;
                                                                                                                                                                                                                                                                                                                                                           23-APR-1991;
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                                                                                                                                                                                                                                                                                           13-NOV-1992.
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                                                                                  AAR29621;
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                    RESULT 6
AAR29621
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Length 20;

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Rosen CA, Ruben SM;
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                                                                                                                                                                                                                                     20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000.
                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                             Query Match
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                         The specification describes a method for preventing or ameliorating transplantation rejection reactions for transplantation of immune cells or other tissues. The method comprises treating a source of immune cells or with a hydrolase or hydrolase mixture and administering the treated immune cells to a recipient aimal. The hydrolase especially has a preference for temoving, destroying, inactivating or disabling at least cone of CD4, CD8, CD25, CD29, ICAN-1, CD55, an integrin, CD154, CD and CD80 in contrast to removing, destroying, inactivating or disabling TGR. The methods are useful for preventing graft versus host concuses which are involved in triggering the immune reactions involved in the disease by using hydrolase enzymes to remove the cell surface adhesion cell-cell or cell-virus adhesion syndrome comprisaing inflammation, shock, twocur metastases, autoimmune disease, transplantation rejection contrainal of a hydrolase, which may be used in the method of the
                                                                                                                                                                                                                                                                                                                                                               o'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multifunctional hydrolase, rejection reaction, extra-corporeal, therapy, graft versus host disease, transplantation rejection; autoimmune disease, microbial infection, immune disorder, cytostatic, cystic fibrosis, chronic obstructive pulmonary disease, COPD, atherosclerosis, cancer, asthma, septic shock; toxic shock syndrome, conjunctivitis; reperfusion injury, pain; immunosuppressive; antibacterial; vasotropic; bovine.
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ameliorating, preventing or treating immune rejection reactions, such as graft versus host disease, autoimmune disease, asthma, cancer, by extra-corporeally treating donor tissue with hydrolase such as a
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                                                                                                                                                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                            82.0%; Score 82; DB 21; Length 20;
78.9%; Pred. No. 5.2e-07;
"Mismarches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminal of bovine serine multifunctional hydrolase.
Disclosure; Page 26; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE07941 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PHAI-) PHAIRSON MEDICAL INC.
                                                                                                                                                                                                                                                                                                                                                                                1 IVNGEEAVPHXWXWQVSLQ 19
                                                                                                                                                                                                                                                                                                                                                                                                     1 IVNGEDAVPGSWPWQVSLQ 19
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                                                                                                                                                                                                                                                                                                                                     Local Similarity 78.9
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                                                                                                                                                                                                                                                                                             20 AA;
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                                                                                                                                                                                                                                                                                             Sequence
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Best Local 3
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Disclosure, Column 15-16; 27pp; English.

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The present invention relates to a method for ameliorating transplantation rejection reaction. The method comprises treating extra-corporally donor tissue or donor source of immune cells with a rejection ameliorating effective amount of a hydrolase enzyme. The method is useful for ameliorating, treating or preventing immune rejection reactions such as graft versus host diseases, organ or tissue transplantation rejection, autoimmune disease and associated conditions, obstructive pulmonary disease (COPP), atheroscierosis, chronic obstructive pulmonary disease (COPP), atheroscierosis, cancer, asthma, septic shock, toxic shock syndrome, conjunctivitis, reperfusion injury of bovine serine multifunctional hydrolase, used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins, called pancreatic cancer antigens, given in AAB54068 to AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be used in gene therapy. The polynucleotide and proteins can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, pancreas; pancreatic cancer; pancreatic cancer antigen; detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinfiammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC98773 to AAC99231 encode the human pancreatic cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human pancreatic cancer antigen protein sequence SEQ ID NO:643.
                                                                                                                                                                                                                                                                                                                                                                                   82.0%; Score 82; DB 22; Length 20; 78.9%; Pred. No. 5.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB54191 standard; Protein; 146 AA
                                                                                                                                                                                                                                                                                      exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IVNGEEAVPHXWXWQVSLQ 19
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                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
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preventing, treaturing, transcribing in minutary.

for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to design nucleic Agonists and antagonists to the antigens can be used to design nucleic pancreatic cancer antigen polynucleotides can be used to design nucleic can hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to generate minutely proteins can be used to protein cand in vitro diagnostic and therapeutic methods. The proteins can gastrointestinal pulmonary, cardiovascular, renal or proteins can gastrointestinal pulmonary, cardiovascular, represent proliferative disorders. AAC99222 to AAC99240 and AAB54467 represent sequences used in the exemplification of the present invention. or ameliorating a medical condition or in assays

146 AA; Sequence

Gaps ö Score 82; DB 21; Length 146; Pred, No. 4.9e-06; 3; Indels 1; Mismatches 82.0%; 78.9%; Local Similarity 78.9 (es 15, Conservative Query Match Matches

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AAB98504 standard; Protein; 231 AA

(first entry) 03-AUG-2001 AAB98504;

Human chymotrypsin serine protease catalytic domain.

Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer; tumour antigen-derived gene 15; serine protease; chymotrypsin.

Homo sapiens

WO200129056-A1.

26-APR-2001

99US-0421213 20-OCT-1999;

20-OCT-2000; 2000MO-US29095

(UYAR-) UNIV ARKANSAS

O'Brien TJ,

WPI; 2001-381031/40.

The present invention relates to human tumour antigen-derived gene 15 (TADG-15) protein and coding sequence (see AAH33601 and AAB98500).
TADG-15 is an extracellular serine protease. It was found that TADG-15 is over-expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20 residues that lack TADG-15 protease activity are useful for at risk of getting an individual against TADG-15, having, suspected of having or at risk of getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15. Novel extracellular serine protease, termed tumor antigen-derived gene 15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, Example 10; Fig 1; 130pp; English. ovarian cancer

ö Gaps ö Score 82; DB 22; Length 231; Pred. No. 8.1e-06; 1; Mismatches 3; Indels 1; Mismatches 82.0%; 78.9%; 0.0 Query Match Best Local Similarity 78.9 Matches 15; Conservative 231 AA; Sequence X S

2 IVNGEDAVPGSWPWOVSLO 20 1 IVNGEEAVPHXWXWQVSLQ 19 셤

RESULT 12

AAU82738 standard; Protein; 263 AA.

AAU82738;

(first entry) 23-APR-2002 Amino acid sequence of novel human protease #37.

Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme

Homo sapiens.

WO200200860-A2

03-JAN-2002

26-JUN-2001; 2001WO-US20171.

26-JUN-2000; 2000US-214047P

(SUGE-) SUGEN INC

Sudarsanam S, Manning G, Whyte D, Charydczak G; Plowman G,

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Caenepeel

WPI; 2002-139913/18.

N-PSDB; ABK31780.

Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory disorders inflammatory disorders

Claim 6; Fig 2M; 313pp; English.

The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (c.g. inflammatory diseases and atchma), cardiovascular diseases and disorders (e.g. inflammatory diseases and atchma), cardiovascular diseases and disorders (e.g. the invental associated (e.g. restenosis and coronary thrombosis), brain or neuronal associated disearces (e.g. rheumatoid arthritis and psoriasis), central or corribberal nervous system diseases, migraines, pain, sexual dysfunction, peripheral nervous system diseases, migraines, pain, sexual dysfunction, psychotic disorders, cognition disorders, hypotension, hypotension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias.

The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular characters.

263 AA; Sequence

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AAP70759 standard; Protein; 270
                                                                                                       99WO-JP06473.
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                                                                                                                                       (FUSO ) FUSO PHARM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-APR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human pancreas elastase-1.
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Best Local Similarity 78.9
Matches 15, Conservative
                                                                                                                                                                           WPI; 2000-400058/34.
                                                                                                                                                          Uemura H, Okui A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 264 AA;
                                                                                                                                                                                   N-PSDB; AAA61734.
                                                                   WO200031243-A1.
                                                                                                     19-NOV-1999;
                                                                                                                       20-NOV-1998;
                                                                                    32-JUN-2000.
                                                    Mus sp.
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ID AAP7
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AC AAP7
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                        Gaps
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0
  Score 82; DB 23; Length 263;
Pred. No. 9.4e-06;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                  New genetically engineered human pancreatic elastase - obtd.
using hosts modified DNA coding for enzyme
                                                                                                                                                                                                                                                                                                                                   Ohmine T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                 Kawashima I, Eurukawa H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse serine protease BSSP5 (mBSSP5) SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.0%; Score 80; DB 7; I
68.4%; Pred. No. 1.9e-05;
tive 4; Mismatches 2;
                                                                                                                                                    Sequence of human pancreatic elastase IIIA.
                                                                                                                                                                     Enzyme; serum lipoprotein metabolism
                                                                                                AAP60060 standard; Protein; 242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB11711 standard; Protein; 264 AA.
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                                                                                                                                                                                                                                                           85JP-0236686.
85JP-0072308.
85JP-0091986.
85JP-0163964.
85JP-0271128.
   82.0%;
78.9%;
                                    1 IVNGEEAVPHXWXWQVSLQ 19
                                                34 IVNGEDAVPGSWPWQVSLQ 52
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           Best Local Similarity 78.9
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                          WPI; 1986-280300/43.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                               (SANY ) SANKYO KK
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                                                                                                                                                                                      Homo sapiens.
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27-APR-1985;
26-JUL-1985;
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   Query Match
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The invention relates to novel serine proteases designated BSSP5 (AAB11710-B11711), and to nucleic acids encoding them (AAA61733-A61734). The invention also relates to vectors and transformants comprising BSSP5 mucleic acids; transgenic animals in which the expression level of BSSP5 can be varied; and an mBSSP5 knockout mouse. The invention additionally encompasses anti-BSSP5 antibodies and methods of production of such antibodies, methods of BSSP5 detection using the antibodies, and the nucle of BSSP5 proteins or fragments as diagnostic markers for certain pancial conditions, e.g., pancreatitis. A method for detecting pancreatitis comprising messuring BSSP5 concentration in the blood or utine, and a pancreatitis diagnostic agent containing an anti-BSSP5 antibody is also disclosed. Nucleotides encoding BSSP5 were initially isolated in a human brain cDNA library using degenerate pCR primers
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BSSP5; serine protease; human; hBSSP5; mouse; mBSSP5; brain; diagnostic marker; antibody; transgenic animal; Alzheimer's disease; epilepsy; cancer; inflammation; infertility; pancreatitis; prostatic hypertrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine proteases BSSP5, useful in detecting homologs, mutants and polymorphic variants as markers for diagnosis of e.g. Alzheimer's disease, epilepsy, cancer and inflammation, using blood, urine, pancreas or other tissues
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Pred. No. 2.1e-05;
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Sequence encoding pancreas elastase may be used to transform an expression system. The product is useful in rejuvenating the elasticity of the arterial wall, and improving unusual serum lipid levels and lipoprotein metabolism.
                                                                                                                                                                                                                                                                                       Pancreas elastase prodn. used to improve lipoprotein metabolism -
comprises isolating RNA coding elastase, synthesising single and
double chain cDNA and introducing recombinant into host
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

80.0%; Score 80; DB 8; Length 270;
Best Local Similarity 68.4%; Pred. No. 2.1e-05;
Matches 13; Conservative 4; Mismatches 2; Indels
                                                              Key Location/Qualifiers Misc-difference 2..28 //note= "May be absent"
                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 481; 18pp; Japanese.
         Lipoprotein metabolism; lipid.
                                                                                                                                                                85JP-0138494.
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                                                                                                                                                                                                                                                  WPI; 1987-040875/06.
N-PSDB; AAN71122.
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                                                                                                                                                                                               25-JUN-1985;
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                                      Sus scrofa.
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Search completed: February 12, 2003, 10:22:24 Job time : 14.4328 secs

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chymotrypsin (EC 3
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                             283224 segs, 96134422 residues
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Maximum Match 100%
Listing first 45 summaries
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plasmin (EC 3.4.21 chymotrypsin (EC 3 plasmin (EC 3.4.21 apolitoproteania) apolitoproteania) chymotrypsin Pml - plasmin (EC 3.4.21 plasmin (EC 3.4.21 ryptase (EC 3.4.21 ryptase (EC 3.4.21 plasmin (EC 3.4.21 ryptase (EC 3.4.21 ryptase (EC 3.4.21 tryptase (EC 3.4.21 tryptase (EC 3.4.21 tryptase (EC 3.4.21 tryptase (EC 3.4.21	e 22-Jun-1999 Bjarnason, J.B. inogen. PID:g468751	0; Gaps	: 07-Aug-1998 Madsen, M.; Hojrup, P Gadus morhua.	0; Gaps 0;
		Score 97; DB 2; Length 263; Pred. No. 1.2e-08; 0; Mismatches 2; Indels	7-Apr-1998 #text_chang lfsson, M.; Norregaard nt B from Atlantic cod 5; PMID:8841380	Score 95; DB 2; Length 244; Pred. No. 2.4e-08; J; Mismatches 2; Indels
1 PLPG 2 A328648 2 A328648 2 A328649 2 A61336 2 A61336 1 PLMC 1 PLMS 1 PLMS 2 A5156 2	ALI 1) precursor - (Atlantic cod) 163 karsson, S.; Ea karsson, S.; Ea 19, 211-214, 1 219, 211-34, 1 37; MUD:94368 37; MUD:94368 137; MUD:94368 17; MUD:94368 17; MUD:94368 18; Argustatus rypsin #status homology <try>: His, Asp, Ser</try>		fraç ic c evis 8.; 8.; -56, 5:96 0:96	Pre 0,
799 265 810 810 4548 31 810 812 25 25 270 455 810	1.1) pred (Atlant) (Atlant) (A	ON	lantic cod (fragments) zhua (Atlantic cod) #sequence_revision 17-P) Asgairsson, B.; Thorolfs Acta 1297, 49-56, 1996 Acta 1297, 49-56, 1996 Acta 1297, MUID:96439045; iv r iv	95.0%; 89.5%; vative
6623 6623 6623 6610 6610 6610 6610 6610 6610 6610 661	C 3.4.21.1) morbina (A) 1994 #sequent 1994 #sequent 7537; S4316; r, A.; Oskala r, A.cta 121; c cod cDNA 7537 mRNA c mRNA c squb res: EMBL:X7 rypsin; try rolase; prot scolase; prot colase;	tch al Similarity 89. 17. Conservative IVNGEBAVPHSWSWQVSLQ IVNGEBAVFHSWSWQVSLQ	- Atlantic 1998 * Morbua 1998 * Segur 2219 R.; Asgeir R.; Asgeir R.; Asgeir R.; Asgeir R.; Asgeir E. Actor Atla: Atla: A	Similarity 89.7; Conservative
8 8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9	ypsin (E es: Gada es: Gada sion: S4 ndsdotti Biophy : Atlant ence num ence ence ence ence ence ence ence ence	# B H—H	hymotrypsin B - Atlantic cod (fragments /Species: Gadus morbhua (Atlantic cod) /Date: 19-Mar-1998 #sequence_revision 1/Accession: S72219 /Heth-Larsen, R.; Asgeirsson, B.; Thoroicohim. Blophys. Acta 1297, 49-56, 1996 /Title: Structure of chymotrypsin varia /Accession: S72219; MUID:9643904 /Accession: S72219; MUID:9643904 /Accession: S72219; MUID:9643904 /Accession: 1-14,15-244 <- Accession: S72219; MUID:9643904 /Accession: S72219; MUID:9643904 /Accession: S72219 /Accession: S72219 /Accession: S72219 /Accession: S72219 /Accession: S72219 /Accession: Accession: Accessi	Local Sim
	RESULT 1 847537 Chymotrypsin (EC : C;Species; Gade 19 C;Accession: S475: R;Gudmudsdottir, Biochim Biophys. A;Title: Atlantic A;Reference number A;Accession: S475: A;Residues: 1-263 A;Cross reference C;Superfamily: try C;Keywords: hydrol F;1-18/Domain: try F;75,120,213/Activ: E;75,120,213/Activ:	Query Ma Best Loc Matches Qy 1 Db 34 RESULT 2	chymotrypsin B - Atlantic cod (C)Species: Gadus morhua (Atlant C)Date: 19-Mar-1998 #sequence_rv C;Accession: S72219 R;Leth-Larsen, R.; Asgairsson, 18 jochim. Biochiw. Biochiw. Biochiw. Biochiw. Biochiw. Structure of chymotryp A;Reference number: S72219; MUII A;Accession: S72219; MUII A;Accession: S72219; MUII A;Accession: S72219; MUII A;Accession: 114;15-24 <-LET>C;Superfamily: trypsin trypsin p;15-237/Domain: trypsin homolog Ouerv Match	Best Lo Matches

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1 IVNGEEAVPHXWXWQVSLQ 19

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A; Molecule type: mRNA
A;Residues 1.270 cTAN.
A;Cross-references: GB:M18692; NID:g607029; PIDN:AAA58454.1; PID:g182035
R;Shen, W.; Fletcher, T.S.; Largman, C.
Biochemistry 26, 3447-3452, 1987
A;Ttele: Primary structure of human pancreatic protease E determined by sequence analysis:
A;Reference number: A90516; MUID:88000545; PMID:3477287
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A; Residuce: (G', 5-63, (G', 65-78, 'W', 80-163, 'P', 165-270 < FLE>
R; Residuce: (G', 5-63, (G', 65-78, 'W', 80-163, 'D'; Puigserver, A.
R; Aviles, F. X.; Pascual, R.; Salva, M.; Bontcel, J.; Puigserver, A.
Biochem. Biophys. Res. Commun. 163, 1191-1196, 1989
Biochem. Generation of a subunit III-11ke protein by autolysis of human and porcine prop:
A; Reference number: A33257; WUID: 89392022; PMID: 2675835
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A;Reaidues: 18-57 <AVI>
R;Guy-Crotte, O.; Barthe, C.; Basso, D.; Fournet, B.; Figarella, C.
Biochem. Biophys. Res. Commun. 156, 318-322, 1988
A;Title: Characterization of two glycoproteins of human pancreatic juice: P35, a truncaté
A;Reference number: A28932; MUID:89025862; PMID:3178837
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A;Accession: 804999
A)Contents: annotation; X-ray crystallography
C;Comment: Chymotrypsinogens are synthesized in the acinar cells of pancreas.
C;Comment: Chymotrypsinogens are synthesized in a fully active enzyme (pi-chymotrypsi c;Comment: Tryptic Cleavage after Arg-15 results in a fully active enzyme (pi-chymotrypsidelta-chymotrypsin); tryptic cleavage liberates the dipeptide Thr-147 and Asr dan-148 directly from chymotrypsinogen, which leads to the degraded form neochymotrypsin (c;Nuperfamily: trypsin); trypsin, trypsin thomology, which leads to the degraded form neochymotrypsin F;1-245/Product: chymotrypsinogen #status experimental <2YM>
F;1-245/Product: chymotrypsinogen #status experimental <2XM>
F;1-13,16-146,149-245/Product: alpha-chymotrypsin #status experimental <MPT>
F;1-12,3-42-58,136-201,168-182,191-220/Disulfide bonds: #status experimental
F;1-12,102,195/Active site: His, Asp, Ser #status experimental
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A,Residues: 'G',5-63,'G',65-78,'W',80-118,'G',120-163,'P',165-270 <SHE>
R,Fletcher, T.S.
submitted to GenBank, August 1987
A,Reference number: A94507
A,Contents: revision to residue 119
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85.0%; Score 85; DB 1; Length 245;
Best Local Similarity 84.2%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 3; Indels
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A;Reaidues: 'X',32-52,'X',54-55,'XXX',59-63 <GUY>
R;Moulard, M.; Kerfelec, B.; Mallet, B.; Chapus, C.
FEBS Lett, 250, 166-170, 1989
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Chymotrypsin (EC 3.4.21.1) A precursor - bovine
Nylternate names : Aphatrypsingen A
Cispecies: Bos primigenius taurus (catte)
Cispecies: Bos primigenius taurus
Cispecies: Bos primigenius taurus
Biochem. 3. 1011, 211-228. 1966
A,Fittle: Contents: Bos primigenius taurus
A,Rolecute type: protein
A,Rolecute type: Protein
A,Rolecute type: Protein
Biochim. Biophys. Act 130, 431-546, 196
A,Fittle: Role of a burited acid group in the mechanism of action of chymotrypsin.
Biochim. Biophys. Act 130, 431-546, 196
A,Fittle: Role of a burited acid group in the mechanism of action of chymotrypsin.
Biochim. Biophys. Act 130, 431-546, 196
A,Fittle: Role of a burited acid group in the mechanism of action of chymotrypsin.
Biochim. Biophys. Act 130, 431-546, 196
A,Fittle: Role of a burited acid group in the mechanism of action of chymotrypsin.
Biochim. Biophys. Actal 130, 431-546, 196
A,Rolecute type: protein
A,Rolecute type: Brotein
A,Rolecute to atalyse tate
R,Bittle: B, A,Rolecute to atalymotry and the act
                                                                                                                                                                                                                                                         pancreatic elastase (EC 3.4.21.36) III - pig (fragment)
N.Alcernate names: proteinase E
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 21-Reb-1990 #sequence_revision 21-Reb-1990 #text_change 30-Jun-1995
C;Accession: B33257
R;Aviles, F.X.; Pascual, R.; Salva, M.; Bonicel, J.; Puigserver, A.
Biochem. Biophys. Res. Commun. 163, 1136, 1186, 1889
A;Title: Generation of a subunit 113-1116, 1889
A;Aitle: Generation of a subunit lial-like protein by autolysis of human and porcine prop. A;Accession: B3257
A;Accession: B3257
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Pred. No. 1.2e-07;
3; Mismatches 2
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A,Molecule type: protein
A,Residues: 1-31 AAVI-
C,Superfamily: trypsin homology
C,Keywords: hydrolase; serine proteinase
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Best Local Similarity 73.7%;
Matches 14; Conservative
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Chymotrypsin (EC 3.4.21.1) B precursor - bovine
N'Alternate names: chymotrypsinogen B
N'Alternate names: chymotrypsinogen B
N'Alternate names: chymotrypsinogen B
C'Species: Bos primigenius taurus (cattle)
C'Bate: 08-0ct-1981 #sequence_revision 08-0ct-1981 #text_change 18-Jul-1997
C'Accession: A00953
R'Smillie, L.B.; Furka, A.; Nagabhushan, N.; Stevenson, K.J.; Parkes, C.O.
Nature 218, 343-346, 1968
A;Ttle: Structure of chymotrypsinogen B compared with chymotrypsinogen A and trypsinogen
A;Reference number: A00953; MUD:68238908; PMID:5649671
A;Molecule type: protein
A;Molecule type: protein
A;Residues 1-245-SMI-
C;Comment: Chymotrypsinogen B is synthesized, along with chymotrypsinogen A, in the acinc
C;Comment: Chymotrypsinogen B is synthesized, along with chymotrypsinogen A, in the acinc
C;Comment: Chymotrypsinogen B is synthesized, along with chymotrypsin B, occurs in the sar
C;Comment: Chymotrypsinogen B is synthesized, along with chymotrypsin B, occurs in the sar
C;Comment: Chymotrypsinogen B is synthesized, along with chymotrypsin B, occurs in the sar
C;Comment: Chymotrypsinogen B is synthesized, along with chymotrypsin B, occurs in the sar
C;Comment: Chymotrypsinogen B is synthesized, along with chymotrypsin B, occurs in the sar
C;Comment: Chymotrypsin B #status experimental <PRO>
F;16-238/Domain: trypsin homology <PRO>
F;16-238/Domain: trypsin homology <PRO>
F;16-238/Domain: trypsin homology <PRO>
F;16-238/Domain: trypsin homology <PRO>
F;17,102,195/Active site: His, Asp, Ser #status experimental
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CiSpecies: 27-Jul-1999 #sequence_revision 27-Jul-1990 #text_change 22-Jun-1999
CiAccession: A21195
RiPinsky, S.D.; LaForge, K.S.; Luc, V.; Scheele, G.
Proc. Natl. Acad. Sci. U.S.A. 80, 7486-7490, 1983
A;Title: Identification of cDNA clones encoding secretory isoenzyme forms: sequence detental and a secretory 
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C;Species: Homo sapiens (man)
C;Date: 08-Jun-1989 #sequence_revision 08-Jun-1989 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Readus: 1-263 < PIN>
A;Reducs: 1-263 < PIN>
A;Cross-references: GB:K01173; NID:g163945; PIDN:AAA30841.1; PID:g163946
C;Superfamily: trypsin; trypsin homology
C;Reywords: hydrolase; protein digestion; serine proteinase
F;34-256/Domain: trypsin homology < TRY>
F;75,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 245;
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78.9%; Pred. No. 3.8e-06;
tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IVNGEEAVPHXWXWQVSLQ 19
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                                                                                                                                  13 IVNGEEAVPHTWYWQV 28
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                                                                                 1 IVNGEEAVPHXWXWQV 16
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(Species Bos primigenius taurus (cattle)
(Species: Bos primigenius taurus (cattle)
(Species: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 22-Apr-1995
(SAccession: PU0036; pu0039
(R.TSUJ): A.: Sakiyama, K.; Edazawa, K.; Nagata, K.; Sasaki, Y.; Nagamune, H.; Matsuda, Y submitted to JIPID, September 1994
A.Description: Purification and characterization of a novel serine proteinase from bovin
A.Reference number: PU0036
R;Wendorf, P.; Geyer, R.; Sziegoleit, A.; Linder, D.
FEBS Lett. 249, 275-278, 1989
A;Title: Localization and characterization of the glycosylation site of human pancreatid
A;Reference number: S04490; MUID:89289996; PMID:2737288
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Cispecies Gadus morthua (Atlantic cod)

Cispecies: 15-0ct-1994 #sequence_revision 15-0ct-1994 #text_change 11-May-2000

CiAccession: A61229

Rivageirsson, B.; Bjarnsson, J.B.

Rivageirsson, B.; Bjarnsson, J.B.

A;Title: Structural and Kinetic properties of chymotrypsin from Atlantic cod (Gadus morth A):Reference number: A61529; MUID:92111252; PMID:1764912

A;Status: preliminary

A;Status: preliminary

A;Residues: 1-28 eASGs

C;Superfamily: trypsin; trypsin; homology
                                                                                                                                                                   A.Accession: 804490
A.Molecule type: protein
C.Superfamily: trypsin; trypsin homology
F.1-17/Domain: signal sequence #status predicted <ACT>
F.1-17/Domain: activation peptide #status predicted <ACT>
F.29-27/Pomain: activation poptide #status predicted <AMT>
F.29-27/Pomain: activation poptide #status predicted <AMT>
F.73-27.37/Active site: His, Aspp. Ser #status predicted
F.13.123.217/Active site: His, Aspp. Ser Mstatus experimental
F.13.Minding site: carbohydrate (Asn) (covalent) #status absent
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C,Superfamily: trypsin; trypsin homology
C,Keywords: hydrolase; protein digestion; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serine proteinase (EC 3.4.21.-) - bovine (fragment)
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A,Molecule type: protein
A,Redudes: 1-23 ATSUA
A,Experimental source: pancreas
C,Superfamily: trypsin; trypsin homology
C,Keywords: hydrolase; serine proteinase
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Best Local Similarity 73.74
Matches 14; Conservative
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Matches 14; Conservat
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Best Local Similarity
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A,Molecule type: DNA
A,Residues: 1.270 cTAN.
A,Gross-references: GB:003516
R,Shirasu, Y.; Takemura, K.; Yoshida, H.; Sato, Y.; Iljima, H.; Shimada, Y.; Mikayama, T.
B, Blochem: 104, 259-264, 1988
A;Title: Molecular cloning of complementary DNA encoding one of the human pancreatic prot
A;Reference number: JX0045; MUID:89034017; PMID:2460440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
*Residues: 1-240, 'G', 242-270 <SHI>
A;Cross-references: GB:D00306; NID:g220013; PIDN:BAA00212.1; PID:g220014
C;Comment: This enzyme is an alanine-specific serine proteinase that has little elastolyt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pancreatic elastase (EC 3.4.21.36) IIIA precursor - human
NyAlternate names: protease E
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A29934; JX0045
S;Tani, T.; Ohsumi, J.; Mita, K.; Takiguchi, Y.
J. Biol. Chem. 263, 1231-1239, 1988 of elastase isozyme, human pancreatic elastase:
A;Title: Identification of a novel class of elastase isozyme, human pancreatic elastase:
A;Reference number: A92664; MUID:88087253; PMID:2826474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: 17-011-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
Cispecies: 17-011-1992 #sequence_revision 17-Jul-1992 #text_change 22-Jun-1999
Cispecies: 17-0131-1992
Rixang, J.; Wiegand, U.; Mueller-Hill, B.
Gene 110, 181-187, 1992
A;Tile: Identification of cDNAs encoding two novel rat pancreatic serine proteases.
A;Reference number: J01471; MUID:92165057; PMID:1537555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Molecule type: mRNA
A, Residues: 1-268 «KAN>
A, Residues: 1-268 «KAN>
A, Residues: 1-268 «KAN>
A, Residues: 1-268 «KAN>
A, Cross-references: EMBL:XS9014; NID:956090; PIDN:CAA41753.1; PID:956091
C, Superfamily: trypsin; trypsin homology
C, Keywords: hydrolase; serine proteinase; zymogen
F;1-16/Domain: signal sequence #status predicted «SIG>
F;10-29/Domain: activation peptide #status predicted «ACT>
F;30-268/Product: pancreate = lastase IV #status predicted «MAT>
F;30-262/Domain: trypsin homology «TRY>
F;74,121,216/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                         Score 80; DB 2; Length 20; Pred. No. 4.9e-07; 0; Mismatches 4; Indels
                A;Molecule type: protein
A;Residues: 1-20 ePTE>
C;Superfemily: trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase
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C;Keywords: hydrolase; pancreas; serine proteinase
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78.9%;
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nes 15; Conservative
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C;Accession: A31299
R;Tomita, N.; Izumoto, Y.; Horii, A.; Doi, S.; Yokouchi, H.; Ogawa, M.; Mori, T.; Matsub Biochem. Biophys. Res. Commun. 158, 569-575, 1989
A;Title: Molecular cloning and nucleotide sequence of human pancreatic prechymotrypsinog A;Reference number: A31299; MUID:89134264; PMID:2917002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chymotrypsin (EC 3.4.21.1) - edible frog (fragment)
C;Species: Rana esculenta (edible frog)
C;Species: T-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C;Accession: B61313
R;Pies, W.; Zwilling, R.; Woodbury, R.G.; Neurath, H.
PEBS Lett. 109, 45-49, 1980
A;Title: Amino-terminal amino acid sequences and the evolution of frog (Rana esculenta)
A;Reference number: A61313; MUID:80113255; PMID:6965480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NiAlternate names: chymotrypainogen B
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999
C;Accession: A22658
R;Bell, G.I.; Quinto, C.; Quiroga, M.; Valenzuela, P.; Craik, C.S.; Rutter, W.J.
J;Bell, G.I.; Quinto, C.; Quiroga, M.; Valenzuela, P.; Craik, C.S.; Rutter, W.J.
A;Title: Isolation and sequence of a rat chymotrypsin B gene.
A;Reference number: A22658; MUD:85054881; PMID:6209274
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                      A;Accession: A31299
A;Status: preliminary
A;Molecule: type: mRNA
A;Molecule: 1-263 <TOM>
A;Cross-references: GB:M24400; NID:g181189; PIDN:AAA52128.1; PID:g181190
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:CTRB1; CTRB
A;Cross-references: GDB:119820; OMIM:118890
A;Map position: 16623.1.16623.1
C;Superfaully: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase
P;34-256/Domain: trypsin homology <TRY>
P;75,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.0%; Score 82; DB 2; I
78.9%; Pred. No. 3.8e-06;
tive 1; Mismatches 3;
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Best Local Similarity 78.9
Matches 15; Conservative
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Matches 14; Conserva
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Gaps

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Length 268;

us-10-036-371-4.rpr

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pancreatic elastase (EC 3.4.21.36) isoform 2 precursor - human
NiAtternate names: caldecrin isoform 2
C;Species: Homo sapiens (man)
C;Date: 04-Dec.1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998
C;Accession: 586826
R;Tomomura, A.; Akiyama, M.; Itoh, H.; Yoshino, I.; Tomomura, M.; Nishii, Y.; Noikura, T
FEBS Lett. 386, 26-28, 1996
R;Tomomura, A.; Akiyama, M.; Itoh, H.; Yoshino, I.; Tomomura, M.; Nishii, Y.; Noikura, T
FEBS Lett. 386, 26-28, 1996
A;Tomomura, P.; Akiyama, M.; Itoh, H.; Yoshino, I.; Tomomura, M.; Nishii, Y.; Noikura, T
A;The: Molecular Cloning and expression of human caldecrin.
A;Reference number: $68826
A;Nolecula F.; Yope: mRNA
A;Residues: 1-268 ATOM-
A;Experimental source: pancreas; serine proteinase; zymogen
C;Superfamily: trypsin homology
C;Geywords: hydrolase; pancreas; serine proteinase; zymogen
C;Geywords: hydrolase; pancreas; serine proteinase; zymogen
F;17-20/Domain: signal sequence #status predicted <PRO>
F;30-268/Produc: pancreatic elastase isoform 2 #status predicted <MAT>
F;30-268/Domain: trypsin homology <TRY>
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F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-29/Domain: propeptide #status predicted <PRO>
F;29-270/Product: pancreatic elastase IIIA #status experimental <MAT>
F;29-263/Domain: trypsin homology TRY>
F;29-263/Domain: trypsin homology CRY>
F;21-263/217/Active site: His, Asp, Ser #status predicted
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29 VVHGEDAVPYSWPWQVSLQ 47
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"48U) NNAJA 3DA9 SIHT

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                                     erinaceus e
homo sapien
homo sapien
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homo sapien
    meriones un
             rattus norv
equus cabal
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MEDLINE-92111252; PubMed=1764912;
MSDLINE-92111252; PubMed=1764912;
MSGLINE-92111252; PubMed=1764912;
Structural and kinetic properties of chymotrypsin from Atlantic cod (Gadus morhua). Comparison with bovine chymotrypsin.";
Comp. Blochem. Physiol. 998:327-335(1991).
-- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                                                          01-FBB-1996 (Rel. 33, Created)
01-FBB-1996 (Rel. 31, Last sequence update)
15-UWA-2002 (Rel. 31, Last amotation update)
Chymotrypsin A precursor (EC 3.4.21.1).
Gadus morhua (Atlantic cod).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Bueeleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00089; trypsin; 1.
PRINTS: PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN—HIS; 1.
PROSITE; PS00135; TRYPSIN—HIS; 1.
PROSITE; PS00135; TRYPSIN—SER; 1.
STAPACIASE; Scrine procease; Digestion; Pancreas; Zymogen; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                         "Atlantic cod cDNA encoding a psychrophilic chymotrypsinogen.";
Bjochim. Biophys. Acta 1219:211-214(1994).
                            002844
029485
099233
P08246
015661
P20231
P15157
P099582
            P27435
P80010
                                                                                                                                                                                                                                                                                     TISSUE-Pyloric caeca;
MEDLINE-94368860; PubMed-8086467;
Gudmundsdottir A., Oskarsson S., Eakin A.E., Craik C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYILC A. Phe-|-Xaa.
Phe-|-Xaa, Leu-|-Xaa.
-!- SUBCELDULAR LOCATION: EXTRACEILULAR.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                       263 AA
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                                                                                                                            ALIGNMENTS
          MCT7_RAT
PLMN_HORSE
MCT7_MOUSE
PLMN_ERIEU
TRYD_HUMAN
                                                             TRB1_HUMAN
TRB2_HUMAN
TRYA_HUMAN
KLK4_HUMAN
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X78490; CAA55242.1; -.
                                                                                                                                                                     STANDARD;
273
273
3338
2273
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2275
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275
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NCBI_TaxID=8049;
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                                                                                                                                                                     GADMO
RESULT 1
CTRA_GADMO
homo sapien
mus musculu
rattus norv
bos taurus
sus scrofa
homo sapien
homo sapien
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rattus norv
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P80646 gadus morhu
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Q99895
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P00774
Q29461
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    GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                    112892 segs, 41476328 residues
                                                                                                                                                                                                                                                                                                           SUMMARIES
                                   OM protein - protein search, using sw model
                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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MOUSE
RAT
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PLMN SHEEP
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COG1 CHIOP
TMS4 HUMAN
PLMN MACMU
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HUMAN
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EL2 RAT
EL2 BOVIN
EL2 PIG
CTRL HUMA
ELAS HUMA
ELAS GADN
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length: 2000000000
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Match Length
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CHARGE RELAY SYSTEM (BY SIMILARITY)

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PIR; A25065; CPBOA3.
PDB; 1FON; 14-OCT-96.
MEROPS; S01.983; -
                                                                                                                                                                                             Similarity
                                                                                                                                             245 AA;
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135
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P05805;
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MEDLINE=96439045; Pubmed=8841380;
Leth-Largen R., Asgeirsson B., Thorolfsson M., Noerregaard-Madsen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R InterPro; 1PR001254; Ser_protease_Try.

R InterPro; 1PR001254; Ser_protease_Try.

R InterPro; 1PR001254; Ser_protease_Try.

R PRINTS; PR00722; CHYMOTRYSIN.

R SMART; SM00020; TRYPSIN.

R PROSITE; PS00134; TRYPSIN. DOM; 1.

R PROSITE; PS00135; TRYPSIN. DIS; 1.

R PROSITE; PS00135; TRYPSIN. DSR; 1.

R PROSITE; PS00135; TRYPSIN. SER; 1.

T CHAIN 1 13 CHYMOTRYPSIN B. A CHAIN.

T ACT SITE 57 CHARGE RELAY SYSTEM (BY SIMILARITY).

T ACT SITE 101 101 CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                               Gaps
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
NCBI_TaxID=8049;
 (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
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"Structure of chymotrypsin variant B from Atlantic cod, Gadus
                                                                                                                                                                                                                                               97.0%; Score 97; DB 1; Length 263;
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2; Indels
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 CHARGE RELAY SYSTEM (F
CHARGE RELAY SYSTEM (F
CHARGE RELAY SYSTEM (F
BY SIMILARITY.
T -> S (IN REF. 2).
S -> Q (IN REF. 2).
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S -> T (IN REF. 2).
S -> T (IN REF. 2).
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01-0CT-1996 (Rel. 34, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Chymotrypain B (EC 3.4.21.1)
Gadus morbua (Atlantic cod).
                                                                                                                                                                                                                                                                                                                                                                                                                             245 AA.
                                                                                                                                                                                                                                                                Pred. No. 2.7e
0; Mismatches
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Biochim. Biophyø. Acta 1297:49-56(1996).
                                                                                                                                                                                                                    28294 MW;
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Best Local Similarity
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P80646;
        ACT_SITE
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X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).

MEDILINE=$4222022; PubMed=8168476;

Pignol D., Gaboriaud C., Michon T., Kerfelec B., Chapus C.,

Pignol D., Gaboriaud C., Michon T., Kerfelec B., Chapus C.,

To Greetal structure of bovine procarboxypeptidase A-S6 subunit III, a

Highly structured truncated zymogen E.";

I. EMBO J. 3:176-1771(1994).

I. EMBO J. 3:176-1771(1994).

I. PROCARROXYPEPTIONES A AGAINST DENATURATION IN THE ACIDIC

PROCARROXYPEPTIONES A AGAINST DENATURATION IN THE ACIDIC

ENVIRONMENT OF THE RUMINATY DUODENUM.

C.I. SUBUNIT: HETEROTRIMER OF SUBUNIT III; CARBOXYPEPTIDASE A AND

C. I. SUBCELLULAR LOCATION: Extracellular.

C. I. SUBCELLULAR LOCATION: Extracellular.

C. I. SUBCELLULAR EDGENGS TO PERTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Autolysis of proproteinase E in bovine procarboxypeptidase A ternary complex gives rise to subunit III."; FEBS Lett. 277:37-41(1990).
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
115-UN-2002 (Rel. 41, Last annotation update)
116-UN-2002 (Rel. 41, Last annotation update)
117 (Procarboxypeptidase A-S6 subunit III) (PROCPA-S6 III)
118 (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Boyidae; Boyinae; Bos.
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MEDLINE=86220198; PubMed=3519215;
Venot N., Sciaky M., Puigserver A., Desnuelle P., Laurent G.;
"Amino acid sequence and disulfide bridges of subunit III, a
defective endopeptidase present in the bovine pancreatic 6 S
procarboxypeptidase A complex.";
Eur. J. Blochem. 157:91-99(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-11099520; Pubmed=2269366;
Pascual R., Vendrell J., Aviles F.X., Bonicel J., Wicker C.,
Pulgserver A.;
                                                                                                                                                                                                                                                                                                         Score 95; DB 1; Length 245; Pred. No. 5.2e-08;
                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                             4 -> Y (IN REF. 2).
74FE0D425517AB02 CRC64;
                                                                                                                                                             QVT -> VIS (IN REF. 2)
S -> T (IN REF. 2).
PW -> Y (IN REF. 2).
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                          BY SIMILARITY.
BY SIMILARITY.
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
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181
182
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2620 MW,
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us-10-036-371-4.rsp

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MEDLINE-82078042; PubMed=6914389; Cohen G.H., Silverron E.W., Davies D.R.; Refined crystal structure of gamma-chymotrypsin at 1.9-A resolution. Comparison with other pancreatic serine proceases."; J. Mol. Biol. 148:449-479(1981).
                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF CHYMOTRYPSINOGEN. MEDLINE-70177557; PubMed=5442169; Press S.T., Kraut J., Robertus J.D., Wright H.T., Xuong N.H.; Richymotrypsinogen: 2.5 A crystal structure, comparison with alphachymotrypsin, and implications for zymogen activation."; Biochemistry 9:1997-2009(1970).
                Birktoft J.J., Blow D.M., Henderson R., Steitz T.A.;
"I. Serine proteinases. The structure of alpha-chymotrypsin.";
Philos. Trans. R. Soc. Lond., B, Biol. Sci. 257:67-76(1970).
                                                                                                                                                                                                                                                                                                                                                                                                            Phe-|-Xaa, Leu-|-Xaa.
-!- SUBCELLOUIAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-!- DATRAASE: NAME-Worthington enzyme manual;
WWW-"http://www.worthington-biochem.com/manual/C/CHY.html".
PIR; A00952; KYBOA.
                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF GAMMA-CHYMOTRYPSIN
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001284; Ser protease_Try.
Pfam; PR00089; trypsin; CHYMOTRYPSIN,
SMART; SM00020; Tryp_SPC; I
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16 - OCT - 87.
16 - OCT - 87.
16 - OCT - 87.
17 - OCT - 92.
15 - OCT - 92.
15 - OCT - 90.
15 - OCT - 91.
16 - OCT - 91.
17 - OCT - 91.
18 - OCT - 91.
18 - OCT - 91.
18 - OCT - 91.
19 - OCT - 91.
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30-APR-94.
22-JUN-94.
22-JUN-94.
22-JUN-94.
30-SEP-94.
01-NOV-94.
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23-JUL-97.
23-JUL-97.
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1HJA; 14-JAN-98.
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6CHA;
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10G7;
10CD;
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1GMH;
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1AFQ;
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1CBW;
1VGC;
2VGC;
3VGC;
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PDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, DISULFIDE BONDS, AND ACTIVE SITE.
MEDLINE-67181721; Pubmed=5971783;
Brown J.R., Hartley B.S.;
"Location of disulphide bridges by diagonal paper electrophoresis.
The disulphide bridges of bovine chymotrypsinogen A.";
Biochem. J. 101:214-228(1966).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=67183948; PubMed=5972866;
Meloun B., Kluh I., Kostka V., Moravek L., Prusik Z., Vanacek J.,
Keil B., Sorm F.;
                                                                                                                                                                                                                                                                                             0
PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PSS0240; TRYPSIN "DOM; 1.
PROSITE; PS00134; TRYPSIN "HIS; 1.
PROSITE; PS00135; TRYPSIN "BE; 1.
Serine protease homolog; Pancreas; Digestion; 3D-structure.
PROPER PROPER PROFILE PROPERTIE:
CHAIN 12 253 PROPROTEINASE E.
                                                                                                                                                                                                                                                    87.0%; Score 87; DB 1; Length 253; 73.7%; Pred. No. 9.9e-07; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-69106266, PubMed=5764436, Blow D.M., Birktoft J.J., Hartley B.S.; "Role of a buried acid group in the mechanism of action of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smillie L.B., Hartley B.S.;
"Histidine sequences in the active centres of some 'serine'
                                                                                                                                                                                                                       27337 MW; 24663724DBAE409C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hartley B.S.;
"Amino-acid sequence of bovine chymotrypsinogen-A.";
Nature 201:1284-1287(1964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Covalent structure of bovine chymotrypsinogen A.
Biochim. Biophys. Acta 130:543-546(1966).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUM-2002 (Rel. 41, Last annotation update)
Chymotrypsinogen A (EC 3.4.21.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                         245 AA.
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MEDLINE=67181723; Pubmed=5971785;
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MEDLINE=72035052; PubMed=4399050;
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                                                                                                                                                                                                                                                                                                                                      1 IVNGEEAVPHXWXWQVSLQ 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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PRELIMINARY SEQUENCE.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                      Moulard M., Kerfelec B., Mallet B., Chapus C.; indentification of a procarboxypeptidase A-truncated protease binary complex in human pancreatic juice."; PEBS Lett. 250:166-170(1989).
                                                                                                                                                                    TISSUB-Pancreas;
MEDLINE=88000545; PubMed=3477287;
Shen W., Fletcher T.S., Largman C.;
"Primary structure of human pancreatic protease E determined sequence analysis of the cloned mRNA.";
Biochemistry 26:3447-3452(1987)
                                                                       TISSUE FROM N.A.

TISSUE-Pancreas;
MEDLINE-88087253; PubMed=2826474;
Tani T., Ohtawi J., Mita K., Takiguchi Y.;
"Identification of a novel class of elastase isozyme, human pancreatic elastase III, by cDNA and genomic gene cloning.";
                                                                                                                                                                                                                                                                          SEQUENCE OF 94-164, AND CARBOHYDRATE-LINKAGE SITES ASN-114
                                                                                                                                              Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
01-NOV-1988 (Rel. 09, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elastase IIIB precursor (EC 3.4.21.70) (Protease E)
ELA3B.
                                                                                                                                                                                                                               TISSUE=Pancreas;
MEDLINE=89325560; PubMed=2753124;
                                                                                                                                                                 SEQUENCE OF 4-270 FROM N.A.
                                                                                                                                                                                                                       SEQUENCE OF 31-50.
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                       TISSUE=Pancreas;
       85.0%; Score 85; DB 1; Length 245;
84.2%; Pred. No. 2e-06;
ive 0; Mismatches 3; Indels
        PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SRS; 1.
Hydrolase; Serine protesse; Digestion; Pancress; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                25666 MW; 91A9F28E2F3E3142 CRC64;
                                         CHYMOTRYPSIN A, A CHAIN.
CHYMOTRYPSIN A, B CHAIN.
CHYMOTRYPSIN A, C CHAIN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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nes 16; Conservative
                                           235 2
245 AA;
                                   3D-Btructure.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
EMBL; M16630; AAA36482.1; -.
EMBL; BC005216; AAH05216.1; -
EMBL; M18692; AAA58454.1; -.
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SWISS-2DPAGE; P08861; HUMAN.
Genew; HGNC:15945; ELA3B.
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PIR; A27206; A27206.

PIR; S04999; S04499.

PIR; S04490; S04490.

MSSP; P08805; IFON.
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Gaps

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1 IVNGEEAVPHXWXWQVSLQ 19

ઠ 셤 270 AA

STANDARD;

EL3B HUMAN P08861; P11423;

EL3B_HUMAN RESULT 5

us-10-036-371-4.rsp

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NCBI_TaxID=9615;
                 PROSITE; PSC
PROSITE; PSC
Hydrolase; S
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CHAIN
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Smillie L.B., Furka A., Nagabhushan N., Stevenson K.J., Parkes C.O.;
"Structure of chymotrypsinogen B compared with chymotrypsinogen A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Nature 218:343-346 (1968).
-!-CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Phe-|-Xaa, Leu-|-Xaa, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Euteria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. (VCBL_TaxID=9913;
                                                                                                                                                                                                                                                   CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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                        InterPro; iPRUGLES, ...
PERM, PERMORSO; CTYPDELL; I.
PRIMES, PRO0022; CHYPOTAYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00135; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN BOM; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
SIGNAL 15 No. 16 (POTENTIAL).
SIGNAL 16 28 ACTIVATION PEPTIDE (POTENTIAL).
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3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                           EXAMPLE SIGNED (B) SIGNED BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

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N-LINKED (GLCNAC, .).

/FIId=CAR_000212.

A -> G (IN REF. 3).

A -> G (IN REF. 3).

M -> R (IN REF. 3).

M -> R (IN REF. 5).

M -> P (IN REF. 5).

M -> P (IN REF. 3).

M -> P (IN REF. 3).
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ID CTRB_BOVIN STANDARD; PRT; 245 AA.

CTRB_BOVIN STANDARD; PRT; 245 AA.

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-2086 (Rel. 01, Last sequence update)

DT 15-JUL-2002 (Rel. 41, Last annotation update)

DE Chymotrypsingen B (EC 3.4.21.1)
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
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InterPro, IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
SMRINTS; PR00022; CHYMOTRYPSIN.
SMART; SM00020; Tryp. SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 73.7
Matches 14, Conservative
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270 AA;
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73
123
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CCHAIN
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CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 80:7486-7490(1983).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Phe-|-Xaa, Leu-|-Xaa, Leu-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDIMEd=6584866; MEDIME=84170253; PubMed=6584866; Pinsky S.D., Laforge K.S., Luc V., Scheele G.; Independentification of cDNA clones encoding secretory isoenzyme forms: Sequence determination of canine pancreatic prechymotrypsinogen 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; JPR001314; Chymotrypsin.
InterPro; IPR001314; Ser_protease_Try.
InterPro; IPR001314; Ser_protease_Try.
PRINTS; PR001022; CHYMOTRYPSIN.
PROSITE; PS00240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
| TEP | PS00134; TRYPSIN | HIS; 1 | LEP | PS00135; TRYPSIN | SER; 1 | LEP | PS00135; TRYPSIN | SER; 1 | LEP 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.0%; Score 82; DB 1; Length 245
78.9%; Pred. No. 5.9e-06;
iive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25755 MW; 678016446FF5FEB5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TESOLIA

TO CTR2 CANFA STANDARD, PRT; 263 AA.

AC P04813; PT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-UN-2002 (Rel. 41, Last annotation update)

DE Chymotrypsinogen 2 precursor (EC 3.4.21.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; K01173; AAA30841.1; -. PIR; A21195; A21195. HSSP; P00766; IACB. MEROPS; S01.152; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IVNGEEAVPHXWXWQVSLQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 IVNGEDAVPGSWPWQVSLQ 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 78.9
Matches 15; Conservative
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42
136 2
168 1
191 2
245 AA;
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Pancreas;
MEDLINE-89134264; PubMed=2917002;
Tomita N., Izumoto Y., Horii A., Doi S., Yokouchi H., Ogawa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                   Mori T., Matsubara K.; "Molectide sequence of human pancreatic "Molecular Cloning and nucleotide sequence of human pancreatic prechymotrypainogen cDNN."; Biochem. Biophys. Res. Commun. 158:569-575(1989).
                                                                                                                                                         ö
                                                                                                                                  Score 82; DB 1; Length 263;
Pred. No. 6.4e-06;
1; Mismatches 3; Indels
CHYMOTRYPSIN 2, A CHAIN.
CHYMOTRYPSIN 2, B CHAIN.
CHYMOTRYPSIN 2, C CHAIN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                   SIMILARITY.
SIMILARITY.
SIMILARITY.
2A2F449D813B3961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phe-|-Xaa, Leu-|-Xaa.
SUBCELLULAR LOCATION: Extracellular.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CTymotrypainogen B precursor (EC 3.4.21.1).
CTRB1 OR CTRB.
                                                                                                                                                                                                                                                   263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfan; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, BC005385, AAH05385.1, -. PIR, A31299, A31299 HSSP, P00766; LCHG. MEROPS, SO1.152; -. Genew, HGNC:2521; CTRB1.
                                                                                                                  27787 MW;
                                                                                                                                    ch 82.0%;
1 Similarity 78.9%;
15; Conservative 1
                                                                                                                                                                              1 IVNGEEAVPHXWXWQVSLQ 19
                                                                                                                                                                                          34 IVNGEDAVPGSWPWQVSLQ 52
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   31
164
263
75
75
1120
120
140
76
219
219
2200
238
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                                                                                                                                                 Local Similarity
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                                                                                                                  263 AA;
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P17538;
                                 ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
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                                                                                                                  SEQUENCE
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    CHAIN
CHAIN
CHAIN
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                                                                                                                                                            Matches
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"Isolation and sequence of a rat chymotrypsin B gene.";
"Isolation and sequence of a rat chymotrypsin B gene.";
"Isolation and sequence of a rat chymotrypsin B gene.";
"Isolation and sequence of sequence of the case of the content 
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                  CHYMOTRYPSIN B, C CHAIN.
CHYMOTRYPSIN B, B CHAIN.
CHYMOTRYPSIN B, C CHAIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                  Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal
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MEDLINE-85054881; PubMed=6209274;
Bell G.I., Quinto C., Quiroga M., Valenzuela P., Craik C.S.
Rutter W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.0%; Score 82; DB 1; Length 263; 78.9%; Pred. No. 6.4e-06; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4C1C055A490B8701 CRC64;
                                                                                                                                                                                                               CHYMOTRYPSINOGEN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AFR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsinogen B precursor (EC 3.4.21.1).
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MEROPS; SOL.152; --
Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Ser protesse_Try.
Pfam; PF00089; trypsin; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS, PRO0722; CHYMOTRIPSIN.
SMRAT; SMO0020; Tryp SF7; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
SMART; SM00020; Tryp_SPC; 1.
SMOSITE; PSS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27870 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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19
167
175
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209
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P07338;
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DISULFID
DISULFID
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ACT_SITE
DISULFID
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SEQUENCE
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 AA.
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                                                                          M18700; AAA66350.1; -...
M18694; AAA66350.1; JOINED.
M18694; AAA66350.1; JOINED.
M18695; AAA66350.1; JOINED.
M18696; AAA66350.1; JOINED.
M18699; AAA6320.1; JOINED.
M18699; AAA6320.1; JOINED.
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01-OCT-1996 (Rel
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CLCR RAT
ID _CLCR_RAT
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                      CHYMOTRYPEIN B, A CHAIN.
CHYMOTRYPEIN B, B CHAIN.
CHYMOTRYPEIN B, C CHAIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
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-!- CATALYTIC ACTIVITY: Preferential cleavage: Ala-|-Xaa. Does not hydrolyse elastin.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. ELASTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: EFFICIENT PROTEASE WITH ALANINE SPECIFICITY BUT ONLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Pancreas;
MEDLINE=89044017; PubMed=2460440;
MEDLINE=89044017; PubMed=2460440;
Shirasu Y., Takemura K., Yoshida H., Sato Y., Iijima H.,
Shimada Y., Mikayama T., Ozawa T., Ikeda N., Ishida A., Tamai Y.,
Matsuki S., Tanaka J., Ikenaqa H., Ogawa M.;
"Molecular cloning of complementary DNA encoding one of the human pancreatic protease E isozymes";
J. Blochem. 104:259-264(1988).
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine procease; Digestion; Pancreas; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-PROCEAS;
MEDLINE-88087253; PubMed-2826474;
Tani T., Ohsumi J., Mita K., Takiguchi Y.;
Tani T., Ohsumi J., Mita K., Takiguchi Y.;
"Identification of a novel class of elastase isozyme, human pancreatic clastase III, by cDNA and genomic gene cloning.";
J. Biol. Chem. 263:1231-1239(1988).
                                                                                                                                                                                                                                                                                                                                                   Score 81; DB 1; Length 263;
Pred. No. 9.2e-06;
                                                                                                                                                                                                                                                                                                                                                                           Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P09033; O9BRW4;
O1-WAR-1989 (Rel. 10, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
15-DM2-2002 (Rel. 41, Last annotation update)
Elastase IIIA precursor (EC 3.4.21.70) (Protease E).
                                                                   CHYMOTRYPSINGEN B
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                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                               27849 MW;
                                                                                                                                                                                                                                                                                                                                                                        81.0%;
73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVNGEEAVPHXWXWQVSLQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 IVNGEDAIPGSWPWQVSLQ 52
                                                                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                            263 AA;
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                     1
19
19
34
167
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SEQUENCE
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18699; AAA66.

Li M1699 AAA66.

Li M1699 AAA66.

M1619 D00306; BAA00212.

EMBL; BC005918, AAH05918.,

PIR, AA3934; AA9334.

UR HSSP; D00305; IFON.

DR GENW; HGNC:1594; ELA1A.

DR INCEPPO: IPRO01254; SELPIOCEASE Try.

DR RINE; PRO0029; TryPSIN II.

DR RINE; PRO0029; TRYPSIN II.

DR ROSTIFS; PSO0039; TRYPSIN II.

DR PROSTIFS; PSO0039; TRYPSIN II.

DR PROSTIFS; PSO00139; TRYPSIN II.S; I.

DR PROSTIFS; PSO0135; TRYPSIN II.S; I.

DR PROSTIFS; PSO0135; TRYPSIN II.S; I.

DR PROSTIFS; PSO0136; TRYPSIN II.S; I.

DR PROSTIFS; PSO0136; TRYPSIN II.S; I.

DR PROSTIFS; PSO0136; TRYPSIN II.S; I.

TRYPE II.S TRYPSIN II.S; I.

DR PROSTIFS; PSO0136; TRYPSIN II.S; I.

TRYPE II.S TRYPSIN II.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Caldecrin precursor (EC 3.4.21.2) (Chymotrypsin C) (Serum calcium-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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268 AA.

PRT;

STANDARD:

(caldecrin).";

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CLCR_HUMAN
                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P -> A (IN REF. 2).
EEGSVYAEVDTIYVHEKWNRLFLWN -> AEAPCTLRWTPS
                                                                                                                                                                             "Caldecrin is a novel-type serine protease expressed in pancreas, but its homologue, elastase IV, is an artifact during cloning derived from caldecrin gene."

J. Biochem. 123:546-554 (1998).

-i- FUNCTION: HAS CHYMOTRYPSIN-TYPE PROTEASE ACTIVITY AND HYPOCALCEMIC.
                                                                                                                                                                                                                                                      -:-CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Tyr-|-Xaa, Phe-|-Xaa, Met-|-Xaa, Trp-|-Xaa, Gln-|-Xaa, Asn-|-Xaa, Tyr-|-Xaa, Tissue Specificity: PANCREAS.
-:-SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
-:- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE ELASTASE IV.
                                                                                                                                                     Yoshino-Yasuda I., Kobayashi K., Akiyama M., Itoh H., Tomomura A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
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SIMILARITY).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .)
                                            MEDLINE=92165057; PubMed=1537555;
Kang J., Wiegand U., Mueller-Hill B.;
"Identification of cDNAs encoding two novel rat pancreatic serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.0%; Score 78; DB 1; Length 268; 68.4%; Pred. No. 2.8e-05; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSMRSGTDSSCGT (IN REF. 2).
29374 MW; 33B67AF34D0F8583 CRC64;
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(BY
(BY
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CHARGE RELAY SYSTEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CALDECRIN.
Biol. Chem. 270:30315-30321(1995)
                                                                                                                                CHARACTERIZATION.
MEDLINE-98207038; PubMed-9538241;
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; S80379; AAB35830.1; -. EMBL; X59014; CAA41753.1; -. HSSP; P00766; ICHG.
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Sene 110:181-187(1992).
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                           SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S01.157;
                                          IISSUE=Pancreas;
                                                                                                                                                                                                                                                   ACTIVITY
                                                                                                                                                                      Saheki T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Caldecrin is a novel-type serine protease expressed in pancreas, but its homologue, elastase IV, is an artifact during cloning derived from caldecrin gene."

J. Blochem. 123:546-554(1998).

-I. FUNCTION: HAS CHYMOTRYPSIN-TYPE PROTEASE ACTIVITY AND HYPOCALCEMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Tyr-|-Xaa, Phe-|-Xaa, Met-|-Xaa, Trp-|-Xaa, Gln-|-Xaa, Asn-|-Xaa. -:- TISSUE SPECIFICITY: PANCREAS.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98207038; PubMed-9538241;
Yoshino-Yasuda I., Kobayashi K., Akiyama M., Itoh H., Tomomura A.,
                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A human pancreatic chymotrypsin: biochemical and molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coville G.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
09985; Q9NUHS; 000765; Catated)
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001314; Chymotrypain.
InterPro; IPR001354; Ser_protease_fry.
Prim; PR00089; trypain; I.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp_SPc; 1.
PROSITE; PS0014; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_IS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANT TRP-80.
TISSUE-Pancreas;
MEDLINE-96221265; PubMed-8635596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; $82198; AAB47104.2; ALT SEQ.
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EMBL, Y13697; CAB74031.1; -
HSSP, P00766; 1CHG.
MEROPES, SOI.157; -
Genew; HGNC:2523; CTRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 17-268 FROM N.A.
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Gaps

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3; Mismatches

Local Similarity 68.4%; hes 13; Conservative 1 IVNGEEAVPHXWXWQVSLQ 19 30 VVGGEDAVPNSWPWQVSLQ 48

Best Loca Matches

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Straubberg R.;
Caraubberg R.;
Caraubterg R.;
Caraub
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM (BY SIMILARITY).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C -> V (IN REF, 3),
A2E05143EFF4987C CRC64;
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Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IFR001314; Chymotrypsin.
InterPro; IFR001254; Ser_protease_Try.
FR. PF00092; Crypain; 1.
FR.NTS; PR0072; CHYMOTRYPSIN.
SMART; SM0020; Tryp SPC; 1.
FROSITE; PS0014; TRYPSIN DOM; 1.
FROSITE; PS00114; TRYPSIN LIS.
HUGHOLASE; Serine protease; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elastase 2 precursor (EC 3.4.21.71).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; MI6631; AAA52374.1; --
EMBL; MI6652; AAA52380.1; --
EMBL; D00236; BAA00165.1; --
EMBL; AL512883; CAC42421.1; --
EMBL; BC007031; AAH07031.1; --
PIR; A27432; A27432
PIR; B26823; B26823
HSSP; P00772; IEIG.
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28888 MW;
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29 VVGGEEARPNSWPWQVSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Conservative
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SEQUENCE FROM N.A.
                  TISSUE=Pancreas;
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1D ELZ MOUSE

AC POSSES

DT 13-AUG-1987

CS Mamwalla, ENCOLOR ENKAROPE, ENCOLOR ENKAROPE, ENKAROPE, ENKAROPE, ENCOLOR ENCOL
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CONFLICT
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MEDLINE=Bal98076, PubMed=2834346;
Shitasu Y., Yoshida H., Matsuki S., Takemura K., Ikeda N., Shimada Y., Ozawa T., Mikayama T., Iljima H., Ishida A., Sato Y., Tamai Y., Tanaka J., Ikenaga H.;
Tanaka J., Ikenaga H.;
"Molecular cloning and expression in Bscherichia coli of a cDNA encoding human pancreatic elastase 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                (BY SIMILARITY).
(BY SIMILARITY).
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MEDLINE-87217962; PubMed=3646943;
Kawabaina L., Tani T., Shimoda K., Takiguchi Y.;
Kawabaina L., Tani T., Shimoda K., Takiguchi Y.;
"Characterization of pancreatic elastase II cDNAs: two elastase II
mRNAs are expressed in human pancreas.";
DNA 6:163-172(1987).
                                                                                                                                                                                                                        BY SIMILARITY.
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N'LINKED (GLCNAC...) (POTENTIAL).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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SECULNE-88107669; PubMed=3427074;
Fletcher T.S., Shen W.P., Largman C.;
"Primary structure of human pancreatic elastase 2 determined by sequence analysis of the cloned mRNA.";
Biochemistry 26:7256-7261(1987).
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      Glycoprotein; Zymogen; Signal;
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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-> D (IN REF. 3).
460BF33B4A96516F CRC64;
                                                     POTENTIAL.
ACTIVATION PEPTIDE.
CALBERIN.
CHARGE RELAY SYSTEM (F
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/FTId=VAR_010928.
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O1-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Elastase 2A precursor (EC 3.4.21.71)
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   Serine protease;
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108 12; Conservative
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                            Polymorphism.
SIGNAL
Hydrolase;
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Nikovits W., Rutter W.J.;
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                                                                                                                                                                                                                                                                                                                                            This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
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Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                           **Stevenson b.J., Hagenbuckle O., Wellauer P.K.;

"Sequence organisation and transcriptional regulation of the mouse elastase II and trypsin genes.";

Nucleic Acida Res. 14:8307-8330(1986).
-!- FUNCTION: ACTS UPON BLASTIN.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Met-|-Xaa and Phe-|-Xaa. Hydrolyzes elastin.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: PANCREAS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
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McDonald R.J., Swift G.H., Quinto C., Swain W., Pictet R.L.,
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3; Mismatches 4
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MEDOSS, SOI.155; -...
MGD, MGI:95316; Ela2.
InterPro; IPRO01234; Ser_Drotease_Try.
InterPro; IPRO01234; Ser_Drotease_Try.
Pfam; PF000089; trypsin; 1.
PRINTS; PR00722; CTWMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elastase 2 precursor (EC 3.4.21.71).
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         MEDLINE=87066713; PubMed=3641189;
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Matches 12, Conservative
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E12_RAT
LD PEL2_RAT
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DT 21-JU
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rat pancreatic preproelastases
the complete cloned messenger
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InterPro; IPRO01314; Chymotrypsin.
InterPro; IPRO01254; Ser_protease_Try.
Fam. PRO01254; Ser_protease_Try.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50034; TRYPSIN LDM; 1.
PROSITE; PS00314; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN LSR; 1.
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"Primary structure of two distinct determined by sequence analysis of ribonucleic acid sequences.";
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EMBL; L00123; AAA98780.1; JOINED.
PIR; A00961; ELRT2.
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                                                                        Biochemistry 21:1453-1463(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; V01233; CAA24543.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L00124; AAA98780.1; -
EMBL; L00118; AAA98780.1; JG
EMBL; L00120; AAA98780.1; JG
EMBL; L00120; AAA98780.1; JG
EMBL; L00121; AAA98780.1; JG
EMBL; L00122; AAA98780.1; JG
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Matches 12; Conservative
                                                                                                                              SECUENCE FROM N.A.
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us-10-036-371-4.rspt

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O9pwq6 gadus morhu
Q9d7t9 mus musculu
Q9cq52 mus musculu
Q9w7q3 paralichthy
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010913 macaca mula
09dc86 mus musculu
09dc75 mus musculu
09d56 mus musculu
09d960 mus musculu
09d7pg mus musculu
                                                         February 12, 2003, 10:16:06; Search time 14.1493 Seconds (without alignments) 291.248 Million cell updates/sec
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                                                                                                                                                                                                     671580
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                             671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
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1 IVNGEEAVPHXWXWQVSLQX 20
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09D7T9
09C052
09W7Q3
09SKW7
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Q9DC86
Q9DRX8
Q9DGC35
Q9D960
Q9D7P8
Q9EQZ8
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Gapop 10.0 , Gapext 0.5
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
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OGW704 maralichthy			Oglose gadis morhi	4444	~		O9w7dl navalichthy			2	O91674 xenonis lae		Ogbk47 luidia foli	or protection			Ol8783 macrobus en		α	SUF	ع,	O9r0w3 raffus norv		OBact Associate	e Lodge one		O96871 trichinalla	-	
09W704	O9PRR4	50V5	091039	74N3	O9PRR3	79953	9W701	9W700	09W702	5T73	1674	O9PRT8	3K47	488	OBWR11	E86	018783	092077	Q8VHK8	QBVDV1	146	Q9R0W3	11475	OBOGF6	030	OBTORG	096871	Q921N4	
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261	20	269	270	474	20	1004	249	266	268	492	1524	20	267	265	270	405	806	266	417	417	810	812	812	264	268	271	270	273	
71.0	0.69	0.69	69.0	0.69	0.89	67.0	0.99	0.99	0.99	0.99	0.59	63.0	63.0	62.0	62.0	62.0	62.0	61.0	61.0	61.0	-4		ö	ó,	6.	59.0	θ.	58.0	
71	69	69	69	69	68	67	99	99	99	99	9	63	63	62	62	62	62	61	61	61	61	09	60	59	59	59	28	28	
17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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O99W06 PRELIMINARY; PRT; 263 AA.
O9PW06
O1.MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CHYB.
CHYB.
CHYB.
CHYB.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Actinopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUB-FULDANCE CAECA;
MEDLINE-20464334; PubMed=11011764;
Spilliaert R., Gudmundsdottir A.;
Molecular Confing of the Atlantic Cod Chymotrypsinogen B.";
Microb. Comp. Genomics 5:41-50(2000)
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
EMBL, ALZ42521; CAB43766.1; --
HSSP, PO0766; LCAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 CHYMOTRYPSIN B.
28175 MW; EF61B18A34EE587C CRC64;
                                                                                                                                                                                                                                                                                                                                                                   MEROPS; SOI.152; --
InterPro; IRRO01314; Chymotrypsin.
InterPro; IRR001314; Chymotrypsin.
InterPro; IRR001314; Ser_protease_Try.
Pfam; PR00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN. 1.
Hydrolase; Serine protease; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 AA;
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SEQUENCE
RESULT 1
                90Md60
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09eq28 rattus norv 09er05 mus musculu

09psp2 gallus gall 096q18 homo sapien 08t4n2 rhipicephal

Q96QL8 Q8T4N2 Q9PSP2

13

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Query Match
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290062
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RE STRING-STRIL/64; TISSUE-STOMACH;

RA KARAWA T. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA ALAKAWA T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA ALAKAWA T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA AIZAWA K., IZAWA M., Shibata K., Yoshino M., Yamanaka I.,

RA AIZAWA K., IZAWA M., Shibi K., Sono H., Kasukawa T., Saito R.,

RA AIZAWA K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

RA Kuchi P., Lewis S., Mateuo Y., Gissi C., King B., Kochiwa H.,

RA Kuchi P., Lewis S., Mateuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Beffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Wordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Saaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Hayashizaki Y.,

RA HAYASHIZAKI Y.,
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                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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  Query Match
95.0%; Score 95; DB 13; Length 263;
Best Local Similarity 89.5%; Pred. No. 4.2e-08;
Matches 17; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1915118; Ela3b.
InterPro; IPR001314; Chymotrypain.
InterPro; IPR001214; Ser protease_Try.
Pfam; PR00189; trypain; II
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PR051TE; PS00104; TRYPSIN DOM; 1.
PR051TE; PS001135; TRYPSIN HIS; UNKNOWN I.
                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                            32 IVNGEEAVPHSWPWQVSLQ 50
                                                                                                                       1 IVNGEEAVPHXWXWQVSLQ 19
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nes 16; Conservative
                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2310074F01Rik protein.
ELA3B OR 2310074F01RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
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Matches
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QUELTS

QUEL
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RESULT 3

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RESTAINSCESTBL/60; PubMed=11217851; RATAINSCESTBL/60; PubMed S., Fukuda S., Radota K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Aizawa K., Matsuda H.A., Ashburner M., Bandalov S., Casavana T., Ratochann W., Gasterland T., Gissi C., King B., Kochiwa H., Radota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J., RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Sakai K., Mattil D., Hofmann M., Mume D.A., Kamiya M., Lee N.H., A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Salaski H., Toyo-oka K., Wang K.H., Wettz C., Whittaker C., Wilming L., Mayshiaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., R., Rayashizaki Y., Rayashizak
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Paralichthys Olivaceus (Flounder).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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Nature 409:685-690(2001).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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InterPro, IPR001254; Ser protease_Try.
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                                                                                                        (TrEMBLrel. 17, C
(TrEMBLrel. 17, L
(TrEMBLrel. 21, L
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09C052 PRELIMINARY;
09C022, 01-CTN-2001 (TrEMBLrel. 1'
01-UTN-2001 (TrEMBLrel. 1'
01-UTN-2002 (TrEMBLrel. 2'
2310074F01R1k protein.
ELA3B OR 2310074F01RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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ses 16; Conserv
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1D 009
1D 009
1D 019
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us-10-036-371-4.rspt

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SEQUENCE
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                        RESULT 6
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TISSUE-PANCED KN. M. M.
TISSUE-PANCED KN. M. M.
Seddi R., Guo X.-J., Chaix J.-C., Puigserver A.;
Seddi R., Guo X.-J., Chaix J.-C., Puigserver A.;
Nuclectide sequence of a bovine pancreatic proproteinase E cDNA.";
EMBL, AY057840, AAL236971;
EMBL, AY057840, AAL236971;
PRO0189, Proposity, Lyppsin, 1.
PROSITE, PS50240, TRYPSIN DOM; 1.
PROSITE; PS50240, TRYPSIN DOM; 1.
PROSITE; PS50240, TRYPSIN DOM; 1.
PROSITE; PS50134; TRYPSIN MIS; UNKNOWN 1.
PROSITE; PS01135; TRYPSIN SER; UNKNOWN 1.
HYDROLESE, Serine protease.
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectoidei; Paralichthyidae; Paralichthyidae; Paralichthyidae; Paralichthys.
                                                                                                                                                                   Suzuki T., Srivastava A.S., Kurokawa T.;
"Japanese flounder mRNA for chymotrpsinogen 2.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 92.0%; Score 92; DB 13; Length 260; Local Similarity 84.2%; Pred. No. 1.3e-07; es 16; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                             TherePro; Datis, 1.

InterPro; PR001314; Chymotrypsin.

InterPro; IPR001354; Ser_protease_Try.
Pfam; PR00022; Trypsin; 1.

R NRINTS; R00020; Tryp.SPC; 1.

R ROSITE; PS50240; TRYPSIN DOW; 1.

R ROSITE; PS00134; TRYPSIN JES; UNKNOWN 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

M Hydrolase; Serine protease.

SEQUENCE 260 AA; 27793 MM; 9F583044622F78C0 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 AA.
                                                                                                                                                                                                                                                                   TRYPEIN FAMILY.
EMBL; AB029754; BAA82366.1; -.
HSSP; P00766; 1CHG.
MEROPS; S01.152; -.
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                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                   TISSUE=PANCREAS
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SEQUENCE
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STRAIN=C57BL/6J; TISSUE=SPLEEN;
STRAIN=C108560; Pubmed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa M., Ishahi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saico T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saico R.,
Kadota K., Matsuda H.A., Ashburner M., Beralov S., Casavant T.,
Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
Kuchl P., Lewis S., Matsuo V., Nikaido I., Pesole G., Quackerbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                              Macaca mulatta (Rhesus macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                    "Pancreatic elastase from rhesus monkey.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPEIN PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleoscomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                  Last sequence update)
Last annotation update)
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01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
220000800981K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.0%; Score 85; DB 6;
73.7%; Pred. No. 2e-06;
iive 3; Mismatches
    257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.154; --
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Ffam; PF00089; trypsin. I
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00202; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN. DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_I
PROSITE; PS00135; TRYPSIN HIS; UNKNOWN_I
HYDROIGES; Serine protease.
                                    01-JAN-1998 (TrEMBLrel. 05, Created)
U-JAN-1998 (TrEMBLrel. 05, Last seq
01-WAR-2002 (TrEMBLrel. 20, Last anno
Elastase (EC 3.4.21.36) (Fragment).
  PRT;
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16 VVNGEDAVPYSWPWQVSLQ 34
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Best Local Similarity 73.73
Matches 14; Conservative
PRELIMINARY;
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257 AA;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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TRYPSIN FAMILY
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Q9CR35
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STRAIN=CSTABL/65). PubMed=11217851;

KAMAN=CSTABL/65). PubMed=11217851;

KAMAN=CSTABL/65). PubMed=11217851;

KAMAN=CSTABL/65). PubMed=11217851;

KAMAN=CSTABL/65). PubMed=11217851;

KAMAN=CSTABL/65). PubMed=11217851;

A Arakawa T., Fukuda S.,

A Arakawa T., Saito R.,

A Adota K., Matudia H., Konno H., Kaukawa T., Saito R.,

A Adota K., Matuda H.A., Ashburner M., Batalov S., Casavant T.,

A Adota K., Matuda H.A., Ashburner M., Batalov S., Casavant T.,

A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Sakai K., Statuli F., Sutuki R., Tomita M., Magner L., Washio T.,

B Sakai K., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

B Sakai K., Hill D., Hofmann M., Hue D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,

A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

A Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

A Warshiawa Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A Harashisaki Y.,

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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READES; SOL1.252; CHYOTORY
READES; SOL1.252; CHYOTORY
READES; SOL1.252; CHYOTORY
READES; SOL1.252; CHYOTORY
READES; PSOL1.35; TRYPSIN DOM; 1.
READES; PSOL1.35; TRYPSIN ER; 1.
READES; PSOL1.35; TRYPSIN ER; 1.
READESCE 263 AA; 27821 MW; 2620A27AFBA5D04D CRC64;
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01-JUN-2001 (TrEMBLrel. 17,
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Best Local Similarity 73.7
Matches 14; Conservative
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099888
1D 099888
AC 09988
AC 09988
BDT 01-01
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                                    SOW WE WANTED THE STANDARY OF SOME SOUTH STANDARY SOUTH SOUT
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REGUENCE FROM N.A.

REGUENCE FROM N.A.

RA KARAI J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA KARAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Nibata K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Arakawa T., Hara H., Nibaini K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.P., Suuki R., Tomita M., Wagner L., Washio T.,

RA Kadota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Schriml L.M., Staubli F., Suuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fleccher C., Fujita M., Gariboldi M.,

R Brownstein M.J., Bult C., Fleccher C., Fujita M., Gariboldi M.,

R Brownstein M.J., Bult C., Fleccher C., Fujita M., Gariboldi M.,

R Jone P., Margh B., Ringwald M., Rodriguez I., Sakamoto N.,

R Sasaki H., Sato K., Schoenbach C., Seya T., Whittaker C., Wilming L.,

R Suzuki H., Toyo-oka K., Wang K.H. Weitz C., Whittaker C., Wilming L.,

R Hayashizaki Y.,

R Hayashizaki Y.,

R Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prunctional annotation of a full-length mouse cDNA collection.";
                                            THE
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Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.0%; Score 81; DB 11; Length 263; 73.7%; Pred. No. 9.9e-06; ive 2; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27898 MW; C0638FB8F905A92F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                             MEROPS, 501.152; -.
MGD; MGI:1913723; 220000BD09Rik.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Sar protease_Try.
Pfam; PR00089; trypsin; I.
PRNO125; CHYMOTRYPSIN.
SMART; SM00020; Tryp. SPC; 1.
PROSITE; PS00149; TRYPSIN. DOM; 1.
PROSITE; PS00114; TRYPSIN. JSR; 1.
PROSITE; PS00113; TRYPSIN. JSR; 1.
Hydrolase; Serine protease.
SEQUENCE 263 AA; 27898 MW; C0638FB8F9058
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Q9CR35;
01-JUN-2001 (TrEMBLrel. 17, Created)
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EMBL; AK003079; BAB22553.1; --
EMBL; AK007765; BAB25541.1; --
EMBL; AK007815; BAB2580.1; --
EMBL; AK008129; BAB25661.1; --
EMBL; AK008089; BAB25661.1; --
EMBL; AK008089; BAB25661.1; --
EMBL; AK008089; BAB25661.1; --
                                                                                                                      EMBL, AK007566, BAB25112.1; -. HSSP; P00766; 1GCT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 73.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:685-690(2001)
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2200008D09R1K.
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Mus musculus (Mouse)
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Matches
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RC STRANH-CSTBL/6J; TISSUE=PANCREAS;

MEDLINE=21086660; PubMed=1127851;

RA Maray J., Shinagawa A., Shibara K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Tazawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Arakawa T., Sairo R.,

RA Arakawa T., Sairo R.,

RA Adota K., Matsuda H., Ashburner M., Baralov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Baralov S., Casavant T.,

Radota K., Matsuda H., Ashburner M., Baralov S., Casavant T.,

Ruehl P., Lewis S., Matsud Y., Nigisi C., King B., Kochiwa H.,

Ruehl P., Lewis S., Matsud Y., Nigiado I., Pessole G., Quackenbush J.,

Radota K., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,

RA Schrini L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,

Blake J., Boffelli D., Bolunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Sazki H., Sato K., Schoenbach C., Seyya T., Sakamcto N.,

Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Whittaker C., Whittaker C., Whitshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashiazki Y.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                              27822 MW; 28C4487AF1A26B27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
MEROPS; S01.152; -. MGD; MGI:1913723; 2200008D09Rik.
InterPro: IPR001314; Chymotrypsin.
InterPro: IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CryMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS500240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN LAS; UNKNOWN.1.
Hydrolase; Serine protease.
SEQUENCE 263 AA; 27822 MW; 28C4487AF1A26
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp. SPC; 1.
PR051TE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN SER; 1.
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                      1 IVNGEEAVPHXWXWQVSLQ 19
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CTRL OR 1810004D15RIK.
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RAWAILNE=21096660; PubMed=1127851;

RAWAILNE=21096660; PubMed=1127851;

RAWAI J. Shinagawa A. Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA ATAWA K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,

RA Adota K., Matsuda H.A., Abburner M., Batalov S., Casavant T.,

RA Radota K., Matsuda H.A., Abburner M., Batalov S., Casavant I.,

RA Gota K., Matsuda H.A., Abburner M., Batalov S., Casavant T.,

Rabito T., Colazaki Y., Gissi C., King B., Kochiwa H.,

Rubil D. Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojuga N., Carninci P., de Bonaldo M.P.,

RA Brownstein M., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mastima D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mastima J., Mazzarelli J., Mombaerts P.,

Raski H., Sato K., Scheenbach C., Seya T., Shibata Y., Storch K. F.,

RA Wynshawa Bozis A., Yoshida K., Hasegawa Y., Rawaji H., Kohtsuki S.,

Alavashizaki Y.,
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                  0;
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                                                                                         80.0%; Score 80; DB 11; Length 264; 78.9%; Pred. No. 1.5e-05; tive 0; Mismatches 4; Indels
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78.9%; Pred. No. 1.5e-05;
ive 0; Mismatches 4; Indels
Hydrolase, Serine protease.
SEQUENCE 264 AA; 28151 MW; 1D979719E07C16DE CRC64;
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Last annotation update)
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InterPro; IPRO01314; Chymotrypsin.
InterPro; IPRO01254; Ser_protease_Try.
Pfam; PR00029; trypsin; I.
SMANT; SM00020; CHYMOTYPSIN.
SMANT; SM00020; Tryp. SPC; I.
PROSITE; PS00120; Tryp. SPC; I.
PROSITE; PS00130; TRYPSIN LIS, UNKNOWN I.
PROSITE; PS00135; TRYPSIN LIS, UNKNOWN I.
PHYDrolage; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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HSSP; P00766; 4CHA.
MEROPS; S01.256; -.
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(TrEMBLrel. 17, L
(TrEMBLrel. 21, L
                                                                                                                                                                                                             1 IVNGEEAVPHXWXWQVSLQ 19
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                                                                                      Query Match
Best Local Similarity 78.95
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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01-UN-2001 (TEMBLEE)
01-UN-2002 (TEMBLEE)
1810004015Rik protein
CTRL OR 1810004015RIK.
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Local Similarity 78.9
Les 15; Conservative
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HSSP; P00766; 4CHA.
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                       Query Match
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Q8T4N2;
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Matches
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                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL; AB016228 BAB20275.1; -.
EMBL; AF236365; AAL11034.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                           FIGURINCE FROM N. 1.

TISSUE-RAT PANCREAS;
Sogame Y., Mitsui S., Kataoka K., Kashima K., Kato M., Sakagami J.

Yamaguchi N.;
Wholecular cloning of rat chymopasin.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYESIN FAMILY.

EMBL; AB020757; BAB20287.1; --
HSSP; P00766; 4CHA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%; Score 80; DB 11; Length 264; 78.9%; Pred. No. 1.5e-05; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                          MENDES; SOI.255; --
Interpro; IRR001314; Chymotrypsin.
Interpro; IRR001314; Chymotrypsin.
Interpro; IRR00134; Chymotrypsin.
Interpro; IRR00134; LYPSin. 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SNART; SN00100; TYP_SPO: 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN ER; 1.
PHOILDISE; SOITHE PROFILE SCOUTS; TRYPSIN SER; 1.
FRYDING SOITH STATE SOUTS; TRYPSIN SER; 1.
FROSITE; PS00135; TRYPSIN SER; 1.
FRYDING SOUTS; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Mitsui S., Yamaguchi N.;
"Molecular cloning of mouse chymopasin.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Chymopasin (Chymotrypsin A CTRA-1).
                                                      Q9EQ28 PRELIMINARY; PRT; 264 AA. Q9EQ28; C9EQ28; C9EQ
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STRAIN-129S6/SVEVTAC; TISSUE=SPLEEN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 78.9
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                                                                                                                    Chymopasin.
Rattus norvegicus (Rat).
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Q9ER05;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Midgut serine proceinage-3.
Midjut serine appendiculatus (Brown ear tick).
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Acari, Parasitiformes; Ixodida, Ixodidae, Rhipicephalus.
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TISSUE=PANCREAS.

A Strausberg R.;
Strausberg R.;
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Strausberg R.;
Strausberg R.;
Strausberg R.;
R. Strausberg R.;
R. PEMBL; BCC000383; AAH08383.1; -.
R. MEROPS; S01.154; -.
R. PFG00089; TRYDSIN.F.;
R. PFG00089; TrYPSIN.F.;
R. PFG00089; TrYPSIN.F.; UNKNOWN.1.
R. PROSITE; PS00134; TRYPSIN.ER; UNKNOWN.1.
R. PROSITE; PS00135; TRYPSIN.ER; UNKNOWN.1.
R. PHYDOLASE; PS00135; TRYPSIN.ER; UNKNOWN.1.
R. PHYDOLASE; PS00135; TRYPSIN.ER; UNKNOWN.1.
R. PHYDOLASE; PS00135; TRYPSIN.ER; UNKNOWN.1.
R. PHYDROLASE; PS00135; TRYPSIN.ER; UNKNOWN.1.
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Pred. No. 1.5e-05;
4; Mismatches 2; Indels
| MERCAPS, SO1.256; ---
| MGD; MGI:88558; Ctrl. |
| MGD; MGI:88558; Ctrl. |
| MInterPro; IPR0010134; Ser_protease_Try. |
| InterPro; IPR0010134; Ser_protease_Try. |
| Pfam; PP00089; trypsin; 1. |
| PRINTS; PR00722; CHYMOTRYPSIN. |
| SMART; SM00020; Tryp SPC; 1. |
| PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1. |
| PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1. |
| PROSITE; PS00135; TRYPSIN SER; 1. |
| PHOTOLase; Serine protease. |
| PHOTOLase; Serine protease. |
| SEQUENCE 264 AA; 28135 MW; 1D979709A07056C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q96QL8 PRELIMINARY; PRT; 270 AA. 096QL8; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Similar to elastase 3, pancreatic (protease E).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461 AA
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Best Local Similarity 69.4%;
Matches 13; Conservative '
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29 VVHGEDAVPYSWPWQVSLQ 47
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RA Mulenga A., Onuma M., Sugimoto C.;

RT "Rhipicephalus appendiculatus midgut serine proteinase-3, cDNA cloning
RL and characterization.";

RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

BR EMBL; AYO'R055; AAL79567.1;

SQ SEQUENCE 461 AA, 49581 MW; 641C3DCA5CF2EB68 CRC64;

Query Match

Query Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

MAtches 13; Conservative 2; Mismatches 4; Indels 0;

OY 1 IVNGERAVPHXWWQVSLQ 19

Db 208 IVAGQBAVPHXWWQSLQ 19

Db 208 IVAGQBAVPHSWPWQASVQ 226

Search completed; February 12, 2003, 10:27:23
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APPLICANT: STREET: 3719 Morgan's Creek
APPLICANT: CITY: San Antonio
APPLICANT: STATE: Texas
APPLICANT: STATE: Texas
APPLICANT: POSTAL CODE: 78230
ITLE OF INVENTION: Modulators of Bone Cell Function and
TILE OF INVENTION: Uses Thereof
CORRESPONDENCE: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: OSTEOSA, INC.
STREET: 2040 Babcock Road, Suite 201
CITY: San Antonio
US-08-270-584A-2
US-08-56-031-2
US-08-96-139-2
US-09-96-139-2
US-09-13-304-2
US-09-199-793-2
US-08-944-483-50
US-08-944-483-60
US-08-94-483-60
US-08-97-15-1
US-09-478-957-1
US-09-631-840-2
US-09-61-840-2
US-09-61-840-2
US-09-61-840-2
US-09-06-616-149
US-09-06-616-149
US-09-012-431-149
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STREET: 3530 Hunter's Sound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Rhone-Poulenc Rorer Inc. STREET: 500 Arcola Rd. 3C43 CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 7738 Apple Green
CITY: San Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: IZBICKA, Elzbieta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9516826
GENERAL INFORMATION:
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COUNTRY: USA
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Sequence 11, Appl
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Sequence 62, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 61, Appl
                                                                                                                                        February 12, 2003, 10:18:40; Search time 4.29851 Seconds (without alignments) 136.898 Million cell updates/sec
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1. /cgn2_6/pcdata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/pcdata/1/iaa/6A_COMB.pep:*

3. /cgn2_6/pcdata/1/iaa/6A_COMB.pep:*

3. /cgn2_6/pcdata/1/iaa/6A_COMB.pep:*

5. /cgn2_6/pcdata/1/iaa/faTUSCOMB.pep:*

5. /cgn2_6/ptdata/1/iaa/backfiles1.pep:*
     GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-278-091-10

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US-08-487-173-10

US-08-487-16-10

US-08-487-16-10

US-08-615-271-10

US-09-074-659-10

US-09-074-659-10

US-09-074-659-10

US-09-074-659-10

US-09-106-468-10

US-09-220-711-16

US-09-220-711-16

US-09-220-711-16

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US-09-44-481-53

US-09-944-481-58

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Maximum Match 100%
Listing first 45 summaries
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1 IVNGEEAVPHXWXWQVSLQX 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Perfect score:
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                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                           Run on:
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CINTRY: Ontario COUNTRY: Canada ZIP: MSG 1PF: Canada ZIP: MSG 1PF: Canada ZIP: MSG 1PF: Canada COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: TBM PC Compatible COPERATIOS SYSTEM: PC-DOS/NS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/278,091 FILING DATE: 21-JUL-1994 CLLASSIFICATION: 435 CATORNEY AGENT INFORMATION: NAME: Stewart, Michael I REGISTRATION NUMBER: 24,973 REFERENCE/DOCKET NUMBER: 1038-371 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVNGEEAVPHXWXWQVSLQ 19
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                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOUNCE:
ORGANISM: Homo sapiens
PCT-US95-16826-2
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APPLICANT: STATE: Texas
APPLICANT: COUNTRY: USA
APPLICANT: POSTAL CODE: 78230
TITLE OF INVENTION: Modulators of Bone Cell Function and TITLE OF INVENTION: USes Thereof
NUMBER OF SEQUENCES: 2
CORRESPEDUDENCE ADDRESS:
ADDRESSEE: Rhone-Poulanc Rorer Inc.
STREET: SAO Arcala Rd. 3C43
CITY: Collegeville
STREET: PA
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STREET: 2040 Babcock Road, Suite 201
CITY: San Antonio
STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
85.0%; Score 85; DB 5; 1
Best Local Similarity 73.7%; Pred. No. 2.7e-08;
Matches 14; Conservative 3; Mismatches 2
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363,092
FILING DATE: 20.DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 29,699
REFERENCE/DOCKET 1010/454-3816
TELECOMMUNICATION INFORMATION:
FILEPHONE: (610) 454-3806
TELEPAX: (610) 454-3806
TELEPAX: (610) 454-3806
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: YONEDA, Toshiyuki
STREET: 3530 Hunter's Sound
CITY: San Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 7738 Apple Green CITY: San Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: IZBICKA, Elzbieta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application PC/TUS9516826; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Texas
COUNTRY: USA
POSTAL CODE: 78240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Texas
COUNTRY: USA
POSTAL CODE: 78230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POSTAL CODE: 78229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IVNGEEAVPHXWXWQVSLQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VVNGEDAVPYSWPWQVSLQ 19
                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19002
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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Gaps
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GENERAL INFORMATION
GENERAL INFORMATION;
APPLICANT: LOCAGNORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Raymond P.
APPLICANT: CHONG, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Sim & McBurney
STRRET: Suite 701, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Best Local Similarity 73.7%; Pred. No. 2.8e-08;
Matches 14; Conservative 3; Mismatches 2; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: IEM PC Compatible
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPE, MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16826
FILING DATE:
PLING DATE: 20-DEC-1994
ATTONENEY/AGBRY INPOMER: US 08/363,092
FILING DATE: 20-DEC-1994
ATTONEY/AGBRY INPOMERION:
NAME: SAVILEKY, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/POCKET NUMBER: 29,699
RELECOMMUTCATION INPORMATION:
TELEPHONE: (610) 454-3816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEMETH: 32 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-278-091-10
; Sequence 10, Application US/08278091
; Patent No. 5506139
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us-10-036-371-4.rai

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Gaps
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US-08-472-173-10
Sequence 10, Application US/08472173
Sequence 10, Application US/08472173
Sequence 10, Application US/08472173
Sequence 10, Application US/08472173
APPLICANT: CACSMORE, Sheena M
APPLICANT: CACSMORE, Pale
APPLICANT: CACSMORE, Pale
APPLICANT: CACSMORE, Pale
APPLICANT: CACSMORE, Raymond P.
APPLICANT: CACSMORE, Raymond P.
APPLICANT: CACSMORE, Raymond P.
APPLICANT: CACSMORE, Raymond P.
APPLICANT: CACSMORE, 23
CORRESPONDENCE ADDRESS: 23
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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84.2%; Pred. No. 2.5e-07;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: ParentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,173
APPLICATION NUMBER: US/08/472,173
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
FILING DATE: 26-AUG-1994
FILING DATE: 21-ULL-1994
FILING DATE: 21-ULL-1994
ATTORNEY/AGENT INORMATION:
NAME: 21-ULL-1994
ATTORNEY/AGENT INORMATION:
NAME: 21-ULL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08487167;
PARERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pal-Ping
APPLICANT: COMEN, RAYMOND P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
                                   1 IVNGEEAVPHXWXWQVSLQ 19
                                                                       1 IVNGEEAVPHXWXWQVSLQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 84.2
les 16; Conservative
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STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
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TOPOLOGY: linear

US-08-472-173-10
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US-08-487-167-10
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08483859
Fatent No. 565436
FAPLICANT: LOCEMORE, Sheena M. APPLICANT: LOCEMORE, Sheena M. APPLICANT: CHONG, PIP PIP G. APPLICANT: CHONG, PIP PIP G. APPLICANT: CHONG, PIP PIP G. APPLICANT: COMEN, Raymond P. APPLICANT: COMEN, Raymond P. APPLICANT: KLEIN, Michel H. TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with TITLE OF INVENTION: Reduced Protease Activity CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                  Query Match 85.0%; Score 85; DB 1; Length 228; Best Local Similarity 84.2%; Pred. No. 2.5e-07; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
85.0%; Score 85; DB 1; Length 228;
Best Local Similarity 84.2%; Pred. No. 2.5e-07;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE: 07-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATE: 26-AUG-1994
FILING DATE: 26-AUG-1994
FILING DATE: 26-AUG-1994
FILING DATE: 21-UL-1994
FILING DATE: 21-UL-1994
FILING DATE: 21-UL-1994
FILING DATE: 21-UL-1994
ATTORNEY/GENT INCOMATION:
NAME: CENTRAL AUGUST AUGUST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALVESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-495 MIS:vg
TELECOMMUNICATION INFORMATION:
   (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IVNGEEAVPHXWXWQVSLQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IVNGEBAVPGSWPWQVSLQ 19
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                     LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
                            TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                         / TOPOLOGY: linear
US-08-278-091-10
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TELEPHONE:
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US-08-483-859-10
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Pred. No. 2.5e-07;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LOOSAGNES, Sheena M
APPLICANT: LOOSAGNES, Sheena M
APPLICANT: TOOSAGNES, Sheena M
APPLICANT: TONG, Yan.-Bing
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: COMEN, Raymond P.
TITLE OF INVENTION: Raduced Protease Activity
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBULNEY
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER: LADALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/296,149
FILING DATE:
CLASSIFICATION NUMBER: 105/08/296,149
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-390
TELECOMMUNICATION INFORMATION:
Patentin Release #1.0, Version #1.25
                                                        CURRENT APPLICATION NUMBER: US/08/482,816
FILING DATE: 07-JUN-1995
CLASSIFICATION 135
CLASSIFICATION 135
FILING DATE: 26-MUG-1994
FILING DATE: 26-MUG-1994
FILING DATE: 26-MUG-1994
FILING DATE: 26-MUG-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: SEWART, Michael I
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-494 MIS:VG
TELEFAN: (416) 595-1155
TELEFAN: (416) 595-1163
TELEFAN: (416) 595-1163
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
STRENGENCE/CONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08296149
Patent No. 5939297
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 84.2
Matches 16; Conservative
                                          CURRENT APPLICATION DATA APPLICATION NUMBER: US
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US-08-482-816-10
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Sequence 10, S935573
GENERAL INFORMATION:
APPLICANT: LOSOMORE, Sheena M
APPLICANT: TANG, Yan-Ping
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease Act
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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              APPLICANT: KLEIN, Michel H.

TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
SIME MCBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.2%; Pred. No. 2.5e-07;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                        CITY:
COMPUTER READABLE FORM:
MEDIUM TYRE:
COMPUTER READABLE FORM:
MEDIUM TYRE:
COMPUTER:
COMPUT
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STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IVNGEEAVPHXWXWQVSLQ 19
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Fatent No. 6020183

GENERAL INFORMATION

APPLICANT: LOOSMORE, Sheena M.
APPLICANT: CHONG, Pale
APPLICANT: CHONG, Pale
APPLICANT: CHONG, Pale
APPLICANT: COMEN, Raymond P.
APPLICANT: CALEIN, Michel H.
ITLE OF INVENTION: Raduced Protease Activity
ITLE OF INVENTION: Reduced Protease Activity

NUMBER OF ENGUENCES:
ADDRESSEE SIM & MCBUTNEY

STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: TANG, Yan-Ping
APPLICANT: TONG, Yan-Ping
APPLICANT: COMEN, Yan-Ping
APPLICANT: COMEN, Raymond P.
APPLICANT: COMEN, Michael H.
TITLE OF INVENTION: MACALOG OF HAEMOPHILUS HIN47 WITH REDUCED
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: 23
ADDRESSEE: Sim & MCBURNERY
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84.2%; Pred. No. 2.5e-07;
Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE: 20-JUN-1996
CLASSIETCATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: STEWATCH, MICHAEL: 24,973
REFERENCE/DOCKET NUMBER: 1038-580
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INDOMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TVDD: amino acids
TVDD: Amino acids
TVDD: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                 E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                ; Sequence 10, Application US/08615271; Patent No. 5981503
                     1 IVNGEEAVPGSWPWQVSLQ 19
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COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 84.2*
Matches 16, Conservative
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; TOPOLOGY: linear
US-08-615-271-10
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                                                                                    RESULT 10
US-08-615-271-10
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STATE: Or
COUNTRY:
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US-09-074-660-10
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Sequence 10, Application US/08801499

Patent No. 5962-10

GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: CHONG, Pen-Ping
APPLICANT: CHONG, Pen-Ping
APPLICANT: CHONG, Pen-Ping
APPLICANT: CLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease Act
CORRESPONDENCE ADDRESS:
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                                                                                                                                  Query Match
85.0%; Score 85; DB 2; Length 228;
Best Local Similarity 84.2%; Pred. No. 2.5e-07;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.0%; Score 85; DB 2; Length 228; 84.2%; Pred. No. 2.5e-07; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-671 MIS:jb
TELECOMONICATION INFORMATION:
TELEPAX: (416) 595-1155
INPORMATION FOR SEQ 1D NO: SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Sim & McBurney
6th Floor, 330 University Avenue
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 07-UUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 1-UUL-1994
ATTORNEY/AGRIT INFORMATION:
                                                                                                                                                                                                                       1 IVNGEEAVPHXWXWQVSLO 19
                                                                                                                                                                                                                                                    LENGTH: 228 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-296-149-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IVNGEEAVPHXWXWQVSLQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 84.27
Matches 16; Conservative
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COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6th FlorITY: Toronto STATE: Ontario
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RESULT 13
US-09-106-468-10
US-09-106-468-10
Sequence 10, Application US/09106468
Patent No. 6114125
GENERAL INPORMATION:
APPLICANT: LOCSWORE, Sheena M.
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Bele
APPLICANT: CHONG, ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
TITLE OF INVENTION: PROTEASE ACTIVITY
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Gth Floor, 330 University Avenue
CITY: Toronto
COUNTRY: Canada
ZIP: MGG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PLODS/MS-DOS
SOFTWARE: PATENTIN BYGENER: PCTATION NUMBER: US/09/106,468
FTITING DATE:
FTITING DATE:
FTITING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.0%; Score 85; DB 3; Length 228;
84.2%; Pred. No. 2.5e-07;
tive 0; Mismatches 3; Indels
PRICRAPELCATION DATA:

APPLICATION NUMBER: US 08/487,167
FILING DATE: 07-UNN-1995
FILING DATE: 07-UNN-1995
FILING DATE: 26-MC-1994
FILING DATE: 26-MC-1994
FILING DATE: 26-MC-1994
FILING DATE: 21-WL-1994
ATORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-730 MIS:jb
TELEFAN: (416) 595-1155
TELEFAN: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 228 mmino acide
TYPE: mmino acide
STEMBER: 228 mmino acide
TYPE: mmino acide
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NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REPERENCE FOCKET NUMBER: 1038-825
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/615,271
FILING DATE: 20-UUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IVNGEEAVPHXWXWQVSLO 19
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Best Local Similarity 84.2'
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US-09-074-659-10
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ALTIES OF INVENTION: Analog of Haemophilus Hin47 Protein with TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MEBRINEY
STREET: Sim & MEBRINEY
GITY: Toronto
STREET: 6th Ploor, 330 University Avenue
CITY: Toronto
STREET: GLASSEE SIM & MEBRINEY
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/074,659
FILLING DATE:
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                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,660
FILING DATE:
                                                                                                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNDAER:
APPLICATION UNDAER:
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-UL-1994
ATTORNEY/AGENT INFORMATION:
NAME: SE-WART, Michael I.
REGISTRATION NUMBER: 24,038-731 MIS:jb
TELEFENOR: (416) 595-1155
TELEFENOR: (416) 595-1165
TELEFENOR: (416) 595-1163
TELEFENCE CHARACTERISTICS:
LENGTH: 228 amino acide
TYPE: amino acide
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 10, Application US/09074659; Patent No. 6025342; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LOOSMORE, Sheena M. APPLICANT: YANG, Yan Ping APPLICANT: YANG, Yan Ping APPLICANT: COMEN, Raymond P. APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IVNGEEAVPHXWXWQVSLQ 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
     STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
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Gaps

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APPLICANT: LOGGNER, Sheena M.
APPLICANT: CHONG, Van-Ping
APPLICANT: CHONG, Van-Ping
APPLICANT: CHONG, Pale
APPLICANT: CHONG, Pale
APPLICANT: CHONG, Pale
APPLICANT: CHONG, Pale
APPLICANT: Michal H.
TITLE OF INVENTION: RANLOG OF HAEMOPHILUS HIN47 WITH REDUCED
NUMBER OF SEQUENCES: 23
CORRESSEE: Sim & MCBRITHEY
STREET: Sim & MCBRITHEY
STREET: Sim & MCBRITHEY
STREET: Sim & MCBRITHEY
STREET: COLORIO
STATE: 
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                                                                                                                                                                                                                                                                                                       Query Match
85.0%; Score 85; DB 3; Length 228;
Best Local Similarity 84.2%; Pred. No. 2.5e-07;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 85.0%; Score 85; DB 4; Length 228; Best Local Similarity 84.2%; Pred. No. 2.5e-07; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09106466A; Patent No. 6147057; GENERAL INFORMATION;
TELEFAX: (416) 595-1163
| INFORMATION FOR SEQ ID NO: 10:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 228 amino acids
| TYPE: amino acid
| STRANDEDNESS: single
| TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IVNGEEAVPHXWXWQVSLQ 19
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HERDIT. APPLICATION US/09106467

Sequence 10, Application US/09106467

PATENT NO. 60251500

GREENLINGWARTON

APPLICANT: CONSCREE, Sheena M. APPLICANT: CONSCREE, Sheena M. APPLICANT: CONSCREE, Sheena M. APPLICANT: CONSCREE, SAMENA M. APPLICANT: CONSCREE, SAMENA M. APPLICANT: CONSCREES, SAMENA M. APPLICANT: CONSCREES, SAMENA M. APPLICANT: CONSCREES, SAMENA M. APPLICANT: CONSCREES, SAMENA M. AAPLICANT: CONSCREES, SAMENA M. AAPLICANTON DATA:

CONSTRET. EARL PROPERTIES CONSCREES, SAMENA M. SAMENA
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(OTARU) NNAJB 3DA9 RIHT

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Sequence 932, App Sequence 935, App Sequence 932, App Sequence 112, App Sequence 130, App Sequence 130
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Sequence 4, Application US/10036371

Sequence 4, Application US/10036371

Sequence 4, Application US/10036371

Sequence 4, Application US/10036371

Sequence 4, Application US/20041997A1

GENERAL INFORMATION:

APPLICANT: BJARNARSON, JON B.

TITLE OF INVENTION: FISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND TITLE OF INVENTION: E08811C USE

FILE REFERENCE: 81691/28496

CURRENT PELING DATE: 2002-01-02

PRIOR APPLICATION NUMBER: 09/411,688

PRIOR APPLICATION NUMBER: 5086/99

PRIOR APPLICATION NUMBER: 5086/99

PRIOR FILING DATE: 1999-06-18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 20

TYPE: PRATURE: NO RES

LOCATION: (11)

ONGANISM: Gadus sp.

FRATURE:

ONGANISM: Gadus sp.

FRATURE:

ONGANISM: CALCATION: Sor T
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US-10-012-896-932
US-09-895-793-895
US-09-895-793-895
US-09-895-814-992
US-09-895-814-992
US-09-995-814-932
US-09-995-814-932
US-09-790-669-895
US-09-790-669-895
US-09-780-669-895
US-09-780-669-895
US-09-780-669-895
US-09-812-817-895
US-09-812-817-895
US-09-812-817-895
US-10-10-10-112
US-10-112-112
US-10-112-798-330
US-10-113-706-330
US-10-113-706-330
US-10-117-75-330
      OTHER INFORMATION: S, P or Y FEATURE:
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; OTHER INFORMATION: D or
US-10-036-371-4
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es 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: MOD RES
    NAME/KEY: MOD RES
    Query Match
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Matches
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Sequence 6, Appli
Sequence 96, Appl
Sequence 152, App
Sequence 152, App
Sequence 576, App
Sequence 576, App
Sequence 101, Appl
Sequence 871, App
Sequence 934, App
                                                                                         February 12, 2003, 10:22:36; Search time 3.04478 Seconds (without alignments) 167.821 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO_NEW_PUB.pep:*
        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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2 US-10-036-371-6

3 US-09-925-297-643

3 US-09-923-779-152

6 US-09-925-297-695

6 US-09-925-297-695

6 US-09-925-297-695

6 US-09-925-297-695

6 US-09-925-297-871

6 US-09-925-297-871

7 US-09-988-975A-1

7 US-09-981-353-21

8 US-09-981-353-21

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US-09-780-669-934
US-09-822-827-934
US-10-012-896-895
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                                                             OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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1 IVNGEEAVPHXWXWQVSLQX 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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RESULT 2
US-10-036-371-6
Sequence 6, Application US/10036371
Sequence 6, Application US/10036371
Sequence 6, Application US/10036371
GENERAL INFORMATION:
APPLICANT: BARANARSON, JON B.
TITLE OF INVENTION: FISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND TITLE OF INVENTION: COSMETIC USE
FILE REFERENCE: 81691/264560
CURRENT APPLICATION NUMBER: US/10/036,371
CURRENT FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 5086/99
PRIOR PILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 20
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Patent No. US20020081659A1

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105

CURRENT APPLICATION NUMBER: US/09/925,297

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05989

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 928

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 643

LENGTH: 146
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; ORGANISM: Bovine 8p.
US-10-036-371-6
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Best Local Similarity
Matches 16; Conserv
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US-09-925-297-643
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; LOCATION: (143); OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-297-643
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Patent No. US20020076721A1

GENERAL INFORMATION:

APPLICANT: Pyle, Ruth A.

APPLICANT: AL, Jiangchun

APPLICANT: AL, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

FILE REFERENCE: 210121.553

CURRENT APPLICATION NUMBER: US/09/923,779

CURRENT APPLICATION NUMBER: 155

CURRENT APPLICATION NUMBER: 1501-08-06

NUMBER OF SEQ ID NOS: 155

SOFTWARE: FRAESEQ for Windows Version 4.0

FENCENTIAL OF 152
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Best Local Similarity 68.4%; Pred. No. 9.8e-06;
Matches 13; Conservative 4; Mismatches 2; Indels
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82.0%; Score 82; DB 10; Length 26
Best Local Similarity 78.9%; Pred. No. 4.6e-06;
Matches 15; Conservative 1; Mismatches 3; Indels
                                                                                                                                       3, Indels
                                                                                       Score 82; DB 10;
Pred. No. 2.5e-06;
1; Mismatches 3
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APPLICANT: CARNEPEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: SUDARSANAM, SUCHA
TITLE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
FILLE REFERENCE: 030602/1214
CURRENT PFLICA DATE: 2001-06-26
PRIOR PILLING DATE: 2000-06-26
PRIOR PILLING DATE: 2000-06-26
NUMBER: PALCATION NUMBER: 60/214,047
PRIOR FILLING DATE: 2000-06-26
NUMBER: PALCATION NUMBER: 2001-06-26
NUMBER: PALCATION NUMBER: 0477
PRIOR FILLING DATE: 2000-06-26
NUMBER: PALCATION OF: 150
SOUTWARE: PALCATION OF: 2.1
SEQ ID NO 96
LENGTH: 263
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
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Patent No. US20020064856A1
GENERAL INFORMATION:
                                                                                            82.0%;
78.9%;
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                                                                                                 Query Match
Best Local Similarity 78.9
Matches 15; Conservative
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CRGANISM: Homo sapiens
US-09-923-779-152
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US-09-888-615-96
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APPLICANT: PLOCMANIA GREGORY
APPLICANT: PLOCMANIA GREGORY
APPLICANT: CANDEPEL, SAN
APPLICANT: CANDEPEL, SAN
APPLICANT: CANDEPEL, SAN
APPLICANT: GARACOEAK, GLEN
APPLICANT: GARACOEAK, GLEN
APPLICANT: GARACOEAK, GLEN
APPLICANT: GARACOEAK, GUCHA
TITLE OF INVENTING NOVEL PROTEASES
FILE REPERENCE: 038602/114
CURRENT APPLICATION NUMBER: US/99/886,615
CURRENT FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PALENTING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PALENTING DATE: 2001-06-26
INDIRECT SEQ ID NOS: 150
SOFTWARE: PALENTING DATE: 2000-06-26
INDIRECT SEQ ID NOS: 150
SOFTWARE: PALENTING DATE: 2000-06-26
INDIRECT SEQ ID NOS: 150
INDIRECT SEQ ID NOS: 150
INDIRECT SEG 
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ORGANISM: Homo sapiens
US-09-925-297-529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: SITE
LOCATION: (27)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTION: (34)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-297-695
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (8)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/SEX: SITE
LOCATION: (167)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                              US-09-925-297-695

Sequence 695, Application US/09925297

Patent No. US20020081659A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
FILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT APPLICATION NUMBER: PCT/US00/05989
PRIOR PALICATION NUMBER: PCT/US00/05989
PRIOR PLILNG DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 695
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ITILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR PELICATION NUMBER: PCT/US00/65989
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARRE: PATENTIN Ver. 2.0
SEQ ID NO 576
LENGTH: 269
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Patent No. US20020081659A1
GENERAL INFORMATION:
                                             1 IVNGEEAVPHXWXWQVSLQ 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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COCATION: (213)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAMS/KEY: SITE
LOCATION: (220)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAMS/KEY: SITE
LOCATION: (234)
COCATION: (234)
COCATION: (234)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-297-576
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US-09-925-297-529
/ Sequence 529, Application US/09925297
/ Sequence 529, Application US/09925297
/ Patent No. US20020081659A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ CURRENT APPLICATION NUMBER: US/09/925,297
/ CURRENT APPLICATION NUMBER: 05/01-08-10
/ PRIOR PAPLICATION NUMBER: 60/124,270
/ PRIOR FILING DATE: 1999-03-12
/ NUMBER OF SEQ ID NOS: 928
/ SOFFWARE PATENT NOR - 2.0
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JS-10-012-896-934
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APPLICANT:
APPLICANT:
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: SITE
LOCATION: (106)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (112); CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-297-871
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Sequence 871, Application US/09925297

Patent No. US2002008559A1

GENERAL INFORMATION:

APPLICANT: ROSEON et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA105

CURRENT APPLICATION NUMBER: US/09/925,297

CURRENT FILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-08

PRIOR PILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 928

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 871

LENGTH: 113
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GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Bandman, Olga
TITLE OF INVENTION:
FILE REFERENCE: PF-0227-2 CIP
CURRENT APPLICATION NUMBER: US/09/988,975A
CURRENT FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PERL PROGRAME
SEQ ID NO 1
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Best Local Similarity 63.2%; Pred. No. 0.00023;
Matches 12; Conservative 3; Mismatches 4; Indels
                                                     Score 70; DB 10; Length 970;
pred. No. 0.0015;
                                                                                               6; Indels
                                                                                               1; Mismatches
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                                                         Query Match 70.0%;
Best Local Similarity 63.2%;
Matches 12; Conservative
                                                                                                                                          1 IVNGEBAVPHXWXWQVSLQ 19
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ORGANISM: Homo sapiens
, ORGANISM: Homo sapiens
US-09-888-615-101
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US-09-988-975A-1
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US-09-925-297-871
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Sequence 23, Application US/09981353

Patent No. US202016038241

GENERAL INFORMATION:

APPLICANT: Lasek, Amy W.

APPLICANT: Jones, David A.

TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER

TITLE PERFERENCE: PA-0038 US

CURRENT APPLICATION NUMBER: US/09/981,353

CURRENT FILING DATE: 2001-10-11

WINHER OF SEQ ID NOS: 194

SOFTWARE: PELL Program

SOTTWARE: PELL PROGRAM

SOFTWARE: PRT

CORGANISM: Homo sapiens

FRATURE:

FRATURE:

NAME/KEY: misc feature

CHER INFORMATION: Incyte ID No. US20020160382A1 991163CD1

US-09-981-353-23
                                                                                                                                                                                                                         Score 66; DB 10; Length 283;
Pred. No. 0.0018;
1; Mismatches 5; Indels
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Pred. No. 0.0025;
1; Mismatches 5; Indels
                                      FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020119531A1 556016
FEATURE:
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Publication No. US2002018351A1
GENERAL INFORMATION:
APPLICANT: Nu. Jiangchun
APPLICANT: Nu. Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: AAFIOCKET, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Retter, Marc W.
APPLICANT: Recter, Marc W.
APPLICANT: Scilk, John A.
APPLICANT: Scilk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Catter, Day, Craig H.
                                                                                                                            NAME/KEY: unsure

1. LOCATION: 235

7. OTHER INFORMATION: unknown or other

US-09-988-975A-1
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Hepler, William T.
Henderson, Robert A.
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Best Local Similarity 66.7%;
Matches 12; Conservative
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Best Local Similarity 66.7
Matches 12, Conservative
TYPE: PRT
ORGANISM: Homo sapiens
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1 IVNGEEAVPHXWXWQVSL 18

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157 IVGGESALPGAWPWQVSL 174
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                                                             APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: OMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
GURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: Falls DATE: 201-12-10
SOFTWARE: Falls DATE: Anidows Version 3.0
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APPLICANT: Henderson, Robert A.

APPLICANT: Houghton, Raymond L.

APPLICANT: Houghton, Raymond L.

APPLICANT: Winals de Bassols, Carlota

APPLICANT: Vinals de Bassols, Carlota

APPLICANT: Farger, Gary R.

APPLICANT: Farger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210.15.34C2

CURRENT FILING DATE: 2010-06-29

NUMBER OF SEQ ID NOS: 982

SOFTWARER: FastSEQ for Windows Version 3.0

LENGTH: 393
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Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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) Sequence 944, Application US/09895793
; Publication No. US2020192763A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Miccham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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Hepler, William T.
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                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-934
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; ORGANISM: Homo sapiens
US-09-895-793-934
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APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER.
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER.
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT PAPLICATION NUMBER: US/09/895,814
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 934
LENGTH: 393
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Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
RESULT 15
US-09-895-814-934
Sequence 914, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
                                                                                                        APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Miccham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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Hepler, William T.
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ORGANISM: Homo sapiens
US-09-895-814-934
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APPLICANT:
APPLICANT:
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APPLICANT:
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| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT;*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT;*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT;*
| SIDS2/gcgdata/geneseqg-emb1/AA1983.DAT;*
| SIDS2/gcgdata/geneseqg-emb1/AA1983.DAT;*
| SIDS2/gcgdata/geneseqg-emb1/AA1986.DAT;*
| SIDS2/gcgdata/geneseqg-emb1/AA1986.DAT;*
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| SIDS2/gcgdata/geneseqg/geneseqg-emb1/AA2000.DAT;*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                  OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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68
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	New Arthur Lidady to Manager and Manager a	Amino tominal and	Neutrophil action	Posting absented	Himen namerical	Amino pancieacio c	Mentancharia sequenc	Neutrophil - activat	Heart Print activat	Human panciedtic c Human serine prote	
SUMMARIES	ID	AAY50209	AAB31577	AAY50207	AAY99596	AAB54191	AAU82738	AAY50208	AAY50210	AAB54077	AAB11710	
	DB	20	22	20	21	2	23	20	50	21	21	
	Query Match Length DB	13	13	15	245	146	263	15	15	192	264	
مد	Match	100.0	100.0	100.0	100.0	95.6	95.6	91.2	91.2	72.1	72.1	
	Score	68	69	68	68	63	63	62	62	49	4.9	
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	Propionibacterium S. pneumoniae derium Olegatovate Human olfactovate Human olfactova	ed peptide 9. cardiovascular disease; tr ses; arthritis; diabetes; disease; myocardial infa	hy; venous insufficiency; on; sepsis.
AAB117 AAY502 AAY502 ABG146 AAU685 AAU18 AAG718 AAG724 AAG724 AAG724 AAG718	AAVIS-542.1 AAVIS-542.1 AAVIS-1199 AAVIS-1199 AAVIS-1199 AAVIS-1199 AAVIS-1199 AAVIS-1199 AAVIS-1199 AAVIS-1199 AAVIS-11993	de; 13 AA. y) ncreatic deriv s; treatment; s; treatment; a; Alzheimer's	retinopiyperten
	525 525 525 525 525 525 525 525 525 525	otide, prick, pancre, pancre, pancre, mautoimmaia, Al	abetic re litor; hyp .05247. 38894. N INC. A. ST.
264 113 1007 1144 1144 1170 1133 1339 1339	55.73 9.73	Pepti t entr ing pa ancrea se, au	diab hhibit -USOS; -O038(TION : RNIA. INST
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	6 ° ° ° ° ° ° ° ° ° ° ° ° ° ° ° ° ° ° °	1 1750 1750 1750 1750 111 111 111	haemorrhagic trauma; prot Bos taurus. W09946367-AK 16-SEP-1999, 11-MAR-1999, 11-MAR-1998, (CELL-) CELL (REGC) UNIV (SCRI) SCRI Stoughton RB
44444444444444444444444444444444444444	420000000000000044444 100000000000044444	SUL	XW haek XX

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fungal infection; autoimmune disease.
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                                                                                                                                                                                                                      15-JUN-2000; 2000WO-IS00005
                                                                                                                Best Local Similarity 100.
Matches 13; Conservative
                                                                                                        13 AA;
                                                                                                                                                                                                          WO200078332-A2
                                                                                                                                                                                                                            18-JUN-1999;
                                                                                                                                                            20-APR-2001
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                                                                                                                                                      AAB31577;
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                                                                                                              Query Match
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                                                                                                                                             AAB3157'
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Bjarnason JB; Sequence Query Match 요 ઠે This invention describes a novel method for the use and preparation of cell activating compositions which involves preparing a cell activating cell activating composition compositions which involves preparing a cell activating composition comprising (a) homogenizing pancreatic tissue in buffer at about neutral or higher ph to produce a homogenate, (b) removing particulates from the homogenate, (c) optionally incubating the particulates removed, with a protease; and cell activation activity. The methods can be used for improving treatment outcome or reducing risk of treatment of e.g. cardiovascular celseament outcome or reducing risk of treatment of e.g. cardiovascular celseamer, inflammatory disease, trauma, autoimmune diseases, arthritis, organ rejection, disbetes and diabetic complications, stroke, ischemia, cretingathy, disbetes, venous insufficiency, unstable angina or trauma. They can be used in the veterinary treatment of a non-human subject. They can be used in the veterinary treatment of a non-human subject. They can be used to lower cell activation resulting from the veterinary preatment of an elevated level of hydrogen peroxide in plasma or whole blood and in the elevated level of hydrogen peroxide dismitase (SOD) indicates leukocyte up to presence of superoxide dismitase (SOD) indicates leukocyte up to presence of by indicative of the onset of an acute cardiovascular disorders, such as disease onset or ischemic complications. An elevated correct of hydrogen peroxide in plasma or whole blood and in the presence of SOD is indicative of a chronic or immune compromised confittion e.g. hypertension or sepsis. AAYSO201-YSO334 represent peptides confittion e.g. hypertension or sepsis. AAYSO201-YSO334 represent peptides ô Use of cell activating compositions in developing products for diagnosis and treatment of e.g. cardiovascular, inflammatory, autoimmune or Alzheimer's disease, trauma, arthritis, organ rejection, diabetes, stroke or ischemia -Gaps ö 100.0%; Score 68; DB 20; Length 13; 100.0%; Pred. No. 5.1e-05; ive 0; Mismatches 0; Indel8 Example 9; Page 182; 184pp; English. 1 CGVPAIQPVLSGL 13 1 ccvphiópvisci 13

Amino terminal sequence of bovine trypsin A chain. AAB31577 standard, peptide; 13 AA. (first entry)

CELL ACTIVATION INC. UNIV CALIFORNIA. SCRIPPS RES INST. 98US-0038894. 99WO-US05247. 11-MAR-1998; 11-MAR-1999; W09946367-A2 16-SEP-1999. Bos taurus. (REGC) (SCRI) arthritis, inflamed joint; bursitis; osteoarthritis; septic arthritis; rheumation; arthritis; inflamed joint; bursitis; osteoarthritis; septic arthritis; rheumatoid arthritis; fibromyalgia; systemic lupus erythematosus; phlebitis; tendinitis; rash; psoriasis; acne; eczem; facial seborrheic eczema; foreskin infection; athlete's foot; fistulae infection; ulcer; navel infection; wrinkle; scar; kelloid; boil; wart; allergic itch; hemorrhoid; wound;

The specification describes a fish serine proteinase. The proteinases are useful as medicaments, for treating and preventing a disease in a human or an animal such as pain, acute inflammation, chronic chronic chromic atthritis, inflamed joints, bursitis, osteoarthritis, inflamed joints, bursitis, septic arthritis, inflamed joints, bursitis, septic arthritis, resh, cheumatoid arthritis, luvenile ritheumatosus, phiebitis, tentritis, rash, psoriasis, acne, eczema, facial seborrheic eczema, eczema of the hands, face or neck, foreskin infections, athlete's foot, fistulae infections, infected topical ulcers, navel infections in newborns, wrinkles, scars, infections, wounds from burns, fungal infections and immunological and infections and immunological and infections ö cell activation; pancreas; treatment; cardiovascular disease; trauma; inflammatory disease; autoimmune diseases; arthritis; disbetes; atroke; organ rejection; ischamia; Alzheimer's disease; myocardial infarction; haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina; trauma; protease inhibitor; hypertension; sepsis. Pish serine proteinase, useful as a cosmetic, medicament for treating eczema, psoriasis, arthritis, and in the manufacture of the medicament for treating, preventing pathogenic diseases involving receptor mediated binding Gape ö 100.0%; Score 68; DB 22; Length 13; 100.0%; Pred. No. 5.1e-05; tive 0; Mismatches 0; Indels Neutrophil-activating pancreatic derived peptide 7. AAY50207 standard; Peptide; 15 AA. Disclosure, Page 5; 38pp; English. 12-JAN-2000 (first entry) Matches 13; Conservative 1 CGVPAIQPVLSGL 13 1 CGVPAIQPVLSGL 13 (BJAR/) BJARNASON J B. Best Local Similarity WPI; 2001-091493/10. 13 AA; AAY50207; RESULT 3

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Lin X,
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                                                                                                                                                 This invention describes a novel method for the use and preparation of cell activating compositions which involves preparing a cell activating compositions composition comprising of a homogenizing pancreatic tissue in buffer at composition comprising (a) homogenizing pancreatic (b) removing about neutral or higher pH to produce a homogenate; (b) removing the about neutral or higher pH to produce a homogenate; (c) optionally incubating the about the homogenate and selecting fractions that exhibit resulting the homogenate and selecting fractions that exhibit cell activation activity. The methods can be used for improving treatment outcome or reducing risk of treatment of e.g. cardiovascular corgan rejection, diabetes and diabetic complications, stroke, ischemia, Alzhenmer's disease, myocardial infarction, heamorthagic shock, diabetic retinopathy, diabetes, wence insufficiency unstable angina or trauma. Criby can be used in the veterinary treatment of a non-human subject. Protease inhibitors can be used to lower cell activation realting from hydrogen peroxide can be used to lower cell activation realting from clevated level of hydrogen peroxide in plasma or whole blood and in the regulation, e.g. indicative of the onset of an acute cardiovascular disorders, such as disease onset or ischemic complications. An elevated level in plasma or whole blood and a low level in the presence of SoD is indicative of an acute cardiovascular condition e.g. hyperension or sepsis. AAVSGO21-YSGO314 represent peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·,
                                                     Use of cell activating compositions in developing products for diagnosis and treatment of e.g. cardiovascular, inflammatory, autoimmune or Alzheimer's disease, trauma, arthritis, organ rejection,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 68; DB 20; Length 15; 100.0%; Pred. No. 6e-05;
       Kistler E;
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heart attack; stroke; blood clotting disorder.
      Hugli TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
 Schmid-Schonbein GW,
                                                                                                                              Example 9; Page 182; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY99596 standard; protein; 245 AA,
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0
                                                                                                   diabetes, stroke or ischemia -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGVPAIQPVLSGL 13
                            WPI; 1999-580234/49.
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 Stoughton RB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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The present sequence is bovine chymotrypsinogen. It was included in a review of sequence homologies of several plasminogen activators.

Plasminogen is the principal serine protease zymogen in the prample of vertebrates. Its active form, plasmin, is implicated in pericellular proteolysis associated with a wide range of physiological and pathological processes. Plasminogen expression is physiological and pathological processes. Plasminogen expression is plasminogen to convert it to plasmin or form tight binding complexes plasminogen to spontaneously convert it to plasmin or form tight binding complexes with plasminogen to spontaneously convert it to plasmin. The sequence concluded in this peptide is particularly useful when inserted basminogen activation. This peptide is particularly useful when inserted between amino acid residues 64 and 645 of full length human inserted plasminogen. Novel plasminogen activators have been made based upon the plasminogen are useful in preparing thrombolytic agents for treating the plypeptides are useful in preparing thrombolytic agents for treating concluded the plant of the plasminogen are useful in preparing thrombolytic agents for treating concluded the plant of the plasminogen are useful in sentered.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                               Polypeptide with plasminogen activator activity useful as thrombolytic agent for treating blood clot disorders e.g. heart attack, comprises 10 amino acid peptide fragment for recognition or activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, pancreas, pancreatic cancer, pancreatic cancer antigen, detection, diagnosis, identification, cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, antiinflammatory, cardiant, gene therapy, chromosome mapping, linkage analysis, tissue identification; tissue typing, forensic, neural; immune system, muscular; reproductive, gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 68; DB 21; Length 245; 100.0%; Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                      Disclosure; Page 35-36; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB54191 standard; Protein; 146 AA.
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     Tang JJN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Conservative
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                                                  WPI; 2000-422975/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Zhang XC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                 plasminogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB54191;
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AAC98773 to AAC99231 encode the human pancreatic cancer associated processing called pancreatic cancer antigens have cytosteria.

Expectens, called pancreatic cancer antigens have cytosteria.

ABS5466. The human pancreatic cancer antigens have cytosteria.

Compression of the control of the control of the called for cardiant and antinflammatory relaxant, contraceptive, conversing the cardiant and antinflammatory activities, and can be used for in gene therapy. The polynucleotide and proteins can be used for the preventing treating, or ameliorating a medical condition or in assays or subject. Binding partners to the proteins and the activity of the cambiect. Binding partners to the proteins and the activity of the control or an engage of the control of the cardiant of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; protease, cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection;
     New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenepeel S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.6%; Score 63; DB 21; Length 146; 92.3%; Pred. No. 0.0051; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of novel human protease #37.
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                                                                                                                  Claim 11; Page 1081; 1379pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU82738 standard; Protein; 263 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CGVPAIQPVLSGL 13
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Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200200860-A2
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Charydczak G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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AAU82738
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The present invention relates to the isolation of novel human processes, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immne-related diseases and disorders and concers (e.g. inflammatory diseases and acthma), cardiovascular diseases (e.g. inflammatory diseases and acthma), cardiovascular diseases (e.g. inflammatory diseases, e.g. diabetes, obseity), inflammatory diseases, metabolic disorders (e.g. diabetes, obseity), inflammatory ciscarders (e.g. rheumatoid arthritis and psoriasis), central or corrigheral nervous system diseases, migraines, pain, sexual dysfunction, condisorders, attention disorders, neurological disorders hypotension, contral or condisorders, and sease, Parkinson's disease) and dyskinesias.

The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections caused by human immunodeficiency virus (HIV), and non-viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell activation; pancreas; treatment; cardiovascular disease; trauma; inflammatory disease; autoimmune disease; arthritis; disbetes; stroke; organ rejection; ischemia; Alzaheiner's disease; myocardial infarction; haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina; trauma; protease inhibitor; hypertension; sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                  infections such as ocular disease (e.g. glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel human proteases of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
                                                         treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory disorders -
                                              proteases, useful for useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63; DB 23; Length 263;
pred. No. 0.0096;
0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kistler E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neutrophil-activating pancreatic derived peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hugli TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schmid-Schonbein GW,
                                                 novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY50208 standard; Peptide; 15 AA.
                                                                                                                                      Claim 6; Fig 2M; 313pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CELL-) CELL ACTIVATION INC. (REGC ) UNIV CALIFORNIA. (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US05247.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 92.3
                                                     Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
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WPI; 2002-139913/18.
N-PSDB; ABK31780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 CGVPAIHPVLSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGVPAIQPVLSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stoughton RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9946367-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY50208
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Gaps

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This invention describes a novel method for the use and preparation of cell activating compositions which involves preparing a cell activating composition to higher ph to produce a homogenatic tissue in buffer at about neutral or higher ph to produce a homogenatic in buffer at centifing homogenate, (d) formogenate, (b) removing the particulates removed, with a protease; and fractionating the homogenate and selecting fractions that exhibit compared to treatment outcome or reducing risk of treatment of e.g. cardiovascular circatment outcome or reducing risk of treatment of disease, arthritis, disease, inflammatory disease, trauma, autoimmune diseases arthritis, arthritis or organ rejection, diabetes and diabetic complications, stroke, ischemia, cretinopathy, diabetes, venous insufficiency, unstable angian or trauma. Cretoses inhibitors can be used to lower cell activation resulting from the veterinary treatment of a non-human subject. They can be used in the veterinary treatment of a non-human subject. Creatment elevate can be used to dower cell activation resulting from charges levale of hydrogen peroxide in plasma or whole blood and in the comparation. An indicates leavence of superoxide dismutase (SOD) indicates leuckoyen peroxide of superivor of the neutron of substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulation, e.g. indicative of the onset of an acute cardiovascular disorders, such as disease onset or ischemic complications. An elevated the presence of SoD is indicative of a chronic or immune compromised condition e.g. hypertension or sepsis. AAY$0201-Y$0334 represent peptides used in the method of the invention.
Use of cell activating compositions in developing products for diagnosis and treatment of e.g. cardiovascular, inflammatory, autoimmune or Alzheimer's disease, trauma, arthritis, organ rejection, diabetes, stroke or ischemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell activation; pancreas; treatment; cardiovascular disease; trauma; inflammatory disease, autoimmune disease; arthritis; diabetes; stroke; organ rejection; ischemia; Alzheimer's disease; myocardial infarction; haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina; trauma; protease inhibitor; hypertension; sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.2%; Score 62; DB 20; Length 15; 92.3%; Pred. No. 0.00064; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neutrophil-activating pancreatic derived peptide 10.
                                                                                                           Example 9; Page 182; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY50210 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0038894.
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(REGC ) UNIV CALIFORNIA.
(SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US05247
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Matches 12; Conserv
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This invention describes a novel method for the use and preparation of cell activating compositions which involves preparing a cell activating compositions omprisang (a) homogenizing pancreatic tissue in buffer at composition compusing (a) homogenizing pancreatic tissue in buffer at about neutral or higher pH to produce a homogenate, (b) removing particulates from the homogenate, (c) optionally incubating the creatility homogenate, with particulates removed, with a procease; and cell activation activity. The methods can be used for improving treatment outcome or reducing risk of treatment of e.g. cardiovascular or significant disease, inflammatory disease, frauma, autoimmune diseases, arthritis, disease, myocardial infarction, hemorrhagic shock, diabetic complication be used in the veterinary treatment of a non-human subject.

Alzheimer's disease, worder insufficiency, unstable angina or traumance procease inhibitors can be used to lower cell activation resulting from procease inhibitors can be used to lower cell activation resulting. The presence of superoxide dismutase (SOD) indicates leukocyte up created level of hydrogen peroxide in plasma or whole blood and in the regulation, e.g. indicative of the anche cardiovascular clavel of hydrogen peroxide in plasma or whole blood and in the cell of hydrogen peroxide in plasma or whole blood and a low level in the method of the invention.

Che condition e.g. hypertension or sepsis. AAYSO201-YSO334 represent peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                 Use of cell activating compositions in developing products for diagnosis and treatment of e.g. cardiovascular, inflammatory, autoimmune or Alzheimer's disease, trauma, arthritis, organ rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, pancreas, pancreatic cancer, pancreatic cancer antigen, detection, diagnosis, identification, cytostatic, neuroprotective, nootropic, immunomodulatory; relaxant, contraceptive, gynaecological, antiinflammatory; cardiant, gene therapy; chromosome mapping; linkage analysis, tissue identification; tissue typing; forensic, neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human pancreatic cancer antigen protein sequence SEQ ID NO:529.
                  Stoughton RB, Schmid-Schonbein GW, Hugli TE, Kistler E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.2%; Score 62; DB 20; Length 15; 92.3%; Pred. No. 0.00064; 1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i, Indels
                                                                                                                                                                                                    Example 9; Page 182; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB54077 standard; Protein; 192 AA.
                                                                                                                                                                diabetes, stroke or ischemia
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                                                             WPI; 1999-580234/49.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 AA;
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21-SEP-2000

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AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to proteins, called pancreatic cancer antigens have cytostatic.

C. AAB54466. The human pancreatic cancer antigens have cytostatic, contraceptive, noctropic, immunomodulatory, relaxant, contraceptive, cytostatic, and can antificiammatory activities, and can be used for in gene therapy. The polymucleotide and proteins can be used for cytoring a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the cubject. It is a pathological condition or a susceptibility to one in a cytorian can be identified. The pancreatic cancer antigens can be used to generate cancer antigens to the antigens can be screened for. The Agonists and antagonists to the antigens can be used to design nucleic and hybridisation probes that can be used in chromosome mapping, linkage can diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including which are used to purify, detect and target the polypeptides, including which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods: The both in vivo and in vitro diagnostic and therapeutic methods are proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, remal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BSSP5; serine protease; human; hBSSP5; mouse; mBSSP5; brain; diagnostic marker; antibody; transgenic animal; Alzheimer's disease; epilepsy; cancer; inflammation; infertility; pancreatitis; prostatic hypertrophy.
                                                                                                                                                                                                              New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.1%; Score 49; DB 21; Length 192; 72.7%; Pred. No. 1.7; 1; Indels iive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human serine protease BSSP5 (hBSSP5) SEQ ID NO:2.
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                                                                                                                                                                                                                                                                                                      Claim 11; Page 966; 1379pp; English.
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                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                        99US-0124270.
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08-MAR-2000; 2000WO-US05989
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Best Local Similarity 72.7.
Best Local Similarity 72.7.
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                                                                                                                         Rosen CA, Ruben SM;
                                                                                                                                                                  WPI; 2000-579444/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 AA
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                                                                                                                                                                                       N-PSDB; AAC98842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUN-2000
                                              12-MAR-1999;
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The invention relates to novel serine protesses designated BSSP5

(AABI1710-B11711), and to nucleic acids encoding them (AAA61733-A61734).

(AABI1710-B11711), and to nucleic acids encoding them (AAA61733-A61734).

(The invention also relates to vectors and transformants comprising BSSP5

(The invention also relates to vectors and transformants comprising BSSP5

(Can be varied) and am BSSP5 knockout mouse. The invention additionally compasses anti-BSSP5 knockout mouse. The invention of such cantibodies, methods of BSSP5 detection using the antibodies, and the antibodies, methods of BSSP5 detection using the antibodies, and the canditions of tagments as diagnostic markers for certain use of BSSP5 proteins or fragments as diagnostic markers for certain used calculations of tagments as diagnostic markers for certain and a pancreatitis diagnostic agent containing an anti-BSSP5 urine, and a pancreatitis diagnostic agent containing an anti-BSSP5 contained in a human brain converted regions of serine protesses. The BSSP5 serine protesses and nucleotides encoding them are useful in the protesses and th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BSSP5; serine protease; human; hBSSP5; mouse; mBSSP5; brain; diagnostic marker; antibody; transgenic animal; Alzheimer's disease; epilepsy; cancer; inflammation; infertility; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detecting homologues, mutants and polymorphic variants in biological samples (e.g., blood, wrine, brain, prostate gland, placenta, testis, pancreas and spleen) as diagnostic markers for conditions such as Alzaheimer's disease, epilepsy, cancer, inflammation, infertility, pancreatitis and prostatic hypertrophy, Sequence ABB1710 represents human BSSP5 (hBSSP5), and sequence AAB11711 represents murine BSSP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                    Serine proteases BSSPS, useful in detecting homologs, mutants and polymorphic variants as markers for diagnosis of e.g. Alzheimer's disease, epilepsy, cancer and inflammation, using blood, urine, pancreas or other tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.1%; Score 49; DB 21; Length 264; 72.7%; Pred. No. 2.4; 1; Indels 1; Indels
                                                                                                    Kominami K, Yamaguchi N, Mitsui S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse serine protease BSSP5 (mBSSP5) SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB11711 standard; Protein; 264 AA.
                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 51-52; 70pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-JP06473.
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                  98JP-0347806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 72.7.
B; Conservative
                                                               (FUSO ) FUSO PHARM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostatic hypertrophy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGVPAIOPVLS 11
                                                                                                                                                                  WPI; 2000-400058/34
N-PSDB; AAA61733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 AA;
                                                                                                                    Jemura H, Okui A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||:|||:||
19 CGIPAIKPALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200031243-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUN-2000.
                  20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB11711;
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Cell activation; pancreas; treatment; cardiovascular disease; trauma; disfammatory disease; autoimmune diseases; arthritis; diabetes; stroke; organ rejection; ischemia; Alzheimer; s diseases; myocardial infarction; haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina; trauma; protease inhibitor; hypertension; sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neutrophil-activating pancreatic derived peptide 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
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                                                                                                                                                                                                                                                   The invention relates to novel serine proteases designated BSSP5

(AAB11710-B11711), and to nucleic acids encoding them (AAA61733-A61734).

The invention also relates to vectors and transformants comprising BSSP5

uucleic acids; transgenic animals in which the expression level of BSSP5

can be varied; and an mBSSP5 knockout mouse. The invention additionally

encompasses anti-BSSP5 antibodies and methods of production of such

antibodies, methods of BSSP5 detection using the antibodies, and the

compasses anti-BSSP5 antibodies and adaptositic markers for certain

use of BSSP5 proteins or fragments as diagnostic markers for certain

compareatitis comprising measuring BSSP5 concentration in the blood or

pancreatitis comprising measuring BSSP5 concentration in the blood or

contine, and a pancreatitis diagnostic agent containing an anti-BSSP5

contine, and a pancreatitis diagnostic agent containing an anti-BSSP5

contibody is also disclosed. Nucleotides encoding BSSP5 were initially

contained in a human brain cDNA library using degenerate pCR primers

contained in a human brain cDNA library using degenerate pCR primers

contained and proceases and nucleotides encoding them are useful in

contained and spleen) as diagnostic markers for conditions such as

contained and spleen) as diagnostic markers for conditions such as

conditions and spleen) as diagnostic markers for conditions such as

conditions and spleen) as diagnostic markers for conditions such as

conditions and prostatic hypertrophy. Sequence AAB11711 represents murine BSSP5

conditions and prostatic hypertrophy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell activation; pancreas; treatment; cardiovascular disease; trauma; finflammatory disease; attoimmune diseases; arthritis; diabetes; stroke; organ rejection; ischemia; Alzheimer; a disease; myocardial infarction; haemorrhagic shock; diabetic retinopathy; venous insufficiency; angina; trauma; protease inhibitor; hypertension; sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                   Serine proteases BSSP5, useful in detecting homologs, mutants and polymorphic variants as markers for diagnosis of e.g. Alzheimer's disease, epilepsy, cancer and inflammation, using blood, urine, pancreas or other tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 21; Length 264;
Pred. No. 3.6;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                             Yamaguchi N, Mitsui S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neutrophil-activating pancreatic derived peptide 12.
                                                                                                                                                                                                                             Claim 3; Page 55-56; 70pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY50212 standard; Peptide; 13 AA.
                                                                             Kominami K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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             20-NOV-1998; 98JP-0347806.
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                                           (FUSO ) FUSO PHARM IND LID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                       WPI; 2000-400058/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                        Okui A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGVPAIOPVLS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 CGVPAITPALS 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 264 AA;
                                                                                                                      N-PSDB; AAA61734
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                                                                          Vemura H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAYS0212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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This invention describes a novel method for the use and preparation of cell activating compositions which involves preparing a cell activating compositions which involves preparing a cell activating composition compression to the composition composition composition composition composition composition in buffer at about neutral or higher pH to produce a homogenating buffer at cabut neutral or higher pH to produce a homogenating the new composition of the composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulation, e.g. indicative of the onset of an acute cardiovascular disorders, such as disease onset or ischemic complications. An elevated level of hydrogen peroxide in plasma or whole blood and a low level in the presence of SOD is indicative of a chronic or immune compromised condition e.g. hypertension or sepsis. AAY50201-Y50334 represent peptides used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of cell activating compositions in developing products for diagnosis and treatment of e.g. cardiovascular, inflammatory, autoimmune or Alzheimer's diagease, trauma, arthritis, organ rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                           Stoughton RB, Schmid-Schonbein GW, Hugli TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 9; Page 182; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY50211 standard; Peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetes, stroke or ischemia
                                                                                              98US-0038894.
                                                                                                                                                                                   (CELL-) CELL ACTIVATION INC.
(REGC ) UNIV CALIFORNIA.
(SCRI ) SCRIPPS RES INST.
     99WO-US05247.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-580234/49.
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11-MAR-1999;
                                                                                              11-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-2000
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Matches
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This invention describes a novel method for the use and preparation of cell activating compositions which involves preparing a cell activating composition (a) homogenizing pancreatic tissue in buffer at about neutral or higher pH to produce a homogenate; (b) removing composition composition (a) but to produce a homogenate; (b) removing the creating homogenate, with particulates removed, with a protease; and feating homogenate, with particulates removed, with a protease; and the resulting homogenate, with particulates removed, with a protease; and the retivation activator. The methods can be used for improving creating artivation activator, disease, trauma, etc. organ rejection, diabetes and diabetic complications, stroke, ischemia, alternate of diabetes and diabetic complications, stroke, ischemia, and the vectoriant of a non-human subject.

Cretinapathy, diabetes, venous insufficiency, unstable angina or trauma. They can be used in the vectoriant treatment of a non-human subject.

Cretinapathy, diabetes, venous insufficiency, unstable angina or trauma. They can be used in the vectoriant treatment of anon-human subject.

Cretinapated level of hydrogen peroxide in plasma or whole blood and in the presence of superoxide dismutase (SDD) indicates leukocyte up presence of superoxide dismutase (SDD) indicates leukocyte up presence of superoxide dismutase (SDD) indicates leukocyte up presence of superoxide in plasma or whole blood and in the hydrogen peroxide in plasma or such and allow level in level of hydrogen peroxide in plasma or such and allow level in credition e.g. hydrogen peroxide in plasma or immune compromised condition e.g. hypertension or sepale.
                                                                                                                                                                                                                                                                                                                                                  Use of cell activating compositions in developing products for diagnosis and treatment of e.g. cardiovascular, inflammatory, autoimmune or Alzheimer's diagease, trauma, arthritis, organ rejection, diabetes, stroke or ischemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 72.7%; Pred: No. 1.2;
Matches 8; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                 Stoughton RB, Schmid-Schonbein GW, Hugli TE, Kistler E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #14628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 9; Page 182; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG14637 standard; Protein; 107 AA.
                                                                                               99WO-US05247.
                                                                                                                                          98US-0038894.
                                                                                                                                                                                (CELL-) CELL ACTIVATION INC. (REGC ) UNIV CALIFORNIA. (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                 WPI; 1999-580234/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGVPSIPPNLS 11
                 WO9946367-A2.
                                                                                                     11-MAR-1999;
                                                                                                                                             11-MAR-1998;
                                                          16-SEP-1999.
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The invention relates to isolated polynucleotide (I) and probes, CC polypeptide (II) sequences. (I) is useful as hybridisation probes, cpolypeptide (II) sequences. (I) is useful and hybridisation probes, co polymerase chain reaction (FCR) primers, oligomers, and for chromosome cc and gene mapping, and in recombinant production of (II). The complete of the complete of the control of (II) and the complete of the control of (II) and the complete of (II) is useful for generating antibodies against the detecting or control of (II) is useful for generating antibodies against the detecting or (II). (II) is useful for generating antibodies against the detecting or control of supplement. (II) and its binding partners are useful in medical a food supplement. (II) and its binding partners are useful for treating control of supplement. (II) are useful for treating control of supplements in the polypeptide and polymolectide sequences have applications in the polypeptide and polymolectide sequences have applications in capponsible for generic disorders or other traits to assess biodiversity capponsible for generic disorders or other traits to assess biodiversity capponsible for generic disorders or other traits to assess biodiversity and to produce other types of data and produces dependent on DNA and capponsible for generic disorders of the invention.

Conduction acid sequences of the invention of muran directly from WIPO specification, but was obtained in electronic format directly from WIPO control of the printed produced and produced are control of specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, cytokine, cell proliferation, cell differentiation;
antiinflammatory, stem cell growth factor; activin, inhibin; cancer;
nervous system disease; neuropathy, Alzheimer's disease;
Parkinson's disease; Huntington's disease; spinal cord disorder;
                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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61.8%; Score 42; DB 22; Length 107;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human novel cytokine encoded by cDNA 790CIP2A_11 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 44996; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU68565 standard; Protein; 107 AA.
                                                                                                                                                                                                                                                                                         Tang YT;
                                                                                                                                          30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                 31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JAN-2002 (first entry)
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11 GDPELQPVLAGL 22
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N-PSDB; AAS78824.
                                                                                                                                                                                                                                                                                         Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 107 AA;
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                                                           WO200175067-A2
                      Homo sapiens.
                                                                                                     11-OCT-2001.
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2001-626432/72. Zaho QA, (HYSE-) HYSEQ INC. WPI; 2001-626432/ N-PSDB; AAS59857 WO200175093-A1. Homo sapiens. 31-MAR-2000: 11-OCT-2001. Tang YT, Yang Y,

Zhou P, Xue AJ, Ren F, Zhang J, Wang J, Xu C; hen R, Wang D, Goodrich RW, Liu C, Drmanac RT; head trauma; stroke; myeloid cell disorder; lymphoid cell disorder; platelet disorder; thrombocytopaenia; stem cell disorder; aplateic aneamia, tissue regeneration; wound healing; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; fibrosis; reperfusion; immune disorder; ScID; severe combined immunodeficiency; infection; autoimmune disorder; multiple sclerosis; rheumacoid arthritis; diabetes mellitus; allergy; inflammatory bowel disorder; haemophilia; sepsis; nephritis; inflammatory bowel disease; food supplement; immunogen. Asundi V, Znou. OA, Chen R, V 23-AUG-2000, 2000US-0649167. 22-SEP-2000, 2000US-0668680. 23-OCT-2000, 2000US-0695618. 30-NOV-2000, 2000US-0728711. 30-MAR-2001; 2001WO-US10484 2000US-0540217

The invention relates to isolated human polypeptides (which may be cytokines) and the polymucleotides encoding them. The protein is useful and antagonists and antagonists.

Croidentifying a compound which binds to it (e.g. modulators, agonists and antagonists). The polymucleotides are useful as marray for mismatch sources or supplements. The protein exhibits exhibits activity relating success or supplements. The protein exhibits exhibits activity relating to cytokine, cell proliferation, call differentiation, anticinflammatory, suppressing and activin or inhibin related activities. The proteins (and the diagnosis and treatment of diseases and disorders such as cancer, antibodies raised against them) and mucleic acids are therefore useful in creating and peripheral nervous system diseases and neuropathies, and peripheral nervous system diseases and neuropathies, and peripheral nervous system diseases and neuropathies, lateral sclerosis, sproke, myeloid or lymphoid cell disorders, platelet disorders, lateral sclerosis, sproke, myeloid or lymphoid cell disorders, platelet disorders, capeneration of bone, cartilage, tendon, ligament and/or nerve tissue repair, healing of burns, incisions, ulcers, for periodontal disease, lung or liver fibrosis, reperfusion injury in severe combined immunodeficiency (SCID), bacterial or fungal infections, catching assues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, cautoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis, cutoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis, date asthma or other respiratory problems, coadulation disorders, chaemophilia), septic shock, sepais, arthritis, neptric shock, sepais, New polypeptides and nucleic acids, useful for diagnosis, treatment of inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone degenerative disorders, cancer and promoting wound healing Claim 20; Page 308; 336pp; English.

61.8%; Score 42; DB 22; Length 107; 66.7%; Pred. No. 15;

Query Match Best Local Similarity

107 AA;

0 Gaps ; Indels 5, Mismatches cch completed: February 12, 2003, 10:22:25 time : 9.73134 secs 5; 8; Conservative 2 GVPAIQPVLSGL 13 11 GDPELOPVLAGL 22 Matches Search Job tim 6 g

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GenCore version 5.1.3
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	Copyright (c) 1993 - 2003 Compugen Ltd.
OM protein - pr	OM protein - protein search, using sw model
Run on:	February 12, 2003, 10:17:50 ; Search time 3.2597 Seconds (without alignments) 383.393 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-036-371-5 68 1 CGVPAIQPVLSGL 13
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

ALIGNMENTS

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C;Accession: A00953
R;Smillie, L.B.; Furka, A.; Nagabhushan, N.; Stevenson, K.J.; Parkes, C.O.
Nature 218, 343-346, 1968
Nature 218, 343-346, 1968
A;Title: Structure of chymotrypsinogen B compared with chymotrypsinogen A and trypsinoger
A;Reference number: A00953
A;Accession: A00953
A;Accession: A00953
A;Accession: A00953
A;Mocule type: protein
A;Residues: 1-245 cSMI>
C;Comment: Chymotrypsinogen B is synthesized, along with chymotrypsinogen A, in the acuncy C;Comment: Chymotrypsinogen B is synthesized, along with chymotrypsinogen A, in the sar C;Comment: Chymotrypsin trypsin homology
C;Superfamily: trypsin; trypsin homology
C;Comment: The first activation cleavage, leading to pi-chymotrypsin B, occurs in the sar C;Comment: The first activation cleavage, leading to pi-chymotrypsin B, occurs in the sar C;Comment: Trypsin homology
E;16-2345/Product: chymotrypsin B #status experimental cMAT>
F;16-245/Product: chymotrypsin B #status experimental cMAT>
F;1-122,42-58,136-201,168-182,191-220/Disulfide bonds: #status experimental
F;57,102,195/Active site: His, Asp, Ser #status experimental
chymotrypsin (BC 3.4.21.1) B precursor - bovine N.Alternate names: chymotrypsinogen B C.Species: Bos primigenius taurus (cattle) C.Species: Bos primigenius taurus (cattle) C.Date: O8-Oct-1981 #sequence_revision 08-Oct-1981 #text_change 18-Jul-1997
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A,Status: preliminary
A,Molecule type: protein
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-12;16-27;149-160;181-200 <CUT>
R; Smillie, L.B.; Harriery, B.S.
Biochem. J. 101, 232-241, 1966
A; Title: Histidine sequences in the active centres of some 'serine' proteinases.
A; Reference number: A90216; MUID:67181723; PMID:5971785
A; Contents: annotation; active site
A; Contents: annotation; active site
B; Birktoft, J.J.; Blow, D.M.; Henderson, R.; Steitz, T.A.
A; Reference number: A93754
A; Contents: annotation; X-ray crystallography
A; Title: The structure of alpha-chymotrypsin.
A; Reference number: A93754
A; Comment: Tryptic cleavage after Aqy-15 results in a fully active enzyme (pi-chymotryps
C; Comment: Tryptic cleavage after Aqy-15 results in a fully active enzyme (pi-chymotryps
C; Comment: Tryptic cleavage after Aqy-15 results in a fully active enzyme (pi-chymotryps
C; Comment: Tryptic cleavage after Aqy-15 results in a fully active mochymotryps
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C; Comment: Tryptic cleavage after Aqy-15 results in a fully active chymotryps
C; Comment: Tryptic cleavage after Aqy-15 results experimental <Amyorate Adycolase; pancreas; protein digestion; serine proteinase; zymogen
C; Superfamily: trypsin homology after
B; 1-13, 16-146, 199-245, product: alpha-chymotrypsin #status experimental
F; 1-122, 42-58, 136-201, 168-182, 191-220/Disulfide bonds: #status experimental
F; 57, 102, 195/Active site: His, Asp, Ser #status experimental
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C;Species: Canis lupus familiaris (dog)
C;Date: 27-Unl-1990 #sequence_revision 27-Jul-1990 #text_change 22-Jun-1999
C;Date: 27-Unl-1990 #sequence_revision 27-Jul-1990 #text_change 22-Jun-1999
C;Accession: A21195
Proc. Natl. Acad. Sci. U.S.A. 80, 7486-7490, 1983
Pritle: Identification of cDNA clones encoding secretory isoenzyme forms: sequence dete
A;Reference number: A21195; MUD:84170253; PMID:6584866
A;Retus: pred!minary
A;Residues: pred!minary
A;Residues: 1-23 - ANIS
A;Residues: 1-23 - ANIS
A;Residues: 1-23 - ANIS
C;Superfamily: trypsin, trypsin, bandlogy
C;Keywords: hydrolase; protein digestion; serine proteinase
F;75,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                       A.Accession: A93158
A.Accession: A93159
A.Accession: A.B.A. (101-245 cMEL>
A.Residues: 1-101, N'.103-245 cMEL>
A.Residues: 1-101, N'.103-245 cMEL>
A.Residues: 1-101, N'.103-245 cMEL>
B.A.Note: disulfide bonds were determined
R.Yunter: Ascenzi, P., Barra, D.; Bolognesi, M.; Menegatti, E.; Sarti, P.; Schne
B.Ochim. Biophys. Acta 1161, 201-208, 1993
A.Arities: Selective oxidation of Met-192 in bovine alpha-chymotrypsin. Effect on catalyti
A.Reference number: S29550, MuID:93160238; PMID:8431470
R;Meloun, B.; Kluh, I.; Koetka, V.; Moravek, L.; Prusik, Z.; Vanacek, J.; Keil, B.; Sorm Blochim. Biophys. Acta 130, 543-546, 1966
A;Title: Covalent structure of bovine chymotrypsinogen A.
A;Reference number: A90572; MUID:67183948; PMID:5972866
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Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 13; Conservative 0; Mismatches 0; Indels
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C;Species: Chryeemys picta (painted turtle)
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
B;Bhargava, A.K.; Barnard, B.A.
J; Mol. Bvol. 2, 187-198, 1973
A;Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determ A;Reference number: A61414; MUID:76146602; PMID:4807189
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c;Species: Pseudemys scripta (slider)
c;Species: 09-Sep-1994 #text_change 07-May-1999
C;Accession: C61414
R;Bhargava, A.K.; Barnard, E.A.
J, Mol. Evol. 2, 187-198, 1973
A;Pitle: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determinals. Afreference number: A61414; MUID:76146602; PMID:4807189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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92.6%; Score 63; DB 2; Length 263;
Best Local Similarity 92.3%; Pred. No. 0.0043;
Matches 12; Conservative 0; Mismatches 1; Indels
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Pred. No. 0.00042;
0; Mismatches 1; Indels
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A;Molecule type: protein
A;Residues: 1-16 <BHA>
C;Keywords: hydrolase; protein digestion; serine proteinase
chymotrypsin (EC 3.4.21.1) precursor - human
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Best Local Similarity 92.3%;
Matches 12; Conservative
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chymotrypsin (EC 3.4.21.1) - snapping turtle (fragment)

c;Species Chelydra serpentina (snapping turtle)

c;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999

C;Accession: A61414 #senard, E.A.

B;Bhargava, A.K.; Barnard, E.A.

J. Mol. Bvol. 2, 187-198, 1973

A;Yille: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determ A;Reference number: A61414; MuID:76146602; PMID:4807189
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R;Gorr, S.U.; Hamilton, J.W.; Cohn, D.V.
A;Ederence number: A5109; MUID: 93016107; PMID: 1400470
A;Reference number: A45109; MUID: 93016107; PMID: 1400470
A;Reference number: A5109; MUID: 93016107; PMID: 1400470
A;Reference number: A5109; MUID: 93016107; PMID: 1400470
A;Residues: 1-25 AGOR>
A;Residues: 1-25 AGOR>
A;Residues: 1-25 AGOR>
A;Residues: aperimental source: pancreas
A;Note: sequence extracted from NCBI backbone (NCBIP: 116723)
C;Superfamily: trypsin homology
C;Keywords: hydrolase; serine proteinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chymotrypsin (EC 3.4.21.1) homolog p31 - pig (fragment)
C.Species: Sus scrofa domestica (domestic pig)
C.Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 31-Mar-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                         A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-20 <BHA>
C/Keywords: hydrolase; protein digestion; serine proteinase
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A;Introns: 18/1; 52/3; 79/2; 106/3; 167/1; 211/3
C;Superfamily: trypsin; trypsin homology
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Best Local Similarity 84.6'
Matches 11, Conservative
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Cispecies: Gadus morbua (Atlantic cod)
Cispecies: Ascession: Asis, 1991
Comp. Biochem. Physiol: B 99, 327-335, 1991
Comp. Biochem. Physiol: B 99, 327-335, 1991
Asitle: Structural and kinetic properties of chymotrypsin from Atlantic cod (Gadus morby Asternse number: A61529; MuID:92111252; PMID:1764912
Asternse protein mary
Asistus: Protein mary
Cisuperfamily: trypsin, trypsin homology
Cisuperfamily: trypsin; trypsin digestion; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chymotrypsin (EC 3.4.21.1) B precursor - rat
N'Allernate names: chymotrypsinogen B
C'Species: Rattus norvegicus (Norway rat)
C'Species: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999
C'Accession: A22658
R'Bell, G.I.; Quinto, C., Quiroga, M.; Valenzuela, P.; Craik, C.S.; Rutter, W.J.
B.B.I. Chem. 259, 14256-14270, 1984
A'Title: Isolation and sequence of a rat chymotrypsin B gene.
A'Reference number: A22658; MUID:85054881; PMID:6209274
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A;Molecule type: DNA
A;Residues: 1-263 - BEL.
A;Cross-references: GB:K02298; NID:g203653; PIDN:AAA98732.1; PID:g203654
C;Genetics:
A;Introns: 18/1; 52/3; 79/2; 105/3; 166/1; 210/3
C;Guperfamily: trypsin; trypsin homology protein digestion; serine proteinase
F;1-18/Domain: signal sequence #status predicted <SIG>F;1-18/Domain: propertide #status predicted <SIG>F;14-263/Product: crymcorypsin B #status predicted <MT>F;34-263/Domain: trypsin homology <TRY>F;34-256/Domain: trypsin homology <TRY>F;75,120,213/Active site: His, Asp, Ser #status predicted
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89.7%; Score 61; DB 1; Length 263;
Best Local Similarity 84.6%; Pred. No. 0.0093;
Matches 11; Conservative 1; Mismatches 1; Indels
                                                                                                                     11arity 91.2%; Score 62; DB 2; Length 17; Pg. 92.3%; Pred. No. 0.00044; Conservative 0; Mismatches 1; Indels
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A,Residues: 1-17 <BHA>
C,Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                    1 CGVPAIOPVLSGL 13
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Best Local Similarity
Fra 12; Conserva
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S47537
Chymotrypain (EC 3.4.21.1) precursor - Atlantic cod
Cippecies: Gadus morbua (Atlantic cod)
Cippecies: Gadus morbua (Atlantic cod)
Cippecies: Gadus morbua (Atlantic cod)
Cipate: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
Cipate: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
Cipate: 36-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
Cipate: 36-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
Riddmundsdottir, A.; Oskarson, S.; Eakin, A.E.; Craik, C.S.; Bjarnason, J.B.
Biochim. Biophys. Acta 1219, 211-214, 1994
A; Reference number: S47537
A; Accession: S47537
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C;Species: Gadus morhua (Atlantic cod)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 1; Indels
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                                                                                                                                 / Match 12.1%; Score 49; DB 2; Length 264; Local Similarity 72.7%; Pred. No. 1; ndels nes 8; Conservative 2; Mismatches 1; Indels
C.Keywords: hydrolase; serine proteinase
F:34-257/Domain: trypsin homology <TRY>
F:75,121,214/Active site: His, Asp, Ser #status predicted
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A; Residues: 1-126 «VER»
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; serine proteinase
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1 CGVPAIKPAL 10
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C;Species: Yersinia postis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AH024.
G;Accession: AH024.
Geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I
A;Parkhill, J.; Wren, B.W.; Simmonds, M.; Skelton, J.; Stevens, R.M.; Mhitehead, S.; Barrell, E.
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, R.; Whitehead, S.; Barrell, E.
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
C,Accession: S72219
R;Leth-Larsen, R.; Asgeirsson, B.; Thorolfsson, M.; Norregaard-Madsen, M.; Hojrup, P. R;Leth-Larsen, R.; Ascta 1297, 49-56, 1996
A;Title: Biructure of chymotrypsin variant B from Atlantic cod, Gadus morhua.
A;Reference number: S72219; MUID:96439045; PMID:8841380
A;Accession: S72219; MUID:96439045; PMID:8841380
A;Actession: S72219
A;Molecule type: protein
A;Reference number: S7219
C;Superfamily: trypsin; trypsin homology
F;15-237/Domain: trypsin homology <FRY>
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Pred. No. 3;
2; Mismatches 2; Indels
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Matches 10; Conservative
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-384 <KUR>
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P04813 canis famil
P17538 homo sapien
P47796 gadus mortus
P008131 homo sapien
P47796 gadus mortus
P00877 chlaudydomon
P91953 hemicentroct
P24620 caenorhabbi
P00778 lysobacter
C9hnx7 halobacteri
C9hnx8 gallus gallu
C90788 gallus gallu
C9188 gallus gallu
C91899 homo sapien
C9189 human cyrom
C92461 bos taurus
P48075 euglena vir
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Copyright (c) 1993 - 2003 Compugen Ltd.
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STANDARD; PRT; 245 AA.

21-JUL-1986 (Rel. 01, Created)

15-JUN-1996 (Rel. 10, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Chymotrypsinogen B (EC 3.4.21.1).

Chymotrypsinogen B (EC 3.4.21.1).

Bos taurus (Bovinha).

Evaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bovoldea;
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Best Local Similarity 100.0%; Score 68; DB 1; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 13; Conservative 0; Mismatches 0; Indels
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                      X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF GAMMA-CHYMOTRYPSIN.
MEDLINE-82078042; PubMed-6914398;
Cohen G.H., Silverton E.W., Davies D.R.;
"Refined crystal structure of gamma-chymotrypsin at 1.9-A resolution.
Comparison with other pancreatic serine protesses.";
J. Mol. Biol. 148:449-479(1981).
                                                                                               X-RAY CRYSTALLOGRAPHY (1.68 ANGSTROMS) OF ALPHA-CHYMOTRYPSIN.
X-RAY CRYSTALLOGRAPHY (1.68 ANGSTROMS) OF ALPHA-CHYMOTRYPSIN.
TBUKADA H., Blow D.M.;
TSUKADA H., Blow D.M.;
SELUCIULE OF ALPHA-CHYMOTRYPSIN refined at 1.68-A resolution.";
O. MOI. Biol. 184:703-711(1985).
I. CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Fer-|-Xaa, Fer-|-Xaa, LoCATION: Extracellular.
I. SIMCELLULAR LOCATION: Extracellular.
I. SIMILARITY: BELONGS TO PEPTIDASE RAMILY SI.
I. DATABASE: NAME-MOTHINGTON PREPTIDASE RAMILY SI.
WWW-"http://www.worthington-biochem.com/manual/C/CHY.html".
PIR; A00952; KYBOA.
      "Chymotrypsinogen: 2.5-A crystal structure, comparison with alpha-chymotrypsin, and implications for zymogen activation."; glochemistry 9:1997-2009(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R InterPro; IPR001254; Ser_protease_Try.
R InterPro; IPR001254; Ser_protease_Try.
R PRINTS; PR00722; CHYMOTRYPSIN.
R PRABT; SW00020; Tryp. SPC; 1.
R PROSITE; PS00144; TRYPSIN IN 115; 1.
R PROSITE; PS00114; TRYPSIN IN 115; 1.
R PROSITE; PS00115; TRYPSIN IN 115; 1.
R Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; 4 3D-seructure.
I CHAIN 16 146 CHYMOTRYPSIN A, B CHAIN.
CHAIN 16 146 CHYMOTRYPSIN A, B CHAIN.
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PDB, 2CGA, 15-APR-90.

PDB, 4CHA, 31-MAY-84.

PDB, 5CHA, 16-OCT-87.

PDB, 1CHO, 16-UCL-88.

PDB, 1CHO, 16-UCL-88.

PDB, 1CHO, 16-UCL-89.

PDB, 1CHO, 15-UCL-90.

PDB, 4GCH, 15-OCT-90.

PDB, 1GCH, 15-OCT-90.

PDB, 1GCH, 15-OCT-91.

PDB, 1GCH, 22-UN-94.

PDB, 1GCH, 23-UU-97.

PDB, 1CHW, 23-UU-97.

PDB, 1CCM, 23-UU-97.

PDB, 1VGC, 12-NOV-97.

PDB, 1HAA, 14-JAN-98.

PDB, 1HAA, 14-JAN-98.
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Gaps

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Bovidae;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way entities statement is not removed. Usage by and for commercial or send an email to license@lisb.ch).
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Interpro; IPR001314; Ser_protease_Try.
Prant; PR00029; trypsin. 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM, 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-20134264; PubMed=2917002;
Tomita N., Izuncto Y., Horii A., Doi S., Yokouchi H., Ogawa M.,
Mori T., Matsubara K.;
"Molecular cloning and nucleotide sequence of human pancreatic
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Biochem. Biophys. Res. Commun. 158:569-575(1989)
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1-140G-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
CTRR1 OR CTRB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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263
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                                                                                                                                                                                                                                    PIR; A21195; A21195.
HSSP; P00766; IACB.
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                                                                                                                                                                                                                                                                            MEROPS; S01.152;
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19
34
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154
186
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ID _CTRB_HUMAN
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ACT SITE
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DISÜLFID
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DISULFID
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                                                                                MEDLINE-68238908; PubMed=5649611;
Smillie L.B., Furka A., Nagabhushan N., Stevenson K.J., Parkes C.O.;
"Structure of chymotrypsinogen B compared with chymotrypsinogen A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                          -:- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Phe-|-Xaa, Leu-|-Xaa, Leu-|-Xaa, Leu-|-Xaa, Leu-|-Xaa, Leu-|-Xaa, Location: Extracellular.
-:- SUNCELLULAR LOCATION: Extracellular.
-:- DATABASE: NAME-MOOS TO PEPTIDASE FAMILY SI.
-:- DATABASE: NAME-MOOTHINGTON enzyme manual;
MWM-http://www.worthington-biochem.com/manual/C/CHY.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 80:7486-7490(1983).
-!- CATMATMIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Phe-|-Xaa, Leu-|-Xaa, Le
                                                                                                                                                                                                                                                PIRATABLE.

HWW=hhtp://w.,

R PIR, A00953; KYBOB.

B HSSP; P0076; 1ACB.

DR HSSP; P0076; 1ACB.

DR InterPro; IPR001254; Ser protease_Try.

BITTEFPO; IPR001254; Ser protease_Try.

DR PRINTS; PR00722; CYMMOTRYPSIN.

DR PROSITE; PS00134; TRYPSIN. ENC.

DR PROSITE; PS00134; TRYPSIN. DM; 1.

DR PROSITE; PS00135; TRYPSIN. DM; 1.

PROSITE; PS00135; TRYPSIN. ENC.; 1.

DR PROSITE; PS00135; TRYPSIN. BR; 1.

TRYPOINTSYPSIN B, A CHAIN.

1 13 CHYMOTRYPSIN B, A CHAIN.

149 CHAIN.

170 CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.
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MEDLINE-84170253; PubMed-6584866;
Pinsky S.D., Laforge K.S., Luc V., Scheele G.;
"Identification of cDNA clones encoding secretory isoenzyme forms: sequence determination of canine pancreatic prechymotrypsinogen 2 mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·`
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 68; DB 1; Length 245; 100.0%; Pred. No. 0.00019; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25755 MW; 678016446FF5FEB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.-A0G-1987 (Rel. 05, Created)
13.-A0G-1987 (Rel. 05, Last sequence update)
15.-VUN-2002 (Rel. 41, Last annotation update)
Chymotrypsinogen 2 precursor (EC 3.4.21.1).
Canis familiaris (Dog)
                                                             SEQUENCE, DISULFIDE BONDS, AND ACTIVE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 AA.
                                                                                                                                                  trypsinogen.";
Nature 218:343-346(1968).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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245 AA;
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es 13; Conserv
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P04813;
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CTR2_CANFA
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                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHYMOTRYPEIN B, A CHAIN.
CHYMOTRYPEIN B, B CHAIN.
CHYMOTRYPEIN B, C CHAIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                              MENCAS, SOL.152; --.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
Pram; PR00089; Trypsin; N.
SMART; SM00020; Trypsin; N.
SMART; SM00020; Tryp SPC; 1.
SMART; SS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=94093544; PubMed=8268911;
MEDLINE=94093544; PubMed=8268911;
Lareen F., Solheim J., Kristensen T., Kolsto A.B., Prydz H.;
"A tight cluster of five unrelated human genes on chromosome 16q22.1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 61, DB 1; Length 263;
Pred. No. 0.0031;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsin-like protease CTRL-1 precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAFDBACF8C4DA6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hum. Mol. Genet. 2:1589-1595(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHYMOTRYPSINOGEN B
                                                            81.
                         Phe-|-Xaa, Leu-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27849 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.7%;
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Best Local Similarity 84.6
Matches 11; Conservative
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31
1164
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263
275
140
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210
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263 AA;
                                                                                                                                                                                                                                                                                         HSSP; P00766; 1CHG.
                                                                                                                                                                                                                                                                   PIR; A22658; KYRTB
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ACT_SITE
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CTRL_HUMAN
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                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHYMOTRYBEIN B, A CHAIN.
CHYMOTRYBEIN B, B CHAIN.
CHYMOTRYBEIN B, C CHAIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
               CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; i.
SMART; SM00020; Tryps SPc; 1.
SMART; SS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
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MEDLINE=85054881; PubMed=6209274;
Bell G.I., Quinto C., Quiroga M., Valenzuela P., Craik C.S.,
Rutter W.J.;
"Isolation and sequence of a rat chymotrypsin B gene.";
J. Biol. Chem. 259:14265-14270(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 63; DB 1; Length 263;
Pred. No. 0.0014;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4C1C055A490B8701 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHYMOTRYPSINOGEN B.
                                      Phe-|-xaa, Leu-|-xaa.
SUBCELLULAR LOCATION: Extracellular.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-ARR-1988 (Rel. 07, Created)
01-ARR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CCHymotrypsinogen B precursor (EC 3.4.21.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27870 MW;
                                                                                                                                                                                                                                                          EMBL; M24400; AAA52128.1; -.
EMBL; BC005385; AAH05385.1; -.
PIR; A31299; A31299.
HSSP; P00766; 1CHG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.152; -. Genew; HGNC:2521; CTRB1.
MIM; 118890; -.
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186 2
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263 AA;
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SEQUENCE
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DISULFID
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RESULT 5 CTRB_RAT

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PRT;
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213
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154
209
21
25
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44
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ID _CTRB_GADMO
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DISULFID
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CONFLICT
CONFLICT
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SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Pyloric caeca;
MEDLINE=92111252; PubMed=1764912;
MSDLINE=92111252; PubMed=1764912;
MSGLTUSSON B., Bjarnason J.B.;
"Structural and kinetic properties of chymotrypsin from Atlantic cod (Gadus morhua). Comparison with bovine chymotrypsin.";
                                                                                                                                                                                                                                                                      CHYMOTRYPSIN-LIKE PROTESSE CTRL-1.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FBB-1996 (Rel. 33, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsin A precursor (EC 3.4.21.1).
Gadus morbhua (Allantic cod)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Meanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Atlantic cod cDNA encoding a psychrophilic chymotrypsinogen.";
Biochim. Blophys. Acta 1219:211-214(1994)
                                                                                                                                                                                                                                                           ACTIVATION PEPTIDE (POTENTIAL).
                                                                                                                                       InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001354; Ser_protease_Try.
Frant; Pr00089; trypsin; I.
RRINTS; RR00020; Tryp.SRC; I.
SWART; SM00020; Tryp.SRC; I.
SWART; SR000134; TRYPSIN DOM; I.
PROSITE; PS001134; TRYPSIN SRC; I.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                      72.1%; Score 49; DB 1; Length 264; 72.7%; Pred. No. 0.35; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94368860; PubMed=8086467; Gadmundsdottir A., Oskarsson S., Eakin A.E., Craik C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 263 AA.
                                                                                                                                                                                                                                                                                                                                                                                  28002 MW;
                                                                          EMBL, X71874, CAASO710.1, -.
EMBL, X71877, CAASO711.1, -.
HSSP, P00763, 1DPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                               HSSP, P00763; 1DPO.
MEROPS, S01.256; -
Genew; HGNC:2524; CTRL.
MIM; 118888; -
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                                                                                                                                                                                                                                                                                                                 114
141
76
220
                                                                                                                                                                                                                                                                                                                                                                       210 2
264 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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ACT SITE
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CARBOHYD
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p. Biochem. Physiol. 99B:327-335(1991).
CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MEDLINE=96439045; PubMed=8841380;
Leth-Larsen R., Asgeirsson B., Thorolfsson M., Noerregaard-Madsen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Paracanthopterygii, Gadiformes, Gadidae, Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                     THEOPEO, IPRO01314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001324; Ser_protease_Try.
Ffam; PF00089; trypsin; 1.
PRINTS, PR00022; CHYMOTRYPSIN.
PROSITE; PS0240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
SIGNL
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(BY SIMILARITY).
(BY SIMILARITY).
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"Structure of chymotrypsin variant B from Atlantic cod,
morhua.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47AAC699A0A64FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHYMOTRYPSIN A.

CHARGE RELAY SYSTEM (F
CHARGE RELAY SYSTEM (F
CHARGE RELAY SYSTEM (F
BY SIMILARITY.
TO SIMILARITY.
                                                Phe-|-Xaa, Leu-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P00646;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsin B (EC 3.4.21.1)
Gadus morhua (Atlantic cod).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.78;
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2; Mismatches
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ACT_SITE
SEQUENCE
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Jule) Compat.

ALYTIC ACTIVITY: Pre.

ALYTIC ACTIVITY: Pre.

SIMILARITY: BELONGS TO BEPTIDA.

ASSP. POOTOG; 1CHG.

MEROPS; S01.152.

InterPro; IPRO01214; Chymotrypsin.

DR PRINTS; PRO0122; CHYMOTRYPSIN.

BRART; SMOON22; TYPPEST; 1.

DR PROSITE; PSO0134; TRYPSIN DOM; 1.

DR PROSITE; PSO0134; TRYPSIN DOM; 1.

PROSITE; PSO0135; TRYPSIN DOM; 1.

DR PROSITE; PSO0135; TRYPSIN DOM; 1.

PROSITE; PSO0135; TRYPSIN DOM; 1.

PROSITE; PSO0135; TRYPSIN DOM; 1.

TO THYMOTRYPSIN B, B CHAIN.

"THE 13 CHYMOTRYPSIN B, B CHAIN.

"THE 25 STAILARITY:

101 101 CHARGE RELAY SYSTEM (BY SIMILARITY:

121 BY SIMILARITY:

BY SIMILARITY:

121 BY SIMILARITY:

122 BY SIMILARITY:

123 BY SIMILARITY:

124 BY SIMILARITY:

125 BY SIMILARITY:

127 BY SIMILARITY:

128 BY SIMILARITY:

129 BY SIMILARITY:

120 BY SIMILARITY:

121 BY SIMILARITY:

122 BY SIMILARITY:

123 BY SIMILARITY:

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125 BY SIMILARITY:

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14PODOGO STORM 
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-2000 (Rel. 39, Last annotation update)
Ribulose bisphosphate carboxylase large chain precursor (EC 4.1.1.39)
(RubisCO large subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=83189072; PubMed=6302265; Dron M., Rahlre M., Rochaix J.-D.; Dron M., Rahlre M., Rochaix J.-D.; Sequence of the chloroplast DNA region of Chlamydomonas reinhardii "Sequence of the chloroplast DNA region of ribulose bisphosphate containing the gene of the large subunit of ribulose bisphosphate carboxylase and parts of its flanking genes."; J. Mol. Biol. 162:775-793 (1982).
                                                                                                                                                MEDLINE-9211122: "EPDMed=1764912;
MEDLINE-9211122: PubMed=1764912;
MEDLINE-9211122: PubMed=1764912;
MEDLINE-9211122: Missination J.B.;
Structural and kinnetic properties of chymotrypsin from Atlantic cod "Structural and kinnetic properties of chymotrypsin.";
(Gadus morhus). Comparison with bovine chymotrypsin.";
-1- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Lou-|-Xaa, Lou-|-Xaa, Lou-|-Xaa, Location: Extracellular.
-1- SUBCELLULAR LOCATION: Extracellular.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast.
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 1; Length 245;
Pred. No. 1.1;
2; Mismatches 2; Indels
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               Biochim. Biophys. Acta 1297:49-56(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydomonas reinhardtii.
                                                                                       SEQUENCE OF 1-12 AND 16-31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                rissum=Pyloric caeca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 8; Conserv
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ID_RBL_CHLRE
AC P00877;
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MEDLINE=9733490; PubMed=9188724;
Nommara K., Shimizu T., Kinoh H., Sendai Y., Inomata M., Suzuki N.;
Nommara K., Shimizu T., Kinoh H., Sendai Y., Inomata M., Guzuki N.;
Saa urchin hatching enzyme (envelysin): cDNA cloning and deprivation
"Sea urchin hatching enzyme (envelysin): cDNA cloning and deprivation
of protein substrate specificity by autolytic degradation.";
Biochemistry 36:7225-7238(1997).
Hemicentrotus pulcherrimus (Sea urchin).
Bukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euchinoidea, Echinacea, Echinoida, Strongylocentrotidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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P91953;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annocation update)
16-OCT-2001 (Rel. 40, Last annocation update)
                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) = 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000685; RuBisCO large.
Pfam; PF0001685; RuBisCO large, 1.
Pfam; PF000168; RuBisCO large N; 1.
PROSITE; PS00157; RUBISCO LARGE; 1.
PROSITE; PS00157; RUBISCO LARGE; 1.
Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Acetylation.
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                                                                                                                                                                                                                                                                                                         phospho-D-glycerate.
-!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + 0(2)
3-phospho-D-glycerate + 2-phosphoglycolate.
-!- SUBUNIT: 8 LARGE CHAINS + 8 SWALL CHAINS.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SUBCELLULAR LOCATION: Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 1; Length 475;
Pred. No. 22;
2; Mismatches 4; Indels
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ACETYLATION.
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475 AA;
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                                                                                                                                                                                                                                                                     ACTIVE SITE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bulky hydrophobic residues, Leu, Ile, Phe, as well as Tyr.
SUBUNIT: DURING HATCHING, THE 50 kDa MATURE ENZYME IS
AUTOLYTICALLY CLEAVED TO PRODUCE A MAJOR 38 kDa AND A MINOR 15 kDa
FORM WHICH MAY BE DISGLETED LINKED. SUBSEQUENT CLEAVAGE OF THE 38
kDa SPECIES YIELDS A 32 kDa NON-SPECIFIC PROTEASE.
DEVELOPMENTAL STAGE: EMBRYO, BLASTULA STAGE. HIGHEST ACTIVITY AT
                                                                                                                                                                                                                                                                                                                                MEDLINE-93223852; PubMed-8467915;
Nomura K., Suzuki N.,
"Stereo-specific inhibition of sea urchin envelysin (hatching enzyme)
by a synthetic autoinhibitor peptide with a cysteine-switch consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: ALLOWS THE SEA URCHIN TO DIGEST THE PROTECTIVE ENVELOPE DERIVED FROM THE BGG EXTRACELLULAR MATRIX THUS ALLOWING THE SEA
                                                                     MEDLINE=91283488; PubMed=1711895; Nomura K., Tanaka H., Kikkawa Y., Yamaguchi M., Suzuki N.; The specificity of sea urchin hatching enzyme (envelysin) places it in the mammalian matrix metalloproteinase family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: Preferential cleavage: on the amino side of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Widecatalytic case; | Widecatalytic case; | Widecatalytic case; | Widecatalytic cleavage; | Signal; | Calcium. | Calciu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- DOMAIN: THERE ARE TWO DISTINCT DOMAINS IN THIS PROTEIN; THE CATALYTIC N-TERMINAL, AND THE C-TERMINAL WHICH IS INVOLVED IN SUBSTRATE SPECIFICITY.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY MIOA.
-!- SIMILARITY: CONTAINS I HEMOPEXIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NON-SPECIFIC)
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CLEAVAGE (AUTOLYTIC DURING HATCHING)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zinc; Glycoprotein, Zymogen;
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InterPro; IPR001818; Matrixin.
InterPro; IPR001818; Matrixin.
InterPro; IPR001818; Matrixin.
Pfam; Pr00413; Peptidase M10, 1.
PRINTS; PR00139; MATRIXIN.
SWART; SM00120; Hr; 4.
SWART; SM00235; ZnM0; 1.
PR0SITE; PS00024; HEMOPEXIN, 1.
PROSITE; PS00044; ZINC PROTEASE; 1.
PROSITE; PS00046; CYSTĒNE SWITCH; 1.
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HSSP; P03956; 1CGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 321:84-88(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       URCHIN TO SWIM FREELY.
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CLEAVAGE SPECIFICITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mison R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Cardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Riffen L., Smith A., Sanders D., Shownkeen R.,
Suls M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Walerston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
T -> N (IN REF. 1; AA SEQUENCE).
L -> I (IN REF. 1; AA SEQUENCE).
L -> I (IN REF. 1; AA SEQUENCE).
E -> N (IN REF. 1; AA SEQUENCE).
F -> N (IN REF. 1; AA SEQUENCE).
S -> R (IN REF. 1; AA SEQUENCE).
P -> L (IN REF. 1; AA SEQUENCE).
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                                                                                                                                                                                                                                                         58.8%; Score 40; DB 1; Length 591;
                                                                                                                                                                                                                                                                                                3; Indels
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 42.2 kDa protein ZK1236.4 in chromosome III.
                                                                                                                                                                                                                           SDCB448C6758C70D CRC64;
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364 AA; 42163 MW; B7BACBF8FEBDFB0B CRC64;
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2; Mismatches
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MEDLINE=94150718; PubMed=7906398;
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Wormbep; S74226-4; CE00531.
InterPro; IPR000477; RVTse.
Pfam; PF00078; rvt; 1
Hypothetical protein.
SEQUENCE 364 AA; 4213 MW;
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Best Local Similarity 58.3.,
A: Conservative
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Nature 228:438-442(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brayer G.D., Delbaere L.T.J., James M.N.G.; and Errom Myxobacter 495 "Molecular structure of the alpha-lytic protease from Myxobacter 495 at 2.8-A resolution.";
                                                                                                                                                                                                                                                      Epstein D.W., Wensink P.C.;
"The alpha-lytic protease gene of Lysobacter enzymogenes. The nucleotide sequence predicts a large prepro-peptide with homology to pro-peptides of other chymotrypsin-like enzymes.";
J. Blol. Chem. 263:16586-16590(1988).
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).

MEDLINE=86011557; PubMed=3900416;

Pujinaga M., Delbaere L.T.J., Brayer G.D., James M.N.G.;

Pujinaga M., Delbaere L.T.J., Brayer G.D., James M.N.G.;

"Refined structure of alpha-lytic procease at 1.7-A resolution.

Analysis of hydrogen bonding and solvent structure.";

Analysis of hydrogen bonding and solvent
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=ATCC 29487;
MEDLINE=89172068; PubMed=3234766;
Silen J.L., McGrath C.N., Smith K.R., Agard D.A.;
Molecular analysis of the gene encoding alpha-lytic protease:
evidence for a preproenzyme.";
Gene 69:237-244(1988).
                                                                                                                                                                                      Lysobacter enzymogenes.
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                       3,
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BEDILNES-88833457; PubMed=9724517;
PETGTE R.J., Shiau A.K., Sohl J.L., Anderson D.E., Tang G.,
Silen J.L., Agard D.A.;
     DB 1; Length 364;
                                                                                                                          21-JUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-July-10 protease precursor (EC 3.4.21.12) (Alpha-lytic endopeptidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 29487;
MEDLINE=71039222; PubMed=5482494;
Olson M.O.J., Nagabhushan N., Dzwiniel M., Smillie L.B.,
                       3; Indels
                                                                                                                                                                                                                                                                                                                              Epstein D.M.;
Submitted (MAY-1989) to the EMBL/GenBank/DDBJ databases.
    Score 39.5; DB; Pred. No. 20; 1; Mismatches
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MEDLINE=89034140; PubMed=3053694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.8-A resolution.";
Mol. Biol. 131:743-775(1979).
      58.1%;
Query Match
Best Local Similarity 56.4.
Best Local 9, Conservative
                                                                                                              STANDARD;
                                            1 CGVP---AIQPVLSGL 13
                                                             79 CGVPQGSVISPVLFGI 94
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 199-396.
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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"pro region C-terminus;protease active site interactions are critical in catalyzing the folding of alpha-lytic protease."; Biochemistry 37:12058-12067(1998).
                                                          Lacepro, 198064236; AL protease.
Interpro, 198001316; Endopptdse52A.
Interpro, 198001254; Ser protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00089; trypein; I.
Pfam; PF02983; AL procease; 2.
PRINTS; PR00861; ALYTCPTASE:
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
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EMBL; M22763; AAA74111.1; -.
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15-APR-90.
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15-APR-90.
15-APR-90.
15-APR-90.
15-JAN-93.
15-JAN-93.
17-APR-97.
12-AUG-98.
18-UNN-99.
18-UNN-99.
27-APR-99.
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2PRO;
3PRO;
4PRO;
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5LPR;
6LPR;
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SEQUENCE FROM N.A.
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ID UL21 PR
AC Q00703;
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99HNÄ7;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Probable inorganic polyphosphate/ATP-NAD kinase (EC 2.7.1.23)

(Poly(P)/ATP NAD kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.1%; Score 39.5; DB 1; Length 397;
40.0%; Pred. No. 22;
live 3; Mismatches 0; Indels 9
     protease; 3D-structure; Zymogen; Signal.
24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41077 MW; 267FE6EBF57F33CB CRC64;
                                       ALPHA-LYTIC PROTEASE
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Best Local Similarity '
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          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     maturation.";
J. Virol. 66:7096-7103(1992).
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21,
EHV-1 40, EHV-4 UL21, AND VZV 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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46.2%; Pred. No. 19;
ive 4; Mismatches 3; Indels
                               Archaea, Euryarchaecta, Halobacteria, Halobacteriales,
Halobacteriaceae, Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE005089; AAG20093.1; -.
InterPro; IPR002504; ATP NADK.
Pfam: PF01513; NAD_kinase; NAD;
Transferase; Kinase; NAD; NADP; Complete proteome.
SEQUENCE 282 AA; 29120 MW; SDAIAF25147D7500 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE NAD KINASE FAMILY.
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01-APR-1993 (Rel. 26, Last sequence update)
01-UUL-1993 (Rel. 26, Last annotation update)
01-UUL-1993 (Rel. 26, Last annotation update)
Procein UL21 homolog.
Viruses, GaDNA viruses, (PRV).
Viruses, GaDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
Halobacterium sp. (strain NRC-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
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or send an email to license@isb.ch).
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Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Speciars From N.T.
Specials And PubMedal1677609;
MEDLINE-21534948; PubMedal1677609;
MCDLINE-21534948; PubMedal1677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., McClelland M., Sanderson K.E., Spieth J., Dante M., Du F., Hou S., Layman D., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Leorea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                 Gaps
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"Mutants defective in the energy-conserving NADH dehydrogenase of Salmonella typhimurium identified by a decrease in energy-dependent protecolysis after carbon starvation.";
proceolysis after carbon starvation.";
proc. Natl. Acad. Sci. U.S.A. 90:9877-9881(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 611-907 FROM N.A.
SPECIES-S. Lyphimurium; STRAIN-F98;
MEDLINE-98037521; PubMed-9371470;
Zhang-Barber L.Z., Turner A.K., Martin G., Fraenkel G., Dougan G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Influence of genes encoding proton-translocating enzymes on suppression of Salmonella typhimurium growth and colonization."; J. Bacteriol. 179:7186-7190(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
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                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NADH dehydrogenase I chain G (EC 1.6.5.3) (NADH-ubiquinone oxidoreductase chain G) (NUO?).
                                                                                                                                                                     Ouery Match
57.4%; Score 39; DB 1; Length 523;
Best Local Similarity 54.5%; Pred. No. 35;
Matches 6; Conservative 3; Mismatches 2; Indels
                                                                                                                                        PFam; PF03252; UL21; 1.
SEQUENCE 523 AA; 55019 MW; 9E69949DAE94CAC6 CRC64;
                                                                                                                                                                                                                                                                                                                    907 AA.
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MEDLINE-21534947; PubMed-11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=S.typhimurium;
MEDLINE=94052195; PubMed=8234329;
                                                                                               EMBL, M95285; AAA47474.1; -. PIR; A44195; A44195. Interpro; IPR004936; Herpes_UL21.
                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium, and Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-611 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                       STANDARD;
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187 GIPGVRPPLSG 197
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Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
Reltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
Reltwell T., Hamlin N., Lasther S., Moule S., O'Gaora P., Parry C.,
A. Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
A. Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
A. Complete genome sequence of a multiple drug resistant Salmonella
T. — enterica serovar Typhi CT18.",
T. — enterica serovar Typhi CT18.",
T. — hature 413:848-852(2001).
T. — FUNCTION: TARSPER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
TO BE UBIQUINONE. DOES COUPLE THE REDOX REACTION TO PROTON
TO BE UBIQUINONE AND THUS CONSERVES THE REDOX ENERGY IN A PROTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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-!- COFACTOR: BINDS 1 2FE-2S CLUSTER AND 1 4FE-4S CLUSTER (POCENCI.)
-!- SUBUNIT: COMPOSED OF 13 DIFFERENT SUBUNITS. SUBUNITS NUOCD, E,
-!- SIMILARITY: BELONGS TO THE PERIPHERAL SECTOR OF THE COMPLEX.
-!- SIMILARITY: BELONGS TO THE COMPLEX. 1 75 kDa SUBUNIT FAMILY.
-!- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS IN POSITIONS 714 AND 805.
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InterPro; IPR001461; FerreddoxIn.

R InterPro; IPR001467; Prok_Mboxred.

R Pfam; PF00111; fer2; I. r.

R PROSITE; PS00641; COMPLEX1 75K_1; I.

R PROSITE; PS00642; COMPLEX1 75K_1; I.

R PROSITE; PS00643; COMPLEX1 75K_2; I.

A Oxidoreductase; NAD; Ubiquinone; Iron-sulfur; 4Fe-48;

Complete proteome.

BY SIMILARITY.

INIT MET 22 22 IRON-SULFUR (2PR-2C) (PORTENT)

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W, 5DE802178260C65E CRC64;
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Pred. No.
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EMBL; L22504; AAA16063.1; ALT INIT.
EMBL; L42521; -; NOT ANNOTATED CDS.
EMBL; AL627274; CAD07555.1; ALT_INIT.
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Matches 7; Conservative
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kuchi P., Lewis S., Matsuno T., Gissi C., King B., Kochiwa H.,
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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G.,
RA Blake J., Boffelli D., Bolyunga N., Cartinoi P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Mashima J., Mandaserte P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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MEROPS; SO1.152; --
MGD; MGI:1913/23; 2200008B09Rik.
InterPro; IPR001314; Chymotrypain.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin, 1.
SNANT; SMO020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                      PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SMO0202; TRYP SF2; 1.
PROSTITE; PSSO240; TRYPSIN DOM; 1.
PROSITE; PSSO134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PSO135; TRYPSIN SER; 1.
HYMOLSE; SO1108; TRYPSIN SER; 1.
SEQUENCE 263 AA; 27821 MW; 2620A27AFP
   EMBL, AK003060, BAB22539.1; -. HSSP, P00766; IGCT. MRCDES, SQ1.152; -. IGCT. MGD, MGI:1913723; 2200008D09Rik. InterPro; IRRO01314; Chymotrypsin. InterPro; IRRO01254; Ser Exctease_Try. PF00089; trypsin; I.
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STRAIN=C57BL/6J; TISSUE=PANCREAS;
MEDLINE=21085660; PubMed=11217851;
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01-JUN-2002 (TrEMBLrel. 21,
2200008D09R1K protein.
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Nature 409:685-690(2001).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                     Query Match
Best Local Similarity 92.3%; Pred. No. 0.0025;
Matches 12; Conservative 1; Mismatches 0; Indels
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PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
SEQUENCE 263 AA; 27898 MW; C0638FB8F905A92F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) 2200008D09Rik protein.
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InterPro; IPR001314; Chymctrypain.
InterPro; IPR001234; Ser_protease_Try.
InterPro; IPR00124; Ser_protease_Try.
PRINTS; PR00089; trypsin; 1.
PROSITE; PR00020; Tryp_SRo; 1.
PROSITE; PS00130; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN HIS; UNKNOWN_1.
PROSITE; PS0135; TRYPSIN HIS; UNKNOWN_1.
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EMBL; AK003079; BAB22553.1; --
EMBL; AK007061; BAB25241.1; --
EMBL; AK008129; BAB25280.1; --
EMBL; AK008888; BAB25861.1; --
EMBL; AK008888; BAB25954.1; --
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MEDLINE-96043258; PubMed=7584866;
Raae A.J., Flengsrud R., Sletten K.;
"Chymotrypsin isoenzymes in Atlantic cod; differences in kinetics and substrate specificity.";
Comp. Biochem. Physiol. 1128:393-398(1995).
HSSP, P00766; 1ACB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suzuki T., Stivatava A.S., Kurokawa T.;

Auzuki T., Stivatava A.S., Kurokawa T.;

Tapanese flounder mRNA for chymotrypsingen 1.";

Submitted (JUL.1999) to the EMBL/GenBank/DDBJ databases.

--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYBEN FAMILY.

EMBL; ABO29753; BAA82365.1; ---

EMBL; ABO29753; BAA82365.1; ---

EMBL; ABO29753; BAA82365.1; ---

EMBL; ABO29753; BAA82365.1; ---

EMBL; ABO01254; Ser protease_Try.

Fam: PF001354; Ser protease_Try.

Fam: PF00189; trypsin; 1.

PRINTS; PR001254; Ser protease_Try.

Fam: PF00189; trypsin; 1.

PROSITE; PS00240; TRYPSIN D1;

PROSITE; PS00134; TRYPSIN D1;

PROSITE; PS00134; TRYPSIN D1;

PROSITE; PS00134; TRYPSIN D1;

RHYDROJABE; Serine protease.

SQ SEQUENCE 261 AA; 28184 MW; D7090A9D65395B7D CRC64;
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OL-NOV-1999 (TEMBLEL) 12, Created)

O1-NOV-1999 (TEMBLEL) 12, Last sequence update)

O1-JUN-2002 (TEMBLEL) 12, Last annotation update)

O1-JUN-2002 (TEMBLEL) 11, Last annotation update)

Chymotrypsinogen 1.

Paralichhys olivacens (Flounder).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopteryqii, Neopteryqii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopteryqii; Percomorpha; Pleuronectiformes; Pentonectiformes; Pentonectifo
                     OPPRSI;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Chymotrypsin isoenzyme CHTI (Fragment).
Gadus morhua (Arlantic cod).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopeerygii; Neoprerygii; Teleostei; Euteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
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    24 AA.
    PRT;
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Conservative
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    PRELIMINARY;
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                             NCBI_TaxID=8049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE - PANCREAS;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                           SEQUENCE
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                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=93285747; PubMed=8509158; Kim Y.J., Zhou A.S., Pescovitz M.D., Kim Y.J., Zhou Z., Hurtado J., Wood D.L., Choi A.S., Pescovitz M.D., Warfel N.A., Vandagriff J., Davis J.K., Kwon B.S.; IDDM patients' sera recognize a novel 30-kD pancreatic autoantigen related to chymotrypsinogen."; Imminol. Invest. 22:219-227 [1993). SEQUENCE IS AA: 1826 MW; 38105D1037CA6837 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chymotrypsinogen homolog (Fragment).
Sus scrofa (Pig)
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93016107; PubMed=1400470;
Gorr S.U., Hamilton J.W., Cohn D.V.;
"Regulated, but not constitutive, secretory proteins bind porcine
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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95.6%; Score 65; DB 11; Length 263; 92.3%; Pred. No. 0.0025; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.4%; Score 54; DB 4; Length 18; 91.7%; Pred. No. 0.014; cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53; DB 6; Length 25; Pred. No. 0.03;
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HSSP, P00766; 1ACB.
SEQUENCE 25 AA; 2439 MW, F69AE003F1ACB136 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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nes 11; Conservative
                        Best Local Similarity 92.3
Matches 12; Conservative
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Matches 11, Conservative
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                                                                                         1 CGVPAIQPVLSGL 13
                                                                                                                    19 CGVPAIQPVLTGL 31
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                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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    Query Match
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Matches
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nactum juryegitum (zar.).
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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TISSUE=RAT PANCREAS;
Sogame Y., Miteui S., Kataoka K., Kashima K., Kato M., Sakagami J.,
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 11; Length 264;
Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28167 MW; 1D979469A07056C2 CRC64;
   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD, MGI 88558; Ctrl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR00124; Ser_Protease_Try.
PRN0185; PR00132; CHYMOTRYPSIN.
SMART; SM00202; CHYMOTRYPSIN.
PROSITE; PS02040; TRYPSIN DOM; I.
PROSITE; PS00134; TRYPSIN DEM; I.
PROSITE; PS00134; TRYPSIN SER; I.
PROSITE; PS00135; TRYPSIN SER; I.
PROTITE; PS00135; TRYPSIN SER; I.
PROTITE; PS00135; TRYPSIN SER; I.
PROTICE: 264 AA; 28167 MW; ID979469A0705
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81.8%;
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Best Local Similarity 81.87
Than 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattue norvegicus (Rat)
                     1810004D15Rik protein.
CTRL OR 1810004D15RIK.
                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P00766; 4CHA.
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                                                                                                                     NCBI_TaxID=10090;
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Q9EQZ8
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Inverse Matsur Familia.
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                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28151 MW; 1D979719E07C16DE CRC64;
                                                                                                                                                                         Last sequence update)
Last annotation update)
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Last sequence update)
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MGD; MGI:88558; Ctrl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001354; Ser protease_Try.
Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
PR03TTE; PS50240; TryP.SPC; I.
PR0SITE; PS50240; TRYPSIN DOM; I.
PR0SITE; PS00134; TRYPSIN HIS; UNGNOWN I.
PR0SITE; PS00135; TRYPSIN HIS; UNGNOWN I.
PR0SITE; PS00135; TRYPSIN HIS; UNGNOWN I.
PR0SITE; PS00135; TRYPSIN HIS; UNGNOWN I.
PROSITE; PS01355; TRYPSIN HIS; UNGNOWN I.
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                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUB=PANCREAS;
MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                             01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%;
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Matches 9; Conservative
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                                                                                                                 PRELIMINARY:
                                                                                                                                                                       01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                           1810004D15Rik protein.
CTRL OR 1810004D15RIK.
17 CGVPSIKPQVSG 28
                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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Gaps

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2; Indels

Query Match

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Q9D7P8 RESULT 9
Q9D7P8
ID Q9D71
AC Q9D71
DT 01-J1
DT 01-J1 us-10-036-371-5.rspt

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Gaps
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Ol-MAY.2000 (TrEMBLrel. 13, Last sequence update)
Ol-MAY.2000 (TrEMBLrel. 19, Last sequence update)
Chymotrypsin isoenzyme (THZ (Fragment).
Chymotrypsin isoenzyme (THZ (Fragment).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
NCBI_TAXID=8049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chymotrypsinogen 2.

Paralichthys olivaceus (Flounder).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suzuki T., Srivastava A.S., Kurokawa T.;
"Japanese flounder mRNA for chymotrpsinogen 2.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-I. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TYPENI FAMILY.
EMBL; ABO29754; BAA82366.1; -.
HSSP; PO0766; 1CHG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.1%; Score 47; DB 13; Length 23; 66.7%; Pred. No. 0.3; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27793 MW; 9F583044E22F78C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 AA
                                                                                                                                                        23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; 501.152; ---
Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS, PRO0089, ETYPENIN, I.
PRINTS, PR00722; CHYMOTRYPSIN.
SMART, SM00202; TTYP_SPO. 1.
PROSITE; PS00134; TRYPSIN DOM; I.
PROSITE; PS00134; TRYPSIN SER; I.
Hydrolase; Serine protease.
SEQUENCE 260 AA; 27793 MW; 9F58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CGVPAIOPVLSG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 CGVPAITPALS 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
1 CGVPAIQPVLS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8255;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                     Q9PRS0
Q9PRS0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bjoernslett M.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
    Yanaguchi N.;
"Molecular cloning of rat chymopasin.";
"Molecular cloning of rat chymopasin.";
Submitted (DEC-1998) to the EMBL/Genbank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
EMBL, ABO20757; BABZ0287.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
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Pred. No. 2.2;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          70.6%; Score 48; DB 11; Length 264; 81.8%; Pred. No. 2.2; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitsui S., Yamaguchi N.;
"Molecular cloning of mouse chymopasin.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                          PEAM; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN,
BMRAT; SM00020; Tryp SPC; 1.
PROSITE; PS0240; TRYPSIN DOM; 1.
PROSITE; PS0134; TRYPSIN HIS; UNKNOWN_1.
Hydrolae; Serine processe;
SEQUENCE 264 AA; 28116 MW; F9ED5D210FD3500E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28135 MW; 1D979709A07056C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TYEMBLRE). 16, Last sequence update)
Chymopasin (Chymotrypsin A CTRA-1).
CTRL OR CTRA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Ser protease_Try.
Fign. PR00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00220; Tryp.SPS: 1.
PROSITE; PS00240; TRYPSIN DOW; 1.
PROSITE; PS00134; TRYPSIN DOW; 1.
PROSITE; PS00134; TRYPSIN SER, 1.
HYGOLASE; Serine protease.
SEQUENCE 264 AA; 28135 WW; 1D979709A0708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 AA
                                                                                                                                                     MEROPS, SOL.256, -...
InterPro, IPR001114; Chymotrypsin.
InterPro, IPR001264, Ser protesse_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
STRAIN=129S6/SVEVTAC; TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:88558; Ctrl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00766; 4CHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGVPAIQPVLS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; S01.256; -
                                                                                                                                       HSSP; P00766; 4CHA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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09ER05
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us-10-036-371-5.rspt

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[1]
SEQUENCE FROM
STRAIN=UTEX 5
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                                                                  Gaps
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 20, Last annotation update)
Ribulose bisphosphate carboxylase large chain (EC 4.1.1.39) (RuBisCO RBCL.
                                                                                                                                                                                                                                                                                                                                                                                                         Gadus morhua (Atlantic cod).
Bukaryota: Metazoda; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=PYLORIC CABCA;
MEDLINE=20464334; PubMed=11011764;
Spillieert R., Gudmundsdottir A.;
"Molecular Cloning of the Atlantic Cod Chymotrypsinogen B.";
Microb. Comp. Genomics 5:41-50(2000).
-1- SIMILARITY: BELONGS TO PEFTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL; AJ242521; CAB43766.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadacae, Chlamydomonas.
NCBI_TaxID=47905,
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66.7%; Pred. No. 5;
tive 2; Mismatches 2; Indels
                 Score 47; DB 13; Length 260;
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS, SOLLSS, --
MEROPS, SOLLSS, --
InterPro; IPRO01314; Chymotrypsin.
InterPro; IPR001324; Ser_protease_Try.
PEAM; PRO0089; trypsin, I.
PRINTS; PRO0722; CHYMOTRYPSIN.
SMRAT; SM00020; TRYPSIN DM; 1.
PROSITE; PSSO240; TRYPSIN DM; 1.
PROSITE; PSSO134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS0135; TRYPSIN HIS; UNKNOWN 1.
                                                               2; Indels
                                                                                                                                                                                                                                                                                             C1-MAR-2000 (TrENBLrel. 13, Created)
01-MAR-2002 (TrENBLrel. 13, Last sequence update)
Chymcrypsin B precursor (EC 3.4.21.1)
CHYB.
Gadus morhus (Arthur)
69.1%; Sco...
66.7%; Pred. No. 3...
2; Mismatches
                                                                                                                                                                                                                                                                         263 AA
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                                                                                                                                                                                                                                                                         PRT;
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            Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                         PRELIMINARY;
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Chloroplast.
                                                                                                       1 CGVPAIQPVLSG 12
                                                                                                                                  16 CGSPAIPPVITG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                         90MG60
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09PW06
DD 01-MA
DD 0
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TELECTE BLEATHS OF LABBILING BLAND CHARLOWS: THE CARBOXYLATION OF D-Plante 2008:365-372 (1999)

C. -- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBUGOSE 1,5-BISHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF THE PENTOSE SUBSTRATE IN THE PHOTORESPHATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SIMILARITY).

C. -- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3 - PHOSPHO-D-CLYCERATE + 2-PHOSPHOGLYCOLATE.

C. -- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 3 - PHOSPHO-D-CLYCERATE + 2-PHOSPHOGLYCOLATE.

C. -- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 3 - PHOSPHO-D-CLYCERATE + 8 SMALL CHAINS (BY SIMILARITY).

C. -- SUBCELLIAR LOCATION: CHLOROPLAST (BY SIMILARITY).

C. -- SUBCELLIAR LOCATION: CHLOROPLAST (BY SIMILARITY).

C. -- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.

EMBL; AB022224; BAA82054.1; -

DR Ffam; PRO0016; RUBISCO LARGE; 1.

DR PROSITE; PS00157; RUBISCO LARGE; 1.

DR PROSITE; PS00157; RUBISCO LARGE; 1.

DR PROSITE; PS00157; AUDISCO LARGE; 1.

DR PROSITE; PS00157; PUDISCO LARGE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                 Morita B., Abe T., Tsuzuki M., Pujiwara S., Sato N., Hirata A., Sonoike K., Nozaki H.;
"Role of pyrenoids in the CO2-concentrating mechanism: comparative morphology, physiology and molecular phylogenetic analysis of closely related strains of Chlamydomonas and Chloromonas (Volvocales).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
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Pred. No. 7.1;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 AA; 41774 MW; 845E743C36FB86A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; Photorespiration; Photosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 12, 2003, 10:27:25 Job time : 11.197 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 58.3
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 CGLPGVMPVASG 370
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FROM N.A.
TEX 578;
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INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIMMEDIATE SOURCE:
CCONE: 364702
US-08-988-876-1
US-08-988-876-1
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 2, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 17, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Appl
                                                                         (without alignments)
136.898 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                           February 12, 2003, 10:18:40 ; Search time 2.79403 Seconds
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Sequence 16,
Sequence 16,
Sequence 16,
Sequence 16,
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Sequence 1
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1. /cgnZ_6/pcdata/1/iaa/5A_COMB.pep:*

2. /cgnZ_6/pcdata/1/iaa/6A_COMB.pep:*

3. /cgnZ_6/pcdata/1/iaa/6A_COMB.pep:*

4. /cgnZ_6/pcdata/1/iaa/6A_COMB.pep:*

5. /cgnZ_6/pcdata/1/iaa/PcTUS_COMB.pep:*

6. /cgnZ_6/pcdata/1/iaa/PcTUS_COMB.pep:*
  GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-278-091-16

US-08-48-95-16

US-08-47-167-16

US-08-48-91-16

US-08-48-91-16

US-08-256-149-16

US-08-256-149-16

US-08-15-271-16

US-09-106-467-16

US-09-106-467-16

US-09-106-467-16

US-09-106-467-16

US-09-109-468-2

US-08-193-2

US-08-193-2

US-09-193-2

US-09-193-2

US-09-193-2

US-09-193-2

US-09-193-3-2

US-08-964-33-2

US-08-964-33-2

US-08-91-37-68-10

                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                           262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        OM protein - protein search, using sw model
                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                      1 CGVPAIQPVLSGL 13
                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                    US-10-036-371-5
68
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Query
Match Length D
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                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                            Run on:
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No.
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, TOPOLOGY: linear
US-08-483-859-16
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                                                                ö
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INDORMATION:
APPLICANT: UCOSMORE, Sheena M
APPLICANT: VANG, Van-Ping
APPLICANT: VANG, Van-Ping
APPLICANT: OWNEN, Raymond P.
APPLICANT: WIGH H.
TITLE OF INVENTION: Reduced Procease Activity
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
CONTRY: Canada
ZIP: MGG IR7
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: PLOPS/MS-DS
SOFTWARE: Patentin Release #1.0, Version #1.25
COMPUTER: BALCANION BATA:
APPLICATION NUMBER: US/08/278,091
CLASSIFICIATION NUMBER: US/08/278,091
CLASSIFICIATION NUMBER: US/08/278,091
TELEPRATION STATE INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
RELEPRATION FOR SEQ ID NO: SEC IN S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
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YANG, Yan-Ping
CHONG, Pele
CHONG, Rele
KLEIN, Michel H.
VENTION: Analog of Haemophilus Hin47 Protein with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 40.0%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 0; Indels
61.8%; Score 42; DB 3; Length 326; 66.7%; Pred. No. 15; 1.1ve 2; Mismatches 2; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/08483859
Patent No. 5656436
GENERALINFORMATION:
APPLICANT: LOCOMONE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemo
                                                                                                                                                                                                                                                                                                     RESULT 2
US-08-278-091-16
'Sequence 16, Application US/08278091
'Patent No. 5506139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||:||
170 CGIPASQRSSLFERLQPILS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGVPA-----IQPVLS 11
          Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                            42 GDPELQPVLAGL 53
                                                                                                                                       2 GVPAIQPVLSGL 13
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US-08-483-859-16
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TITLE OF INVENTION: Reduced Processe Activity
NUMBERS OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESS
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STATE: Ontatio
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: LIBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-08-482-816-16
1. Sequence 16, Application US/08482816
1. Patent No. 593573
1. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                         TELEPHONE: (416) 595-1153
TELEPHONE: (416) 595-1153
INPORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 198 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                       Best Local Similarity 40.0 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-482-816-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Suite
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                           ; TOPOLOGY:
US-08-487-167-16
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-487-167-16
Sequence 16, Application US/08487167
Sequence 16, Application US/08487167
Sequence 16, Application US/08487167
GENERAL INFORMATION:
APPLICANT: COCNORE, Sheena M. APPLICANT: CROK, Pele APPLICANT: CROK, Pele APPLICANT: CROK, Raymond P. APPLICANT: KLEIN, Michel H. TITLE OF INVENTION: Reduced Protease Activity NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
58.1%; Score 39.5; DB 1; Length 198;
Best Local Similarity 40.0%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDESCREE: Sin & MCBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Oncario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: FIPOppy disk
COMPUTER: Date: PC-DOS/MS-DOS
SOFTWARE: Pate: PC-DOS/MS-DOS
SOFTWARE: Pate: PC-DOS/MS-DOS
SOFTWARE: Pate: NC-DOS/MS-DOS
SOFTWARE: PATE: NC-UND-1995
CLASSIFICATION NUMBER: US 08/296,149
FILING DATE: ON-ON-1995
CLASSIFICATION NATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-NUG-1994
FILING DATE: 21-UUL-1994
ATTORNEY/AGRYI INVORMATION:
NAME: STATUS NUMBER: US 08/278,091
FILING DATE: 21-UUL-1994
ATTORNEY/AGRYI INVORMATION:
                                                                                                                                                                                                                                                                                                                                         1038-493 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-508 MIS:vg
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,173
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
FILING DATE: 21-UL-1994
ATTORNEY/AGENT INFORMATION:
REGISTATION NUMBER: 24,973
ATTORNEY/AGENT INFORMATION:
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 138-493 M
TELEFORM (416) 595-1165
FILEFAX: (416) 595-1165
FILEFAX: (416) 595-1165
FILEFAX: (416) 595-1165
FILEFAX: (416) 595-1165
FILEROTH: 198 amino acids
STRANDEDNESS: Single
TYPE: amino acids
STRANDEDNESS: Single
TOPOLOGY: linear
US-08-472-173-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGVPA------IOPVLS 11
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APPLICANT: LOCANORE, Sheena M
APPLICANT: LOCANORE, Sheena M
APPLICANT: WANG, Yan-Ping
APPLICANT: CHONG, Pela-Ping
APPLICANT: COMEN, Raymond P.
APPLICANT: WIEIN, Michel H.
TITLE OF INVENTOR: 23
CORRESPONDERS: 23
CORRESPONDERS: 23
CORRESPONDERS: 23
CORRESPONDERS: 24
SADDRESSEE: Sim & MCBUTNEY
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
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                                                               Gaps
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58.1%; Score 39.5; DB 2; Length 198; 40.0%; Pred. No. 23; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
SOUTHARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOBER: US/08/482,816
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NOBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NOMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATPLING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
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APPLICANT: LOCSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: YANG, Yan-Ping
APPLICANT: WING, Yan-Ping
APPLICANT: WING, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: COMEN, Raymond P.
APPLICANT: MICHAL H.
TITLE OF INVENTION: PROTEASE ACTIVITY
INDER OF SEQUENCES: 23
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Sim & MCBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STRATE: Ontaxio
COUNTY: Canada
ZIP: MSDIWY: Canada
ZIP: MSGIRY
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>ن</u>
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,271
                                                     ZUER MGG IR
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39.5; DB 2;
Pred. No. 23;
                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 514
PIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 07-UN-1995
FILING DATE: 26-MIG-1994
FILING DATE: 26-MIG-1994
FILING DATE: 26-MIG-1994
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-UL-1994
ATTORNEY AGENT INFORMATION:
NAME: 51-WIG-1994
ATTORNEY AGENT INFORMATION:
TELEFACOWMUNICATION INPORMATION:
TELEFACOWMUNICATION INPORMATION:
TELEFACOR (416) 595-1155
TELEFACE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-615-271-16
; Sequence 16, Application US/08615271
; Patent No. 5981503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 40.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGVPA-----IQPVLS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 198 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: Bi
                     Ontario
: Canada
Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-08-801-499-16
                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      요
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APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease Act
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBUrnev
STRDERS.
                                                                                                                                                                                                                                                                                                                                 Analog of Haemophilus Hin47 Protein with
Reduced Protease Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2, Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Toronto
CITY: Toronto
CITY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: APELLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                 IB: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.1%; Score 39.5; 40.0%; Pred. No. 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFENCE/DOCKET NUMBER: 1038-390
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-08-801-499-16
; Sequence 16, Application US/08801499
; Patent No. 5962430
; GENERAL INFORMATION:
; APPLICANT: LOOSWORE, Sheena M
                                                                                                                                                   Sequence 16, Application US/08296149
Patent No. 5939297
                                                                                                                                                                                           APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: YANG, Yan-Ping
APPLICANT: OOMEN, Raymond P.
APPLICANT: COMEN, Raymond P.
APPLICANT: COMEN, Raymond P.
TITLE OF INVENTION: Analog of He
TITLE OF INVENTION: Reduced Prot
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBURNEY
STREET: Suite 701, 330 Univers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||:||
| CGIPASORSSLFERLOPILS 189
                       ||:||
170 CGIPASQRSSLPERLQPILS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGVPA-----1QPVLS 11
1 CGVPA------IQPVLS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 40.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 198 amino
TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-296-149-16
                                                                                                              RESULT 7
US-08-296-149-16
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Gaps

us-10-036-371-5.rai

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Sequence 16, Application US/09074659
Patent No. 6025342
GENERAL INFORMATION
APPLICANT: LOCAGNORE, Sheena M.
APPLICANT: CHONG, Pele
APPLICANT: OMEN, Raymond P.
APPLICANT: OMEN, Raymond P.
APPLICANT: OMEN, Mandog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEGURNCES. 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
                                                                                                                                                                                                                                 6
                                                                                                                                                                Query Match
Best Local Similarity 40.0%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.1%; Score 39.5; DB 3; Length 198; Best Local Similarity 40.0%; Pred. No. 23; Matches 8; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCY/DOCKET NUMBER: 1038-730 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416, 595-1155
TELEPKX: (416, 595-1163
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,167
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26.AUG-1994
APPLICATION NUMBER: US 08/278,091
FILING DATE: 1-JUL-1994
ATTORING DATE: 1-JUL-1994
                                                                                                                                                                                                                                                                                                       170 CGIPASQRSSLFERLQPILS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6th Floor, 330 University: Toronto STATE: Ontario COUNTR: Canada ZIP: MSG 1R7 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                              1 CGVPA-----IOPVLS 11
                         : LENGTH: 198 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLLOGY: linear
US-09-074-660-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGVPA-----1QPVLS 11
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                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-074-659-16
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US-09-074-659-16
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Sequence 16, Application US/09074660

Sequence 16, Application US/09074660

Patent No. 6020NDE

APPLICANT: LOCSMORE, Sheena M.
APPLICANT: COMEN, Pan-Ping

APPLICANT: CHOIG, Pele

APPLICANT: KLEIN Raymond P.

TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with

TITLE OF INVENTION: Reduced Protease Activity

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                 58.1%; Score 39.5; DB 2; Length 198; 40.0%; Pred. No. 23; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/074,660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Sim & McBurney
6th Floor, 330 University Avenue
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-731 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
FILING DATE: 20-JUN-1996
CLASSIFICATION: 514
ATTONEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/COCKET UNDBER: 1038-580
TELECOMMUNICATION INFORMATION:
TELEPAN: (416) 595-1163
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 16; SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRICR APPLICATION
APPLICATION NUMBER: US 08/487,167
FILING DATE: 07-7010-1995
FILING DATE: 07-7010-1995
FILING DATE: 07-7010-1995
FILING DATE: 07-7010-1995
FILING DATE: 26-7010-1994
FILING DATE: 26-7010-1994
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-7010-1994
ATTORNEY/ACENT INFORMATION:
NAME: Stewart, Michael I:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 CGIPASQRSSLFERLQPILS 189
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Best Local Similarity 40.0%
Matches 8; Conservative
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COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6th Flo
CITY: Toronto
STATE: Ontario
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TOPOLOGY:
US-08-615-271-16
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Gaps

a

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RESULT 14

US-09-106-467-16

US-09-106-467-16

Sequence 16, Application US/09106467

GENERAL INFORMATION:

APPLICANT: LOCONGE, Sheena M.

APPLICANT: CHONG, Pele

TITLE OF INVENTION: PROTEASE ACTIVITY

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney

STREET: Gth Floor, 330 University Avenue

CITY: Toronto

STATE: Ontario

CONDITE: CANADA

COMPUTER: LEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

FILING DATE:

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
   NUMBER OF SEQUENCES: 4.5

CORRESPONDENCE SIM & MCBURINEY
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: 0ntario
COUNTRY: Canada
ZIP: MSG 187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
OPERATION NUMBER: US/09/106,466A
FILING DATE:
CLASSIFICATION NUMBER: US/09/106,466A
FILING DATE: 20-JUN-1996
CLASSIFICATION NUMBER: US/09/106,466A
FILING DATE: 20-JUN-1996
CLASSIFICATION NUMBER: 24-973
REFERENCE/DOCKET NUMBER: 1038-826
TELERHANTON NUMBER: 24-973
REFERENCE/DOCKET NUMBER: 1038-826
TELERHANTION NUMBER: 24-973
REFERENCE/DOCKET NUMBER: 1038-826
TELERHANTION NUMBER: 24-973
REFERENCE/DOCKET NUMBER: 1038-826
TELERHANTION NUMBER: 24-973
REFERENCE/DOCKET NUMBER: 24-973
REFERENCE/DOCKET NUMBER: 1038-826
TELERHANTION NUMBER: 24-973
REFERENCE/DOCKET NUMBE
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Best Local Similarity 40.0%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches
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170 CGIPASQRSSLFERLOPILS 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
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TOPOLOGY: linear
US-09-106-466A-16
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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US-09-106-466A-16
Sequence 16, Application US/09106466A
Sequence 10, Application US/09106466A
Sequence 10, Application
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: CHONG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CALIN, Michel H.
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
TITLE OF INVENTION: PROTEASE ACTIVITY
                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: VANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
TITLE OF INVENTION: PROTEASE ACTIVITY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBUINEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: 10x0000
COUNTRY: Canada
ZIP: M5G 1A7
COMPUTER: Canada
ZIP: M5G 1A7
COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,468
FLING DATE: 20-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION:
APPLICATION:
NAME: Stewart, Michael I
REGISTRATION:
NAME: Stewart, Michael I
REFERENCE/DOCKET NUMBER: 1038-825
TELERPHONE: (416) 595-1163
INPORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.1%; Score 39.5; I
40.0%; Pred. No. 23;
tive 3; Mismatches
                                                                                                                                                      RESULT 12
US-03-106-468-16
'Sequence 16, Application US/09106468
'Patent No. 6114125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||:||
170 CGIPASQRSSLFERLQPILS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGVPA-----1QPVLS 11
             ||:|| :|| :|| 170 CGIPASQRSSLFERLQPILS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 198 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 40.00
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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Gaps

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i STRAIN: Kaplan
US-08-681-129-2

Guery Match
Best Local Similarity 54:$\frac{1}{2}$; Pred. No. 77;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps

Qy 2 GVPAIQPVLSG 12

Db 187 GIPGVRPPLSG 197
Search completed: February 12, 2003, 10:30:10
Job time: 3.79403 secs
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; 0 (OTARU) NNAJA 3ĐAG RIHT

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Sequence 643, Application US/09925297
Patent No. US2020001659A1
GENERAL INFORMATION:
APPLICANT Rosen et al.
ITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERBNE: AA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
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CORGANISM: Bovine sp.
US-10-036-371-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-09-925-297-643
                                          Query Match
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Sequence 643, App
Sequence 36, Appl
Sequence 3, Appli
Sequence 34, Appli
Sequence 24, Appli
Sequence 28, Appli
Sequence 28, Appli
Sequence 1817, Appli
Sequence 1817, Appli
Sequence 3131, Appli
Sequence 3131, Appli
Sequence 211, Appli
Sequence 415, Appli
Sequence 415, Appli
Sequence 415, Appli
                                                                                             (without alignments)
167.821 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                February 12, 2003, 10:22:36 ; Search time 1.9791 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*

1: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

2: \cgn1_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: \cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

4: \cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

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9: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

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14: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

14: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-036-371-5

US-10-036-371-5

US-09-925-297-643

US-09-988-615-96

US-09-982-397-33

US-09-662-340-4

US-09-662-340-4

US-09-774-639-283

US-09-774-639-283

US-09-774-639-283

US-09-774-639-33

US-09-774-639-33

US-09-774-6426

US-09-864-761-38817

US-09-84-761-38801

US-09-84-761-3801

US-09-864-133-63

US-09-864-133-63

US-09-864-133-63
                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                      140259 segs, 25548876 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                   1 CGVPAIQPVLSGL 13
                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
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Match Length DB
                                                                                                                                      US-10-036-371-5
68
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Maximum DB seq
                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                      Searched:
                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
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NESULE 1.5

Sequence 5, Application US/10036371

Sequence 5, Application US/10036371

Sequence 5, Application US/10036371

Sequence 5, Application US/10036371

SETECT NO USZO20141987A1

APPLICANT: BJARNARSON, JON B.

TITLE OF INVENTION: FISH SERIES PROTEINASES AND THEIR PHARMACEUTICAL AND TITLE OF INVENTION: COSMETIC USE

FILE REPERENCE: 81691/284960

CURRENT PLING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: 09/411,688

PRIOR APPLICATION NUMBER: 5066/99

PRIOR FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PALENTIN VEY: 2.1

SEQ ID NO 5
                               Sequence 7, Applisequence 12, Applisequence 12, Applisequence 13, Applisequence 13, Applisequence 13, Applisequence 21, Applisequence 20, Applisequence 219, Applisequence 210, Appliseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
      Sequence 1164, Ap
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10 US-09-867-550-1164

10 US-09-764-862-909-7

10 US-09-764-862-909-7

10 US-00-144A-157

10 US-00-789-306-11

10 US-09-789-306-11

10 US-09-789-306-11

10 US-09-789-306-11

10 US-09-726-643-73

10 US-09-726-643-73

10 US-09-726-643-73

10 US-09-989-738-219

10 US-09-989-738-219

10 US-09-999-744-119

10 US-09-990-444-119

10 US-09-990-444-119

10 US-09-990-444-119

10 US-09-990-486-219

10 US-09-991-181-219

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Sequence 3, Application US/10036371

Sequence 3, Application US/10036371

Sequence 10. US2020141987A1

GENERAL INFORMATION:

APPLICANT: BJARNARSON, JON B.

TITLE OF INVENTION: COGMETIC USE

TITLE OF INVENTION: COGMETIC USE

TITLE OF INVENTION: COGMETIC USE

TITLE OF INVENTION: 19194988: US/10/036,371

CURRENT APPLICATION NUMBER: US/10/036,371

CURRENT FILING DATE: 1999-10-12

PRIOR FILING DATE: 1999-10-12

PRIOR FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

TYPE: PATENT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                               US-09-25-297-529

1. Sequence 529, Application US/09925297

2. Sequence 529, Application US/09925297

2. Sequence 529, Application US/09925297

3. GENERAL INFORMATION:

4. TITLE OF INVENTION:

5. TITLE OF INVENTION:

6. CURRENT APPLICATION NUMBER: US/09/925,297

6. CURRENT FILING DATE: 2001-08-10

7. PRIOR APPLICATION NUMBER: PCT/US00/05989

7. PRIOR FILING DATE: 1999-03-12

7. NUMBER OF SEQ ID NOS: 928

7. SOFTWARE: PatentIN Ver. 2.0

7. SEQ ID NO 529

7. LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.1%; Score 49; DB 10; Length 192; 72.7%; Pred. No. 0.31; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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) LOCATION: (10)

) OTHER INFORMATION: I or V

US-10-036-371-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-297-529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (3)
OTHER INFORMATION: R OFERTURE:
NAME/KEY: MOD_RES
                                                    19 CGVPAIHPVLSGL 31
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15 CGIPAIKPALS 25
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NAME/KEY: MOD_RES
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US-10-036-371-3
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (133)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
LICATION: (2)
OTHER THORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (137)
CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (143)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-643
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (126)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 63; DB 10; Length 146;
Pred. No. 0.001;
0; Mismatches 1; Indels
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JOSTON BENEFIELDS
JOSTON BENEFAL INPORMATION:
JOSTOLICANT:
JOSTON:
JOS
PRIOR APPLICATION NUMBER: PCT/USO0/05989;
PRIOR FILING DATE: 2000-03-08;
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12;
NUMBER OF SEQ ID NOS: 928;
SOFTWARE: PatentIN Ver. 2.0;
SEQ ID NO 643;
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 92.6%;
Best Local Similarity 92.3%;
Matches 12; Conservative
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ORGANISM: Homo sapiens
US-09-888-615-96
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US-09-888-615-96
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1 CGVPAIQPVLSGL 13

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Gaps

us-10-036-371-5.rapb

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Sequence 283, Application US/09774639
Sequence 283, Application US/09774639
Publication No. US200300035551
GENERAL INFORMATION:
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REPERENCE: P2013P1
CURRENT APPLICATION NUMBER: US/09/774,639
CURRENT FILING DATE: 2001-07-09
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
NUMBER OF SEQ ID NOS: 371
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 283
LENGTH: 24
TYPE: PRT
CORGANISM: Homo sapiens
US-09-774-639-283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.9%; Score 38; DB 9; Length 565; 58.3%; Pred. No. 70; ative 1; Mismatches 4; Indels
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                                                      GENERAL INFORMATION:

APPLICANT: Lambeth, J. David

APPLICANT: Cheng, Guangjie

TITLE OF INVENTION: Micceptic Oxygenase Regulators

FILE BERERNCE: 05501-0180 43150-566489

CURRENT FILIO DATE: 2001-11-15

CURRENT FILING DATE: 2001-11-16

PRIOR PELING DATE: 2001-11-16

PRIOR PELING DATE: 2000-11-16

PRIOR PELING DATE: 2001-11-16

PRIOR PELING DATE: 2001-12-05

PRIOR PELING DATE: 2001-05-07

PRIOR APPLICATION NUMBER: US 60/289,172

PRIOR PLING DATE: 2001-05-07

TRYPE: PLOR PRIOR PLING DATE: 2001-05-07

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 565

TYPE: PRIOR PRIOR SAPIENS

US-09-99-248-4
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US-09-774-619-282
Sequence 282, Application US/09774639
Fublication No. US2003000355A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FLLE REPRENCE: P2013H
CURRENT APPLICATION NUMBER: US/09/774,639
CURRENT FILING DATE: 2001-07-09
Sequence 4, Application US/09999248
Patent No. US20020176852Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 58.33
Matches 7; Conservative
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Matches 7; Conservative
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US-09-774-639-283
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US-09-662-540.34
Sequence 34, Application US/09862540
Publication No. US20030023992A1
Sequence 34, Application US/09862540
Publication No. US20030023992A1
GENERAL INFORMATION:
ITILE OF INVENTION: No. US20030023992A1e1 G Protein-Coupled Receptors
FILE REPRENEE: 0252US1
CURRENT APPLICATION NUMBER: US/09/862,540
CURRENT PILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 60/206,138
PRIOR FILING DATE: 2000-05-22
PRIOR PELLING DATE: 2000-05-22
PRIOR PELLING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 61
SOFWARE: Patentin Version 3.0
                                                                Gaps
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US-09-764-869-944
i Sequence 944, Application US/09764869
i Sequence 944, Application US/09764869
i Parent No. US20020061521A1
i GENERAL INFORMATION:
i APPLICANT: Rosen et al.
i TITLE OF INVENTION:
i PILE REFERENCE: PC007
i CURRENT APPLICATION NUMBER: US/09/764,869
i CURRENT FILING DATE: 2001-01-17
i Prior application data removed - refer to PALM or file wrapper
i NUMBER OF SEQ ID NOS: 2442
i SOFTWARE: PALENTIN VEY: 2.0
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       58.8%; Score 40; DB 12; Length 13; 58.3%; Pred. No. 0.54; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 57.4%; Score 39; DB 10; Length 78; Best Local Similarity 53.8%; Pred. No. 5.6; Matches 7; Conservative 1; Mismatches 5; Indels
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Ouery Match 58.8 Best Local Similarity 58.3 Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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; ORGANISM: Homo sapiens
US-09-764-869-944
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                                                                                                  1 CGVPAIOPVLSG 12
                                                                                                                                           1 CGXPAIXPXXTG 12
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; ORGANISM: Homo sapiens
US-09-862-540-34
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; LENGTH: 78
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RESULT 8 US-09-999-248-4

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Sequence 46426, Application US/09864761

Sequence 46426, Application US/09864761

Sequence 46426, Application US/09864761

SERVINAL INFORMATION:
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Hensheng
ITTLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US/09/864,761
                               PEATURE:

ORGANISM: Homo Bapien8
FEATURE:

OTHER INFORMATION: MAP TO AL049733.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.97
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.91
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.91
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
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Pred. No. 7.6;
3; Mismatches 3; Indels
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PRIOR PELLING MATE: AUGIL-US-23
PRIOR PELLING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
PRIOR PELLOATION NUMBER: US 09/632,366
PRIOR PELLOATION NUMBER: US 02/632,366
PRIOR PELLOATION NUMBER: US 60/236,359
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00669
FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 09/608,408
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Best Local Similarity 50.0
Matches 6; Conservative
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US-09-864-761-46426
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PREGRIM, NO. USZOZOGO 49763A1

PREGRIM, NO. USZOZOGO 49763A1

APPLICANT Penn. Sharton G.

APPLICANT Penn. Sharton G.

APPLICANT Penn. Sharton G.

APPLICANT Penn. Membreso

TITLE OF INVERTION HUMAN GROWE-DERIVED SINGLE EXON NUCLEIC ACID FROBES USZPUL FOR TITLE OF INVERTION HUMAN GROWE-DERIVED SINGLE EXON NUCLEIC ACID FROBES USZPUL FOR TITLE OF INVERTION HUMBER: US 60/106,312

PRIOR PLING DATE: 2001-05-23

PRIOR PLING DATE: 2001-05-24

PRIOR PLING DATE: 2001-05-30

PRIOR PLING DATE: 2001-06-30

PRIOR PLING DATE: 2001-01-30

PRIOR PL
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112 PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04 NUMBER OF SEQ ID NOS: 371 SOFTWARE: PALENTIN VEY. 2.0 SEQ ID NO 262 LENGTH: 48
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                                                                                                                                                                                                                                                                                                                                              Score 37; DB 9; Length 48; Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
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SEQ ID NO 36817
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                            Query Match 54.4
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                        TYPE: PRT
GRGANISM: Homo sapiens
US-09-774-639-282
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us-10-036-371-5.rapb

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LaVallie, Edward R.
Collins-Racie, Lisa A.
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                                    APPLICANT: C
APPLICANT: E
APPLICANT: M
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (79)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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| Patent No. US20202094953A1
| GENERAL INFORMATION |
| TITLE OF INVENTION NUCLEIC Acids, Proteins, and Antibodies |
| TILE OF INVENTION NUCLEIC ACIDS, Proteins, and Antibodies |
| TILE REFERENCE | PC008 |
| CURRENT APPLICATION NUMBER: US/09/764,860 |
| CURRENT FILING DATE: 2.001-01-17 |
| Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1198 |
| SOFTWARE: PatentIn Ver. 2.0 |
| SEQ ID NO 305
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CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
CTHER INFORMATION: EST_HUMAN HIT: BE063509.1, EVALUE 2.00e-04
US-09-864-761-46426
                                                                                                                                                                                                                                                                                                                                                                                       54.4%; Score 37; DB 10; Length 52; 63.6%; Pred. No. 7.8; tive 1; Mismatches 3; Indels
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 46426
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, Sequence 313, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
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                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
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US-09-764-860-305
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TYPE: PRT
ORGANISM: Homo sapiens
PEATUME:
OTHER INFORMATION: MAP TO AC009237.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HBLIOO, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 1.1
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PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PLING DATE: 2000-01-30
PRIOR PLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PLICATION NUMBER: US 09/608,408
PRIOR PLICATION NUMBER: US 09/74,203
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SCOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 33801
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Best Local Similarity 70.0
Matches 7; Conservative
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Search completed: February 12, 2003, 10:31:06 Job time : 2.9791 secs

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Gaps

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Human pancreatic c
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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GenCore version 5.1,3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                  908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                     OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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AAY99596
AAY33344
AAY9393
AAE07941
AAE07941
AAB98504
AAB98504
AAB98133
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1 IVNGEEAVPGSWPWQVSLQD 20
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Gapop 10.0 , Gapext
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length: 2000000000
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21 AAB11710 AAW2588 13 AAR2861 14 AAR28621 16 AAR84270 17 AAR860060 17 AAR860060 23 AAR8761759 17 AAR60062 17 AAR60062 18 AAR8761759 18 AAR8761750 18 AAR877750 18 AAR8761750 18 AAR877750 18 AAR877750 18 AAR8761750 18 AAR877750 18 AAR877750 18 AAR8761750 18 AAR877750 18 AAR877770 18 AAR877770 18 AAR877770 18 AAR87770 18 AAR87770 18 AAR87770 18 AAR87770 18 AAR8770 18 AAR87770 18 AAR8770 18 AAR8770 18 AAR8770 18 AAR8770 18 AAR8770 18	AAE0694 AAE0694 AAM01319 ABG6188 ABB9539 ABB9542 AAE1809
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ALIGNMENTS

RESULT 1

Amino terminal sequence of bovine trypsin B chain. AAB31578 standard; peptide; 20 AA (first entry) 20-APR-2001 AAB31578 AAB31578

Fish; serine proteinase; pain; acute inflammation; chronic inflammation; arthritis; inflamed joint; bursitis; osteoarthritis; septic arthritis; rheumatoid arthritis; juvenile rheumatoid arthritis; fibromyalgia; systemic lupus erythematosus; phlabitis; tendinitis; rash; psoriasis; acte; eczema; facial seborrheic eczema; foreskin infection; athlete's foot; fistulae infection; utcer; navel infection; wrinkle; scar; kelloid; boll; wart; allergic tich; hemorrhoid; wound; fungal infection; autoimmune disease.

Bos sp.

WO200078332-A2

28-DEC-2000.

15-JUN-2000; 2000WO-IS00005.

991S-0005086.

18-JUN-1999;

(BJAR/) BJARNASON J B.

Bjarnason JB,

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RESULT 3
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                                                                                                   The specification describes a fish serine proteinase. The proteinases care useful as medicaments, for treating and preventing a disease in a care useful as medicaments, for treating and preventing a disease in a compared to the protein arbititis, inflamed joints, bursatis, osteoarbritis, inflamed joints, bursatis, osteoarbritis, captic arthritis, invenie erythematosus, phlebitis, tendinitis, rash, care, eczema, facial seborrheic eczema, cacema of the hands, caceroriasis, acne, eczema, facial seborrheic eczema, escema of the hands, caceroriasis, or neck, foreskin infections, athlete's foot, fistulae infections, infections, or neck, foreskin infections in newborns, wrinkles, scars, infections in newborns, wrinkles, scars, infections in carecinom and immunological and autoimmune diseases. They are also useful for removing dead or pealing skin from otherwise healthy skin, and for treating or preventing a skin from otherwise healthy skin, and for treating or preventing a disease in which pathogenesis is caused by bacteria, virus, fungus, chalm. The present sequence represents the amino terminal of bovine trypsin B chalm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide with plasminogen activator activity useful as thrombolytic agent for treating blood clot disorders e.g. heart attack, comprises 10 amino acid peptide fragment for recognition or activation of plasminogen
                      Fish serine proteinase, useful as a cosmetic, medicament for treating eczema, psoriasis, arthritis, and in the manufacture of the medicament for treating, preventing pathogenic diseases involving receptor mediated binding
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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heart attack; stroke; blood clotting disorder.
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100.0%; Pred. No. 1.7e-09;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY99596 standard; protein; 245 AA
                                                                                        Disclosure, Page 5; 38pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                          1 IVNGERAVPGSWPWQVSLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine chymotrypsinogen A.
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-422975/36.
     WPI; 2001-091493/10.
                                                                                                                                                                                                                                                                                                                                   20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200032759-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY99596;
                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lin X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY99596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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The present sequence is bowine chymotrypsinogen. It was included in a review of sequence homologies of several plasminogen activators.

C a review of sequence homologies of several plasminogen activators.

C plasminogen is the principal servine processes yengen in the control of the plasmin of the principal servine processes. Its active form, plasmin, is control of the plasminogen activators which hydrolyse a peptide bond in plasminogen to convert it to plasmin or form tight binding complexes with plasminogen to convert it to plasmin or form tight binding complexes with plasminogen to spontaneously convert it to plasmin or form tight binding complexes with plasminogen to spontaneously convert it to plasmin or form tight binding complexes to plasminogen activation. This peptide is particularly useful when inserted between amino acid residues 644 and 645 of full length human control or plasminogen activation/recognition site of plasminogen activation/recognition site of plasminogen binding proteins.

The polypeptides are useful in preparing thrombolytic agents for treating blood clotting disorders such as heart attack.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multifunctional enzyme; treatment; acne; eczema; chymotrypain; trypsin; collagenase; elastase; exopeptidase; cell surface receptor; anti-acne; anti-achesion molecule; ICAM-1; CD4; ICAM-2; VCAM-1; CD4; ICB3; CD5; CD5; CD3; CD4; CD4; CD49; CD62; CD62; GM1 ceramide; krill; bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel method for treating acne and eczema using a krill-derived multifunctional enzyme (1) which comprises 2 or more of the activities of chymotrypain, trypsin, collagenase, elastase or exopeptidase and is reactive with cell surface receptors such as proteins or glycoproceins. The product of the invention have antiseborrheic, anti-acne, dermatological and anti-eczema activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating acne and eczema using a krill-derived multifunctional enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 245;
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100.0%; Pred. No. 2.7e-08;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine chymotrypsin N-terminal fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY33344 Btandard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0600273.
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95US-0486820.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-561004/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 AA;
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07-JUN-1995;
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Gaps

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Indels

97.3%; Score 109; DB 21; 95.0%; Pred. No. 4.6e-09; ive 1; Mismatches 0;

Query Match Best Local Similarity 95.03 Matches 19; Conservative

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The specification describes a method for preventing or ameliorating transplantation rejection reactions for transplantation of immune cells or other tissues. The method comprises treating a source of immune cells with a hydrolase or hydrolase mixture and administering the treated immune cells to a recipient animal. The hydrolase especially has a preference for removing, destroying, inactivating or disabling at least cone of CD4, CD8, CD25, CD29, ICD4, ICD52, OD152, an integrin, CD154, CD40 and CD80 in contrast to removing, destroying, inactivating or disabling TCR. The methods are useful for preventing graft versus host consistent of assabling at least to remove the cell surface adhesion contrast. The methods are useful for preventing or preventing or the diseases. The methods are used for treating or preventing cell-cell or cell-virus adhesion syndrome comprising inflammation, shock, the contrast and disease, transplantation rejection contrast. The methods are used for treating or preventing cell-cell or cell-virus adhesion syndrome comprising inflammation, shock, the actions or microbial infections. The present sequence represents the contrast.
                                                                                                                                                                                                                                                                                                                                                                        ö
(1) removes or inactivates cell surface receptors (proteins and glycoproteins) and adhesion molecules such as ICAM-1 (i.e. CD54), ICAM-2, VCAM-1, CD4, CD5, CD22, CD29, CD3, CD5, CD5, CD10, CD4, CD5, CD5, CD10, CD4, CD5, CD10, CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transplantation rejection; hydrolase; graft versus host disease; cell surface adhesion molecule; immune reaction; inflammation; shock; tumour metastasis; autoimmune disease; Krill derived multifunctional enzyme.
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preventing or ameliorating transplantation rejection reactions using
                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                    Length 20;
                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal of a bovine chymotrpsin hydrolase enzyme.
                                                                                                                                                                                                                                                                                   97.3%; Score 109; DB 20;
95.0%; Pred. No. 4.6e-09;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 26; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY93935 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          1 IVNGEEAVPGSWPWQVSLQD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                (PHAI-) PHAIRSON MEDICAL INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Franklin RL, St Pierre Y;
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                  Local Similarity
es 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-452301/39,
                                                                                                                                                                                                                             20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydrolase enzymes
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                                                                                                                                                                invention
                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                   Query Match
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therapy; graft versus host disease; transplantation rejection; autoimmune disease; microbial infection; immune disease; microbial infection; immune disease; cytostatic; cystic fibrosis; circuit obstructive pulmonary disease; Copb; atheroscierosis; cancer; asthma; septic shock; toxic shock syndrome; conjunctivitis; reperfusion injury; pain; immunosuppressive; antibacterial; vasotropic; bovine.

95US-0385540, 95US-0486820, 96US-0600273,

08-FEB-1996;

98US-0220731

24-DEC-1998; 08-FEB-1995;

US6232088-B1

Bos sp.

15-MAY-2001,

(PHAI-) PHAIRSON MEDICAL INC

St Pierre Y;

Franklin RL,

WPI; 2001-450051/48.

Multifunctional hydrolase, rejection reaction, extra-corporeal, therapy, graft versus host disease, transplantation rejection, autoimmune disease, microbial infection; immune disease, microbial infection; immune disease.

N-terminal of bovine serine multifunctional hydrolase.

(first entry)

01-NOV-2001

AAE07941;

AAE07941 standard; peptide; 20 AA.

1 IVNGEDAVPGSWPWQVSLQD 20

1 IVNGEEAVPGSWPWQVSLQD

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                                                                                                                                                                                                                                                                                                                                                                                                                                       Ameliorating, preventing or treating immune rejection reactions, such as graft versus host disease, autoimmune disease, asthma, cancer, by extra-corporeally treating donor tissue with hydrolase such as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 109; DB 22; Length 20;
Pred. No. 4.6e-09;
1; Mismatches 0; Indels
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Matches 19; Conservative
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                                                                                                                                                                                                                                              detection, diagnosis, identification; cytostatic, neuroprofective; neotropic; immunomodulatory; relaxant; contraceptive; gynaecological; antinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC98773 to AAC99231 encode the human pancreatic cancer associated
                                                                                                                                                                                                    Human pancreatic cancer antigen protein sequence SEQ ID NO:643.
                                                                                                                                                                                                                                 Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 146;
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Pred. No. 4.1e-08;
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                                                                                                               AAB54191 standard; Protein; 146 AA
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      1 IVNGEEAVPGSWPWQVSLQD 20
                           08-MAR-2000; 2000WO-US05989
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                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM;
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Best Local Similarity
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                                                                                                                                                                             09-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                 AAB54191;
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                                                                                                       AAB5419
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TADG-15 is an extracellular serine protease. It was found that TADG-15 is over-expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20 residues that lack TADG-15 protease activity are useful for vaccinating an individual against TADG-15, having, suspected of having or at risk of getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic or therapoutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel extracellular serine protease, termed tumor antigen-derived gene
15 protein overexpressed in carcinomas and DNA encoding it, for
diagnosis, treatment, prevention of cancer, particularly breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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                                                                                                                                                                                                                                                                                                                                                                          Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer; tumour antigen-derived gene 15; serine protease; chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                  Human chymotrypsin serine protease catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of novel human protease #37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.3%; Score 109; DB 22;
95.0%; Pred. No. 6.8e-08;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU82738 standard; Protein; 263 AA.
                                                                                                                                                                                                   AAB98504 standard; Protein; 231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 10; Fig 1; 130pp; English.
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                                                                                   57
                                          IVNGEEAVPGSWPWQVSLQD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-OCT-2000; 2000WO-US29095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0421213.
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                                                                     38 IVNGEDAVPGSWPWQVSLQD
                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tanimoto H;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYAR-) UNIV ARKANSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-381031/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200129056-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ношо варіелв.
                                                                                                                                                                                                                                                                                            03-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Brien TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU82738;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                   AAB98504;
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Matches
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                                                                                                                                                           RESULT 7
                                                                                                                                                                                       AAB9850.
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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and diseases.

C cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. disbetes, obesity), inflammatory constructions are also diseases, metabolic disorders (e.g. rheumatoid archritis and psoriasis), central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypertension, psychotic disorders, neurological disorders, hypertension, psychotic disorders, neurological disorders, and dyskinesias.

C priphers sideses, parkinson's disease) and dyskinesias.

The nucleic acids and polypeptides are also useful for treating viral confections caused by human immunodeficiency virus (HIV), and non-viral conference in infections such as ocular disease (e.g. glaucoma) and macular characters.
                  Human, protease, cancer, immune-related disorder, cardiovascular disease, neuronal-associated disease, metabolic disorder, inflammatory disorder, nervous system disorder, sexual dysfunction, pain, mood disorder, hypertension, psychotic disorder; neurological disorder; dyskinesia, viral infection; human immunodeficiency virus, HIV, non-viral infection; ocular disease, cytostatic, enzyme.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BSSP5; serine protease; human; hBSSP5; mouse; mBSSP5; brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.3%; Score 109; DB 23; Length 26
95.0%; Pred. No. 7.8e-08;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse serine protease BSSP5 (mBSSP5) SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB11711 standard; Protein; 264 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Fig 2M; 313pp; English.
                                                                                                                                                                                                                                                                   26-JUN-2001; 2001WO-US20171.
                                                                                                                                                                                                                                                                                                        26-JUN-2000; 2000US-214047P.
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Les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-139913/18.
N-PSDB; ABK31780.
                                                                                                                                                                                                                                                                                                                                              SUGE-) SUGEN INC.
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                                                                                                                                                                                          WO200200860-A2.
                                                                                                                                                                                                                                                                                                                                                                                  Plowman G, W
Charydczak G;
                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                             03-JAN-2002.
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6
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The invention relates to novel serine proteases designated BSSPS (AAB11710-B11711), and to nucleic acids encoding them (AAA61733-A61734). The invention also relates to vectors and transformants comprising BSSPS nucleic acids; transgenic animals in which the expression level of BSSPS can be varied; and an mBSSPS knockout mouse. The invention additionally components and methods of production of such antibodies, methods of BSSPS detection using the antibodies, and the antibodies, and the antibodies and medical conditions, e.g., pancreatitis. A method for detecting pancreatitis comprising measuring BSSPS concentration in the blood or cinie, and a pancreatitis diagnostic agent containing an anti-BSSPS cuting, and a pancreatitis diagnostic agent containing an anti-BSSPS cuting antibody is also disclosed. Nucleotides encoding BSSPS were initially isolated in a human brain cDNA library using degenerate PCR primers (AAA6144-A6145) based on conserved regions of serine proteases and nucleotides encoding them are useful in detecting homologues, mutants and polymorphic variants in biological conserved regions of serine proteases and signostic markers for conditions such as apparerant and sequence AAB11710 represents channed by pancreatitis and prostatic hypertrophy. Sequence AAB11710 represents channed by mutances.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
epllepsy; cancer; inflammation; infertility; pancreatitis;
prostatic hypertrophy.
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                                                                                                                                                                                                                                                                                                                                                                                   Serine proteases BSSP5, useful in detecting homologs, mutants and polymorphic variants as markers for diagnosis of e.g. Alzheimer's disease, epilepsy, cancer and inflammation, using blood, urine, pancreas or other tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.5%; Score 107; DB 21; Length 264; 95.0%; Pred. No. 1.5e-07; cive 0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                               Yamaguchi N, Mitsui S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 55-56; 70pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB54077 standard; Protein; 192 AA.
                                                                                                                                                                                                                                                                                             Uemura H, Okui A, Kominami K,
                                                                                                                                                                                  99WO-JP06473.
                                                                                                                                                                                                                    98JP-0347806.
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                                                                                                                                                                                                                                                                                                                             WPI; 2000-400058/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 AA;
                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA61734
                                                                                                        WO200031243-A1.
                                                                                                                                                                              19-NOV-1999;
                                                                                                                                                                                                                  20-NOV-1998;
                                                                                                                                              02-JUN-2000.
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AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to proteins, called pancreatic cancer antigens have cytostatic.

AAB54466. The human pancreatic cancer antigens have cytostatic.

Chab54466. The human pancreatic cancer antigens have cytostatic.

Chab54466. The human pancreatic cancer antigens be used for carcer therapy. The polymucleotide and proteins can be used for in gene therapy. The polymucleotide and proteins can be used for cancer antigens can be identified. The pancreatic cancer antigens can be used to proteins and hand antagonists to the antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer. The pancreatic cancer antigens can be used to pancreatic cancer antigens can be used to design nucleic pancreatic cancer antigen polymucleotides can be used to design nucleic and hybridisation probes that can be used in chromosome mapping, linkage and harding methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in viro diagnostic and therapoutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or reproductive, gastrointestinal, pulmonary, cardiovascular, renal or professore.

Cr prodictive, gastrointestinal, pulmonary, cardiovascular, renal or prepresent in vivo and isorders. AAC99240 and AAB54467 respecent
detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences used in the exemplification of the present invention.
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Best Local Similarity 90.0%; Pred. No. 3e-06;
Matches 18; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 966; 1379pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB11710 standard; Protein; 264 AA
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                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                              08-MAR-2000; 2000WO-US05989.
                                                                                                                                                                                                                                                                                                                                             99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-579444/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAC98842.
                                                                                                                                                                                                            WO200055320-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-2000
                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                               12-MAR-1999;
                                                                                                                                                                                                                                                      21-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA,
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The invention relates to novel serine proceases designated BSSP5

(AAB1710-B1711), and to nucleic acids encoding them (AAA61733-A61734).

(AAB1710-B1711), and to nucleic acids encoding them (AAA61733-A61734).

The invention also relates to vectors and transformants comprising BSSP5

Thucleic acids; transgenic animals in which the expression level of BSSP5

can be varied; and an mBSSP5 knockout mouse. The invention additionally

encompasses anti-BSSP5 antibodies and methods of production of such

antibodies, methods of BSSP5 detection using the antibodies, and the

use of BSSP5 proteins or fragments as diagnostic markers for certain

medical conditions, e.g., pancreatings a diagnostic markers for certain

medical conditions, e.g., pancreating BSSP5 concentration in the blood or

pancreatitis comprising measuring BSSP5 concentration in the blood or

contine, and a pancreatitis diagnostic agent containing an anti-BSSP5

urine, and a buman brain cDNA library using degenerate PCR primers

isolated in a human brain cDNA library using degenerate PCR primers

ESSP5 serine proteases and nucleotides encoding them are useful in

BSSP5 serine proteases and nucleotides encoding them are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detecting homologues, mutants and polymorphic variants in biological samples (e.g., blood, urine, brain, prostate gland, placente, testis, pancreas and spleen) as diagnostic markers for conditions such as Alzheimer's disease, epilepsy, cancer, inflammation, infertility, pancreaticis and prostatic hypertrophy. Sequence AAB11710 represents human BSSP5 (HBSSP5), and sequence AAB11711 represents murine BSSP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
      BSSP5, serine protease; human; hBSSP5; mouse; mBSSP5; brain; diagnostic marker; antibody; transgenic animal; Alzheimer's disease; epilepsy; cancer; inflammation; infertility; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine proteases BSSP5, useful in detecting homologs, mutants and polymorphic variants as markers for diagnosis of e.g. Alzheimer's disease, epilepsy, cancer and inflammation, using blood, urine, pancreas or other tissues
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                                                                                                                                                                                                                                                                                                                                               MitBui S;
                                                                                                                                                                                                                                                                                                                                                   Yamaguchi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 51-52; 70pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW02588 standard; peptide; 31 AA.
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                                                                                                                                                                                                                                                                                                                                                     Kominami
                                                                                                                                                                                                                                99WO-JP06473.
                                                                                                                                                                                                                                                                        20-NOV-1998; 98JP-0347806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IVNGEEAVPGSWPWQVSLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 IVNGENAVLGSWPWQVSLQD
                                                                                                                                                                                                                                                                                                             (FUSO ) FUSO PHARM IND LTD.
                                                                        prostatic hypertrophy.
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-400058/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
hes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                       Okui A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA61733.
                                                                                                                                                        40200031243-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-FEB-1997
                                                                                                                                                                                                                                  19-NOV-1999;
                                                                                                                  Homo sapiens
                                                                                                                                                                                             32-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW02588
                                                                                                                                                                                                                                                                                                                                                       Uemura H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Gaps

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AAR29621 standard; Protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                              Porcine pancreatic elastase III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 8; 10pp; Japanese.
                                                                                                                                 Claim 2; Page 8; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           liver function improvers; ss.
         02-DEC-1985; 85JP-0271128.
                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                               1 VVNGEDAVPYSWPWQVSLQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91JP-0092069,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91JP-0092069
                                                                                                                                                                                                                                                                                                                                                          30-APR-1993 (first entry)
                                                                                                                                                                                                                                                 1 IVNGEEAVPGSWPWQVSLQ
                                              Tani T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SANY ) SANKYO CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa domestica.
                                                                           WPI; 1986-280300/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-428826/52.
                          (SANY ) SANKYO KK
                                                                                                                                                                                            242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 AA;
                                                                                  N-PSDB; AAN60075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ31724
                                              Takiguchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                JP04325090-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-NOV-1992.
                                                                                                                                                                                            Sequence
                                                         Ohsumi J;
                                                                                                                                                                                                                                                                                                                                        AAR29621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        improvers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                  RESULT 14
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                                                                                                                                                                                                                                                            AAW02588 is the N-terminal portion of a factor derived from pig pancreatic tissue. The factor was designated PX. PX inhibits the action of osteoclasts and stimulates the action of osteochlasts, hence PX inhibits bone resorption and stimulates bone formation. The mew factor also stimulates the proliferation of human MG-63 osteochast-like cells). The factor is useful for treating bone class of oute to osteochorosis or Paget's disease. The factor may also be used to hasten bone fracture repair. Antibodies osteoblastic of PX can be used to treat osteopetrosis and such bodies.
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
         Pig; bone; calcium; resorption inhibition; formation; osteoporosis; Paget's disease; fracture repair; bone defect; osteopetrosis; metastasis; osteoblast; osteoclast.
                                                                                                                                                                                                   New isolated pancreatic-derived factor - which inhibits bone resorption and increases bone formation, used to develop prods. for diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                          Score 93; DB 17; Length 31;
Pred. No. 1.5e-06;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of human pancreatic elastase IIIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enzyme, serum lipoprotein metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP60061 standard; Protein; 242 AA.
                                                                                                                                                                  Yoneda T;
                                                                                                                                                                                                                                          Claim 1; Fig 14; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          83.0%;
84.2%;
                                                                                                        95WO-US16826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85JP-0236686,
85JP-0072308,
85JP-0091986,
85JP-0163964,
                                                                                                                          94US-0363092
                                                                                                                                                                                                                                                                                                                                                                                                                            1 IVNGEEAVPGSWPWQVSLQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VVNGEDAVPYSWPWQVSLQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86EP-0302557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           16; Conservative
                                                                                                                                                               Izbicka E, Mundy GR,
                                                                                                                                            (OSTE-) OSTEOSA INC.
                                                                                                                                                                                 WPI; 1996-309523/31.
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      31 AA;
                                                                                                      19-DEC-1995;
                                                                                                                          20-DEC-1994;
                                                                 WO9619501-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1985;
05-APR-1985;
27-APR-1985;
26-JUL-1985;
                                                                                    27-JUN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                               Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-0CT-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP198645-A.
                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP60061;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pig; swine; bile acid; gall bladder; bile acid secretion promoters;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents pordine pandreatic elastase III. It was expressed in E. coli YA21 using the expression vector pELEGO1. It may be used in bile acid secretion promoters and liver function
                                                                                                                                                                                                                                                                                                                The genetically engineered prod. can eliminate the dependency on human pancreas supplies for the elastase, and avoids antibody formation and possibility of anaphylaxis using porcine elastase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                     New genetically engineered human pancreatic elastase - obtd.
using hosts modified DNA coding for enzyme
         Ohmine T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pig pancreas elastase protein - used in bile acid secretion promoters and liver function improvers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.0%; Score 93; DB 13; Length 253; 84.2%; Pred. No. 1.5e-05; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
83.0%; Score 93; DB 7; Length 242
Best Local Similarity 84.2%; Pred. No. 1.5e-05;
Matches 16; Conservative 2; Mismatches 1; Indels
      Eurukawa H,
Kawashima I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serum calcium lowering factor obtd. from rat pancreas - useful as drug for treatment of various bone disease e.g. osteoporosis, hyperthyroidism and hypercalcaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serum calium lowering factor; rat; pancreas; calcium; mouse; bone disease; osteoporosis; primary hyperthyroidism; continuous hyperthyroidism; hypercalcaemia; malignant tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

80.4%; Score 90; DB 16; Length 29;
Best Local Similarity 78.9%; Pred. No. 3.8e-06;
Matches 15; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serum calcium lowering factor N-terminal sequence.
                                                                                                                                                                                                                                                        AAR84270 standard; peptide; 29 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 2; 6pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94JP-0027578.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHUS ) CHUGAI PHARM CO LTD.
11-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-317483/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattue rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP07215997-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-AUG-1995.
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                                                                                                                                                                                                                                                                                                                                                AAR84270;
                                                                                                                                                                                           RESULT 15
AAR84270
XX
AAR84
XX
AAR84
DT 11-AP
DT 11-AP
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Search completed: February 12, 2003, 10:22:26 Job time : 14.4328 secs

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OM protein - protein search, using sw model
Run on: February 12, 2003, 10:17:50; Search time 5.01493 Seconds
(without alignments)
12 (without alignments)
11 (without alignments)
12 Sequence: 11 IVNGEAVPGSWPWQVSLQD 20
Scoring table: BLOSUM62

Scoring table: BLOSUM62

Scoring table: Alosum62

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224
Minimum DB seq length: 0
Maximum DB seq length: 0
Maximum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

	Description	- ') L) H) E) E	Chymotrypsin (EC 3	4 C	Chimotrimein D n	, ,	Chymotrypein (EC)			elasta	pancieatic elastas	parametric proceruage	elasta	elasta	c elasta	panciedus elastas	, ,			polyment after	POLYPIOCEIN - ALLI	3 (ACLOSIII (SC. 3.4.41	Procarpoxypeplinas	Chimotramoia (FC 3.4.21	٠, ۲
SUMMARIES	ΩI	KYBOA	KYBOR	A21195	A31299	KYRTB	B61333	A23473	872219	138136	847537	B33257	B29934	A29934	PU0036	B26823	ELRT2	A26823	A25528	J01473	C26823	568826	568825	T30337	829599	802176	CPBOA3	A34170	A61529	T30338
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	Query Match Length	245	245	263	263	263	20	126	244	264	263	31	270	270	23	269	271	269	271	268	269	268	268	1524	421	37	240	415	28	1004
240	Ouery Match	100.0	97.3	97.3	97.3	96.4	91.1	87.5	87.5	86.6	85.7	83.0	83.0	78.6	76.8	76.8	75.0	74.1	74.1	73.2	72.3	71.4	71.4		۲.	67.0	Š.	5.	64.3	۲,
	Score	112	0	109	0	0	102	98	96	97	96	93	93	88	98	98	84	83	83	82	81	80	80	77	16	75	73	73	72	70
	Result No.		7	m	4	Ś	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

ore pitalogenolation	acrossin (EC 3 4 21		actobili (EC 3.4.21	ACTOSIN (EC 3.4.21	prasma Kallikrein	pancreatic elastas	moot ool toom	٠	_	tryptase (EC 3.4.2		Lryptdse (EC 3.4.2	-1	٦ .	tryptase (EC 3.4.2	cryptase (br 3.4.2
A34817	A37344	A55083	7X0172	KOMSDI	233787	A2369A	856160	A45754	12.62.4	23563	735863	S47528	148685	A47246	JC4171	1
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20	418	420	436	638	20	25	270	274	275	275	275	431	230	273	274	
61.6	61.6	61.6	61.6	61.6	60.7	60,7	60.7	60.7	60.7	60.7	60.7	60.7	59.8	59.8	59.8	
69	69	69	69	69	89	68	68	68	89	89	68	68	67	67	67	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

C.Comment: Tryptic cleavage after Arg-15 results in a fully active enzyme (pi-chymotryps)

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chymotrypsin (EC 3.4.21.1) precursor - human chymotrypsin (EC 3.4.21.1) precursor - human chymotrypsin (EC 3.4.21.1) precursor - human cipacides Homo mappiens (man) (C.Date: 08-Jun-1989 #sequence_revision 08-Jun-1989 #sequence_revision 08-Jun-1989 (C.Date: 08-Jun-1989 #sequence (B.Jun-1989 M.; Izumoto, Y.; Horil, A.; Doi, S.; Yokouchi, H.; Ogawa, M.; Mori, T.; Matsuba Biochem. Biophys. Rec Commun. 158, 569-575, 1989 A; Attle: Molecular cloning and nucleotide sequence of human pancreatic prechymotrypsinoge A; Reference number: A31299; MUID:89134264; PMID:2917002 A; Accession: A31299 A; Muid: PMID:2917002 A; Molecule type: mRNA A; Mesidues: 1-263 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Bell, G.I.; Quinto, C.; Quiroga, M.; Valenzuela, P.; Craik, C.S.; Rutter, W.J. J. Biol. Chem. 259, 14265-14270, 1984
A;Title: Isolation and sequence of a rat chymotrypsin B gene.
A;Reference number: A22658; MUID:85054881; PMID:6209274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NiAlterrate names: chymotrypsinogen B
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:K02298; NID:g203653; PIDN:AAA98732.1; PID:g203654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: M24400; NID: g181189; PIDN: AAA52128.1; PID: g181190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AjIntrons: 18/1; 52/3; 79/2; 105/3; 166/1; 210/3
CjSuperfamily: trypsin; trypsin homology
CjSuperfamily: trypsin; trypsin; trypsin; homology
CjSuperfamily: trypsin; trypsin; trypsin; pandicted digestion; serine proteinase
CjSuperfamily: signal sequence #status predicted <SIG>
P;1-18/Domain: signal sequence #status predicted <SIG>
P;1-33/Domain: propeptide #status predicted <PRO>
P;34-263/Porduct: cjMmotrypsin B #status predicted <MAT>
P;34-256/Domain: trypsin homology <TRY>
P;75,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.4%; Score 108; DB 1; Length 263; 90.0%; Pred. No..1.5e-08; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-reference; GDB:119820; OMIM:118890
A;Map position: 16q23.1-16q23.1
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase
F;34-256/Domain: trypsin homology <TRY>
F;75,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

97.3%; Score 109; DB 2;
Best Local Similarity 95.0%; Pred. No. 1e-08;
Matches 19; Conservative 1; Mismatches 0;
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81333
chymotrypain (EC 3.4.21.1) - edible frog (fragment)
C;Species: Rana esculenta (edible frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chymotrypsin (EC 3.4.21.1) B precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
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Best Local Similarity 90.00
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: CTRB1; CTRB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Accession: A22658
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Chymotrypsin (EC 3.4.21.1) B precursor - bowine

Chymotrypsin (EC 3.4.21.1) B precursor - bowine

Chymotrypsin (EC 3.4.21.1) B precursor - bowine

NiAlternate names: chymotrypsinogen B

C;Species: Bos primigenius taurus (cattle)

C;Date: 08-Oct-1981 #sequence_revision 08-Oct-1981 #text_change 18-Jul-1997

C;Date: 08-Oct-1981 #sequence_revision 08-Oct-1981 #text_change 18-Jul-1997

C;Accession: No0953

R;Smillie, L.B.; Furka, A.; Nagabhushan, N.; Stevenson, K.J.; Parkes, C.O.

Nature 218, 343-346, 1968

A;Reference number: A00953; MUD:68238908; PMID:5649671

A;Reference number: A00953; MUD:68238908; PMID:5649671

A;Accession: A00953

A;Molecule type: protein

A;Residues: 1-45 <SMI>

C;Comment: The first activation cleavage, leading to pi-chymotrypsinogen A, in the scirc;Comment: The first activation cleavage, leading to pi-chymotrypsin B, occurs in the scirc;Comment: The first activation cleavage, leading to pi-chymotrypsin B, occurs in the scirc;Comment: The first activation cleavage, leading to pi-chymotrypsin B, occurs in the scirc;Comment: propeptide #status experimental <PRO>

F;1-15/Domain: propeptide #status experimental <AR>

F;1-122,42-58,136-201,168-182,191-220/Disulfide bonds: #status experimental

F;57,102,195/Active site: His, Asp, Ser #status experimental
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C;Species: Canis lupus familiaris (dog)
C;Species: 7-011-1990 #sequence_revision 27-Jul-1990 #text_change 22-Jun-1999
C;Accession: A21195
R;Pinsky, S.D.; LaForge, K.S.; Luc, V.; Scheele, G.
C;Accession: A21195
R;Pinsky, S.D.; LaForge, K.S.; Luc, V.; Scheele, G.
R;Pinsky, S.D.; LaForge, K.S.; MUS. 84866
A;Reference number: A21195; MUD:84170253; PMID:6584866
A;Reference number: A21195
A;Residuasion: A21195
A;Residuasion: A21195
A;Residuasion: A21195
A;Residuasion: A21195
A;Residuasion: A21195
A;Cross-references: GB:KO1173; NID:g163945; PIDN:AAA30841.1; PID:g163946
C;Superfamily: trypsin; trypsin; trypsin; digetion; serine proteinase
F;Sydowachase; protein digetion; serine proteinase
F;34-256/Domain: trypsin homology aTRY:
F;75,120,213/Active site: His, Asp, Ser #status predicted
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C,Species: Canis lupus familiaris (dog)
C,Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 22-Jun-1999
F;16-238/Domain: trypsin homology <TRY>
F;1-122,42-58,136-201,168-182,191-220/Disulfide bonds: #status experimental
F;57,102,195/Active site: His, Asp, Ser #status experimental
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                                                                                                                                           Length 245;
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Best Local Similarity 100.0%; Pred. No. 3.5e-09;
Matches 20; Conservative 0; Mismatches 0;
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pancreatic elastase (EC 3.4.21.36) III - pig (fragment)
NyAlternate names: proteinase E
CiSpecies: Sus scrofa domestica (domestic pig)
CiSpecies: Sus scrofa domestica (domestica pig)
CiSpecies: Sus scrofa domestica (domestica pig)
CiSpecies: Sus sus scrofa domestica pig)
CiSpecies: Sus sus scrofa domestica pig)
Biochem: Biophys: Res. Commun. 163, 1191-1164, 1989
A;Title: Generation of a subunit III-11ke protein by autolysis of human and porcine propi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chymotrypsin (EC 3.4.21.1) precursor - Atlantic cod
C;Species: Gadus morhua (Atlantic cod)
C;Deteise: Gadus morhua (Atlantic cod)
C;Deteise: Gadus morhua (Atlantic cod)
C;Deteise: Schoec-1994 Hesquence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: 847537; 843163
R;Gudmundsdottir, A.; Oskarsson, S.; Eakin, A.E.; Craik, C.S.; Biarnason, J.B.
Biochim. Biophys. Act 1219, 211-214, 1994
A;Title: Atlantic cod cDNA encoding a psychophilic chymotrypsinogen.
A;Reference number: 847537; MUD:94368860; PMID:8086467
A;Accession: 847537
A;Molecule type: mRNA
A;Residues: 1-263 <GUD>
A;Cross-references: EMBL:X78490; NID;9468750; PIDN:CAA55242.1; PID:9468751
C;Keywords: hydrolase; protein digestion; serine proteinase
C;Keywords: hydrolase; protein digestion; serine proteinase
F;1-18/Domain: signal sequence #status predicted <ALT>
F;34-256/Domain: trypsin homology <TRY>
F;75,120,213/Active site: His, Asp, Ser #status predicted
                                                       chymotrypsin-like proteinase (BC 3.4.21.-) CTRL-1 - human C.Sepchase Homos sapiens (man)
C.Sechases Homos sapiens (man)
C.Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 22-Jun-1999
C.Accession: 138136
R.Larsen, F., Sohledm, J.; Kristensen, T.; Kolsto, A.B.; Prydz, H. Hum. Mol. Genet. 2, 1599-1599, 1993
A.Title: A Light cluster of five unrelated human genes on chromosome 16q22.11.
A.Reference number: 138135; MUID:94093544; PMID:8268911
                                                                                                                                                                                                                                                                                                                                      A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-264 <RES>
A,Cross-references: EMBL:X71874; NID:g406226; PIDN:CAA50710.1; PID:g406228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.6%; Score 97; DB 2; Length 264; 90.0%; Pred. No. 6.3e-07; Live 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Map position: 16922.1-16922.1
A;Introns: 18/1; 52/3; 79/2; 106/3; 167/1; 211/3
C;Superfamily: trypsin; trypsin; trypsin; trypsin; homology
C;Kywords: hydrolase; serine proteinase
F;34-257/Domain: trypsin homology <TRY>
F;75,121,214/Active site: His, Asp, Ser #status predicted
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nes 18; Conservative
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                    C. Accession: B6133
R.Pies, W.; Zwilling, R.; Woodbury, R.G.; Neurath, H.
E. Pies, W.; Zwilling, R.; Woodbury, R.G.; Neurath, H.
E. PESS Lett. 109, 45-49, 1980
A. Tittle: Amino-terminal amino acid sequences and the evolution of frog (Rana esculenta)
A. Reference number: A61333 MUID:8013255; PMID:6965480
A. Reference number: A61333
A. Molecule type: protein
A. Residues: 1-20 < PIE>
C. Superfamily: trypsin homology
C. Keywords: hydrolase; protein digestion; serine proteinase
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C;Species: Gadus morhua (Atlantic cod)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Aug-1998
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Aug-1998
C;Accession: S7219
Biochim. Biophys. Acta 1297, 49-56, 1996
A;Title: Structure of chymotrypsin variant B from Atlantic cod, Gadus morhua.
A;Reference number: S72219; MUID:96439045; PMID:8841380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chymotrypsin-like proteinase (EC 3.4.21.-) - pig (tentative sequence) (fragments) N.Alternate names: pancreatic elastase II [misidentification] C.Species: Sus scrofa domestica (domestic pig) C.Bate: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000 C.Accession: A23473 R.Vered, M.; Gertler, A.; Burstein, Y. Int. J. Pept. Protein Res. 27, 183-190, 1986 A.;Reference number: A23473; MUID:86194934; PMID:3634756
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Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
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70.0%; Pred. No. 2e-07;
Live 6; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                       91.1%; Score 102; DB 2; Length 20 90.0%; Pred. No. 6.6e-09; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1-126 <VER>
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14;15-244 <LET>
C;Superfamily: trypsin; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;15-237/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IVNGEEAVPGSWPWQVSLQD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IVNGENAVPGSWPWQVSLQN 20
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nes 18; Conservative
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Best Local Similarity 94.77
Matches 18; Conservative
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Matches 14; Conserv
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Matches
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ecrime proteinase (EC 3.4.21..) - bovine (fragment)
NyAlternate names: trypsin-like proteinase bPTLP
NyAlternate names: trypsin-like proteinase bPTLP
C;Species: Bos prinigenius taurus (cattle)
C;Species: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 22-Apr-1995
C;Accession: PU0036; PU0039
C;Accession: PU0036; PU0039
C;Accession: A; Batylama, K; Bdazawa, K; Nagata, K; Sasaki, Y; Nagamune, H; Matsuda, Y submitted to JPRID, September 1994
A;Description: Purification and characterization of a novel serine proteinase from bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pancreatic elastase (EC 3.4.21.36) IIIA precursor - human pancreatic elastase (EC 3.4.21.36) IIIA precursor - human N.Alternate names: protease E C; Species: Homo sapiens (man) C; Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change_20-Jun-2000 C; Accession: A29344, JX0045 R; Ax Tani, T.; Ohsumi, J.; Mita, K.; Takiguchi, Y. J. Biol. Chem. 263, 1231-1239, 1988 A; Title: Identification of a novel class of elastase isozyme, human pancreatic elastase JA; Reference number: A92664; MuID:080087253; PMID:2826474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1.270 c.TAN>
A; Cross-references: GB:003516
R; Shirasu, Y.; Takemura, K.; Yoshida, H.; Sato, Y.; Itjima, H.; Shimada, Y.; Mikayama, T
J. Biochem. 104, 259-254, 1988
A; Fitle: Molecular cloning of complementary DNA encoding one of the human pancreatic prot
A; Reference number: JX0045; MUID:89034017; PMID:2460440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: JX0045
A;Molecule type: mRNA
A;Residues: 1-240, GY,242-270 <SHI>
A;Cross-references: GB:D00306; NID:g220013; PIDN:BAA00212.1; PID:g220014
C;Comment: This enzyme is an alanine-specific serine proteinase that has little elastolyt
                          Cycoperfamily: trypsin, trypsin, homology
Cykeywords: glycoprotein; hydrolase; serine proteinase; zymogen
E;1-17Domain: adgmal sequence #status predicted <SIG>
F;1-17Domain: activation peptide #status predicted <ACT>
F;18-28/Domain: activation peptide #status predicted <ACT>
F;29-270/Product: (or 31-270) pancreatic elastase IIIB #status predicted
F;29-263/Domain: trypsin homology <TRY>
F;29-263/Domain: trypsin homology <TRY>
F;31-123,121/Active site: His, Asp, Ser #status predicted
F;13,123,127/Active site: Carbohydrate (Asn) (covalent) #status experimental
F;153/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Victions 15/1; 43/3; 76/2; 121/2; 167/1; 214/3; 265/3
C; Superfamily: trypsin, trypsin homology
C; Superfamily: trypsin, trypsin homology
C; Style bydrolase; pancreas; serine proteinase
C; Style bydrolase; pancreas; serine predicted <SIG>
F; 1-15/Domain: signal sequence #status predicted <PRO>
F; 2-270/Product: pancreatic elastase IIIA #status experimental <MAT>
F; 29-263/Domain: trypsin homology <TRY>
F; 73,123,217/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                             Score 93; DB 2; Length 270;
Pred. No. 2.5e-06;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVNGEEAVPGSWPWQVSLQ 19
A;Residues: 94-128;132-164 <WEN>
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Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Conservative
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C;Genetics:
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Matches
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B2931
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PEBS Lett. 249, 275-278, 1989
A;Title: Localization and characterization of the glycosylation site of human pancreatid A;Reference number: S04490; MUID:8928996; PMID:2737288
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                                                                                                                                                                                                                                                                                                            Length 31;
       A;Reference number: A33257; MUID:89392022; PMID:2675835
A;Accession: B33257
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-31 <AVI>C;Superfamily: trypsin; trypsin; homology
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                        Score 93; DB 2; I
Pred. No. 2.3e-07;
2; Mismatches 1;
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84.2%;
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Best Local Similarity 84.2'
Matches 16; Conservative
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A,Molecule type: protein
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Search completed: February 12, 2003, 10:28:52 Job time : 6.01493 secs
                                 29 VVGGEEARPNSWPWQVSLQ 47
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A; Residues: 1-269 cKAW
A; Residues: 1-269 cKAW
A; Residues: 1-269 cKAW
A; Cross-references: GB:MA652; NID:g182057; PIDN:AAA52380.1; PID:g182058
B; Cross-references: GB:MA652; NID:g182057; PIDN:AAA52380.1; PID:g182058
B; Crotemistry 26, 7256-7261, 1987
A; Title: Primary structure of human pancreatic elastase 2 determined by sequence analysis A; Reference number: A27432; MUID:88107669; PMID:3427074
A; Recidues: 1-269 cFLE>
A; Residues: 1-269 cFLE>
A; Residues: 1-269 cFLE>
A; Residues: 1-269 cFLE>
A; Residues: 1-269 cFLE>
A; Rolecule type: mRNA
A; Residues: 1-269 cFLE>
A; MUID:88198076; PMID:2834346
A; Cross-reference number: A41431; MUID:88198076; PMID:2834346
A; Residues: 1-201, VV, 203-269 cSHI>
A; Residues: 1-201, VV, 203-269 cSHI
A; Residues: 201, 179-183, 1990
A; Reference number: S08253; MUID:90169111; PMID:2307232
A; Residues: 1-201, VV, 201-201, VV, 201-
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: B2682; A27432; A1431; S34491
C;Accession: B2682; A27432; Aimoda, K.; Takiguchi, Y.
R;Kawashima, I.; Tani, T.; Shimoda, K.; Takiguchi, Y.
A;Title: Characterization of pancreatic elastase II cDNAs: two elastase II mRNAs are exp
A;Reference number: A90958; MUID:87217962; PMID:3646943
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A.Map position: 12pter-12qter
C.Superfamily: trypsin, tryp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 86; DB 2; Length 23;
Pred. No. 1.8e-06;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                A,Experimental Bource: pancreas
C,Superfamily: trypsin; trypsin homology
C,Keywords: hydrolase; serine proteinase
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68.4%;
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Best Local Similarity 68.4%
Matches 13, Conservative
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Best Local Similarity 78.9%
Matches 15; Conservative
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A; Residues: 'X', 18-50 < MOU>
A;Reference number: PU0036
A;Accession: PU0036
A;Molecule type: protein
A;Residues: 1-23 <TSU>
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P00766 bos taurus
P0081 canis famil
P17538 homo sapien
P17538 homo sapien
P80646 gadus morhu
P40313 homo sapien
P08861 homo sapien
P08861 homo sapien
P08931 homo sapien
P08208 mus musculu
P08208 mus musculu
P08208 homo sapien
P08208 homo sapien
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P0801 sus scrofa
P08208 homo sapien
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P0819 homo sapien
P0801 sus scrofa
P0819 homo sapien
P10626 capra hircu
P0819 homo sapien
P10626 rapra hircu
P0819 mus musculu
P20731 paralithode
P23573 mus musculu
P20731 paralithode
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112892 seqs, 41476328 residues
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1 IVNGEEAVPGSWPWQVSLQD 20
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DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 1-JUL-1986 (Rel. 41, Last annotation update)

DT 15-JUL-1986 (Rel. 41, Last annotation update)

DT 05-JUL-1986 (Rel. 41, Last annotation update)

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CHymotrypsinogen B (EC 3.4.21.1).

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CR C Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CO Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Pred. No. 4.1e-09;
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Matches 20; Conservative 0;
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X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF GAWMA-CHYMOTRYPSIN.

Cohen G.H., Silverton E.W., Davies D.R.;

Cohen G.H., Silverton E.W., Davies D.R.;

Comparison with other pancreatic serine proteases.";

J. Mol. Biol. 148:449-479(1981).

MEDLINE=86011575; PubMed=4046030;

MEDLINE=86011575; PubMed=4046030;

Towada H., Blow D.M.;

"Structure of alpha-chymotrypsin refined at 1.68-A resolution.";

"Structure of alpha-chymotrypsin refined at 1.68-A resolution.";

J. Mol. Biol. 184:703-711(1985).

"C.I. CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Phe-|-Xaa, Leu-|-Xaa.

"Structure of alpha-chymotrypsin nefined at 1.68-A resolution.";

"Structure of alpha-chymotrypsin refined at 1.68-A resolution.";

"Structure of alpha-chymotrypsin nefined at 1.68-A resolution.";
    "Chymotrypsinogen: 2.5-A crystal structure, comparison with alpha-chymotrypsin, and implications for zymogen activation."; Blochemistry 9:1997-2009(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pram; PP00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
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PROSITE; PS00134; TRYPSIN HIS; 1.
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                                                                                                               Smillie L.B., Furka A., Nagabhushan N., Stevenson K.J., Parkes C.O., "Structure of chymotrypsinogen B compared with chymotrypsinogen A and
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-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Pee-|-Xaa, Leu-|-Xaa, Leu-|-Xaa, Leu-|-Xaa, Leu-|-Xaa, Leu-|-Xaa, Leu-|-Xaa, Lox-|-Xaa, Lo
                                                                                                                                                                              "OTALIZE 218:343-346 (1968).
"Nature 218:343-346 (1968).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa, Phe-|-Xaa, Leu-|-Xaa, Leu-|-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-84170253; PubMed=6584866; Pinsky S.D., Laforge K.S., Luc V., Scheele G.; Inforge K.S., Luc V., Scheele G.; Information of cDNA clones encoding secretory isoenzyme forms: sequence determination of canine pancreatic prechymotrypsinogen 2 mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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Pred. No. 1.1e-08;
1; Mismatches 0; Indels
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13.AUG-1987 (Rel. 05, Last sequence update)
15.AUN-2002 (Rel. 41, Last annotation update)
Chymotrypsinogen 2 precursor (BC 3.4.21.1).
Canis familiarie (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 AA.
                                                                    DISULFIDE BONDS, AND ACTIVE SITE.
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                                                                 SEQUENCE, DISULFIDE BONDS, AND AC
MEDLINE=68238908; PubMed=5649671;
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Matches 19; Conserv
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                                                                                                                                                              trypsinogen.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                InterPro; JRR001314; Chymotrypsin.
InterPro; JRR001314; Chymotrypsin.
InterPro; JRR001314; Ser protease_Try.
Pram. PP00089; trypsin.
SWART; SM00020; Tryp SPc; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
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MEDLINE=81914264; PubMed=2917002;
Tomita N. Izunneto Y., Horii A., Doi S., Yokouchi H., Ogawa M.,
Mori T., Matsubara K.;
"Molecular cloning and nucleotide sequence of human pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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95.0%; Pred. No. 1.2e-08;
ive 1; Mismatches 0; Indels
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3, 2A2F4490813B3961 CRC64;
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHYMOTRYPSIN 2, A CHAIN.
CHYMOTRYPSIN 2, B CHAIN.
CHYMOTRYPSIN 2, C CHAIN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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Biochem. Biophys. Res. Commun. 158:569-575(1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (Rel. 15, Created)
U-NAG-1990 (Rel. 15, Last sequence update)
15-JUA-2002 (Rel. 41, Last annotation update)
Chymotrypsinogen B precursor (EC 3.4.21.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 AA
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MEDLINE=96439045; PubMed=8841380;
Leth-Larsen R., Asgeirsson B., Thorolfsson M., Noerregaard-Madsen M.,
     CHYMOTRYPSIN B, A CHAIN.
CHYMOTRYPSIN B, B CHAIN.
CHYMOTRYPSIN B, C CHAIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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01-0CT-1996 (Rel. 34, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
15-UNA-2002 (Rel. 41, Last annotation update)
Chymotrypsin B (EC 3.4.21.1)
Gadus morhua (Atlantic cod).
Gadus morhua (Atlantic cod).
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Paracanthopterygii, Gadiformes, Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protease, Digestion, Pancreas, Zymogen, Signal.
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"Structure of chymotrypsin variant B from Atlantic cod, Gadus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 263;
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Pred. No. 1.6e-08;
2; Mismatches 0; Indels
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001354; Ser_protease_Try.
Pfan; PF00089; trypsin; I
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PR0SITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS001134; TRYPSIN HIS; 1.
PROSITE; PS001135; TRYPSIN HIS; 1.
Hydrolase; Serine protease; Digestion; Pa
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Biochim. Biophys. Acta 1297:49-56(1996).
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                                                                                                                                                                                                                                                                                                                               EMBL; K02298; AAA98732.1; -. PIR; A22658; KYRTB.
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Best Local Similarity 90.0
Matches 18, Conservative
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209 2
263 AA;
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CTRB GADMO
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                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
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CHYMOTRYPEIN B, B CHAIN.
CHYMOTRYPEIN B, C CHAIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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WAY ACICO55A490B8701 CRC64;
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InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
EMAN; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
SMART; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN MIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
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MEDLINE=85054881; PubMed=6209274;
Bell G.I., Quinto C., Quiroga M., Valenzuela P., Craik C.S.,
Rutter W.J., M. Bell G.I., Galander of a rat chymotrypsin B gene.";
J. Biol. Chem. 259:14265-14270(1984).
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1; Mismatches 0;
                       Phe-|-Xaa, Leu-|-Xaa.
SUBCELLULAR LOCATION: Extracellular.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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01-APR-1988 (Rel. 07, Last sequence update)
01-LUN2-2002 (Rel. 41, Last annotation update)
Chymotrypsinogen B precursor (EC 3.4.21.1).
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EMBL; BC005385; AAH05385.1; -.
BIR; A31299; A31299.
HSSP; P00766; 1CHG.
MEROPS; S01.152; -.
Genew; HGNC:2521; CTRB1.
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263 AA,
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Matches

8

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Gaps

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PRT;
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                                   EMBL, X71874; CAASO710.1; -. EMBL, X71877; CAASO711.1; -. HSSP, POOTG3: 1DPO. MEROPS, SO1.256; -. Genew; HGNC:2524; CTRL.
                                                                                                                                                                                                                                                                                                                                                                                             1 IVNGERAVPGSWPWQVSLQD 20
                                                                                                                                                                                                                                                                                                                                                                                                          34 IVNGENAVLGSWPWQVSLQD 53
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                                                                                                                                                                                                                                                                                                                                                                         Conservative
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264
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114
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76
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"Atlantic cod cf
                                                                                        MIM; 118888;
                                                                                                                                                                                                                                                                                                                                                                         18;
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ID CTRA_GADMO
AC P47796;
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                 MEDLINE=9211252; PubMed=1764912;
MSGLINE=9211252; PubMed=1764912;
ASGRESSON B., Bjarnason J.B.;
"Structural and Kinetic properties of chymotrypsin from Atlantic cod (Gadus morhua). Comparison with bovine chymotrypsin.";
Comp. Biochem. Physiol. 99B:127-335(1991).
-! CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-xaa, Trp-|-xaa, Phe-|-xaa, Leu-|-xaa.
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                    CHYMOTREPEN B, A CHAIN.
CHYMOTREPEN B, B CHAIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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BY SIMILARITY.
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BY SIMILARITY.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
MEDULINE-94093544; PubMed-8268911;
Larsen F., Solheim J., Kristensen T., Kolsto A.B., Prydz H.;
"A tight cluster of five unrelated human genes on chromosome 16q22.1.";
                                                                                                                                                                                                                                                                                                                                                                                                 87.5%; Score 98; DB 1; Length 245; 94.7%; Pred. No. 4.2e-07; Live 0; Mismatches 1; Indels
                                                                                                                                    InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam. PF00089; trypsin. 1.
SMART: SM00020; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN JER; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Chymotrypsin-like protease CTRL-1 precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                     1 -> Y (IN REF. 2),
74FE0D425517AB02 CRC64;
                                                                                                                                                                                                                                                                                                                                              QVT -> VIS (IN REF. 2).
S -> T (IN REF. 2).
PW -> Y (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
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                                                                                                                                                                                                                                                                                                                                                                            26260 MW;
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SEQUENCE OF 1-12 AND 16-31.
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57
101
101
121
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201
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           TISSUE=Pyloric caeca;
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                                                                                                                                                                                                                                                                                                                                                                            245 AA;
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es 18; Conserv
                                                                                                                              MEROPS; S01.152;
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57
101
195
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P40313;
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or send an email to license@isb-sib.ch).
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MEDLINE=9211125; PubMed=1764912;
MSDLINE=9211125; PubMed=1764912;
MSDLINE=9211125; PubMed=1764912;
MStructural and kinelic properties of chymotrypsin from Atlantic cod (Gadus morhua). Comparison with bovine chymotrypsin.";
Comp. Blochem. Physiol. 99B:327-335(1991).
-!-CATALYTIC ATTIVITY: Preferential cleavage: Tyr-|-Xaa, Phe-|-Xaa, Leu-|-Xaa, Leu-|-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHYMOTRYPSIN-LIKE PROTEASE CTRL-1.
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
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Biochim. Biophys. Acta 1219;211-214(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001314, Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam, PP00089; trypsin. 1.
SMART; SM00020; Tryp SPC; 1.
PR0STIE; PS50240; TRYPSIN DOM; 1.
PR0STIE; PS00144; TRYPSIN DIS; 1.
PR0STIE; PS00145; TRYPSIN JIS; 1.
Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal.
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MEDLINE=94368860; PubMed=8086467;
Gudmundsdottir A., Oskarsson S., Bakin A.E., Craik C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-5UN-2002 (Rel. 41, Last annotation update)
Chymotrypsin A precursor (EC 3.4.21.1)
Gadus morhua (Atlantic cod).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 AA
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                            SEQUENCE OF 31-50.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                          MEROPS, SOLISI, ...
MEROPS, SOLISI, ...
InterPro; IPRO01314; Chymotrypain.
InterPro; IPRO01324; Ser protease_Try.
Pfam; PPRO0609; trypsin, 1.
PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SMO0206; Tryp_SPC; 1.
PROSITE; PSSO40; TRYPSIN_HIS; 1.
PROSITE; PSSO40; TRYPSIN_HIS; 1.
PROSITE; PSO0134; TRYPSIN_HIS; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal.
SIGNAL
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SIMILARITY).
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"Identification of a novel class of elastase isozyme, human pancreatic elastase III, by cDNA and genomic gene cloning."; J. Biol. Chem. 263:1231-1239(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 96; DB 1; Length 263; Pred. No. 8.6e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47AAC699A0A64FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     P08861; F11423; 01-NOV-1988 (Rel. 09, Created) 01-NOV-1988 (Rel. 09, Lagt sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Elastase IIIB precursor (EC 3.4.21.70) (Protease E)
                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI
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MEDLINE=88087253; Pubmed=2826474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28294 MW;
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                                                                                                                                                           EMBL; X78490; CAA55242.1; -. HSSP; P00766; 1CHG.
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TISSUE=Pancreas;
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AC EL3B_HUMAN
AC 01-NOV-1988
DT 16-OCT-2001
DT 16-OCT-2002
DE Blastase III
GN ELA3B.
GN HOMO Saplens
COC Mammalla; ENASPOCC
NOC NOEL TAXID=S
RN SEQUENCE FRC
TISSUE=Pancy
RX MEDLINE=8880
RA TANI T., Ohe
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RY TANI T., Ohe
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RY TANI T., Ohe
RY TANI T
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Wendorf P., Geyer R., Sziegoleit A., Linder D.; Lecalization site of human "Localization and characterization of the glycosylation site of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                          TISSUE=Pancreas;
MEDLINE=89325560; PubMed=2753124;
Moulard M., Kerfelec B., Mallet B., Chapus C.;
"Identification of a procarboxypeptidase A-truncated protease E binary complex in human pancreatic juice.";
FEBS Lett. 250:166-170(1989).
                     TISSUE-Pancreas;
MEDLINE-88000545; PubMed=3477287;
Shen W., Fletcher T.S., Largman C.;
Primary structure of human pancreatic proteage E determined by sequence analysis of the cloned mRNA.";
Biochemistry 26:3447-3452(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zymogen; Signal; Glycoprotein.
OR 16 (POTENTIAL).
ACTIVATION PEPTIDE (POTENTIAL).
BLASTASE IIIB.
                                                                                                                                                                                                                                                                                                                                                        [5]
SEQUENCE OF 94-164, AND CARBOHYDRATE-LINKAGE SITES ASN-114
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InterPro; IPR001354; Ser protease_Try.
PRam; PR00089; trypain; 1.
PRIMT; R000020; Trypain; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DIS; 1.
PROSITE; PS00135; TRYPSIN LIS; 1.
PROSITE; PS00135; TRYPSIN LIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Pancreas;
MEDLINE=89289996; PubMed=2737288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M16630; AAA36482.1; --
EMBL; BC005216; AAH05216.1; --
EMBL; M18692; AAA58454.1; --
FIR; B22934; B29934.
PIR; A27206; A27206.
PIR; S04499; S04999.
PIR; S04490; S04490.
HSSP; POS805; 1FON.
MEROPS; S01.205; --
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SWISS-2DPAGE; P08861; HUMAN.
Genew; HGNC:15945; ELA3B.
SEQUENCE OF 4-270 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Caldecrin is a novel-type serine protease expressed in pancreas, but its homologue, elastace IV, is an artifact during cloning derived from caldecrin gene."

J. Biochem. 123:546-554(1998).

--- FUNCTION: HAS CHYMOTRYPSIN-TYPE PROTEASE ACTIVITY AND HYPOCALCEMIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Pancreas;
MEDLINE=96107178; PubMed=8510454;
MEDLINE=96107178; PubMed=8510454;
TOmcmura A., Tomcmura M., Fukushige T., Akiyama M., Kubota N.,
Kumaki K., Nishii Y., Noikura T., Saheki T.;
"Molecular cloning and expression of serum calcium-decreasing factor
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -: CATALTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Tyr-|-Xaa, Phe-|-Xaa, Met-|-Xaa, Trp-|-Xaa, Gln-|-Xaa, Asn-|-Xaa, Tsour SPECIFICITY: PRUCERSA.
-: TISSUE SPECIFICITY: PRUCERSA.
-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. ELASTASE SUBFAMILY.
-: CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE ELASTASE IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                      P5SOF1: Q63188;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Caldecrin precursor (EC 3.4.21.2) (Chymotrypsin C) (Serum calcium-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Pancreas;
MEDLINE=92165057; PubMed=1537555;
Kang J., Wiegand U., Mueller-Hill B.;
"Identification of CDNAs encoding two novel rat pancreatic serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98207038; PubMed=9538241;
Voshino-Yasuda I., Kobayashi K., Akiyama M., Itoh H., Tomomura A.,
                                                                                                                                                                                                                             .
                                                                                                                                                                          83.0%; Score 93; DB 1; Length 270;
84.2%; Pred. No. 2.4e-06;
live 2; Mismatches 1; Indels
/FTId=CAR_000212.

* - 5 (IN REF. 3).

* - 5 (IN REF. 3).

* * - 8 (IN REF. 1).

* * - 8 (IN REF. 1).

* * - 9 (IN REF. 5).

* * - 9 (IN REF. 3).

* * * 9 (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                          268 AA
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                     4 4 R
64 64 A
79 79 W
129 131 MT
164 164 R
270 AA; 29293 MW; E
                                                                                                                                                                                                                                                                                           1 IVNGEEAVPGSWPWQVSLQ 19
                                                                                                                                                                                                                     Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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EEGSVYAEVDTIYVHEKWNRLFLWN -> AEAPCTLRWTPS
TSMRSGTDSSCGT (IN REF. 2).
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N-LINKED (GLCNAC. . ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                        MEROPS; SO1.15'; -:
InterPro; IPRO01314; Chymotrypain.
InterPro; IPRO01254; Ser_protease_Try.
Pfam; PF00089; trypsin; I.
R PRINTS; PR00722; CHYMOTRYPSIN.
RMART; SM00020; Tryp SPC; I.
R PROSITE; PS50240; TRYPSIN_DOM; I.
R PROSITE; PS00135; TRYPSIN_SER; I.
R PROSITE; PS00135; TRYPSIN_SER; I.
Mydrolase; Stine protease; Glycoprotein; Zymogen; Signal.
T PROPER IT 29 ACTIVATION PEPTIDE.
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MEDINE=888087253, PubMed=2886474;
MEDINE=888087253, PubMed=286474;
Tani I., Obsumi J., Mita K., Takiguchi Y.;
"Identification of a novel class of elastase isozyme, human pancreatic elastase III, by cDNA and genomic gene cloning."; J. Biol. Chem. 263:1231-1239(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DD _,
), 6.4e-06;
| __haq 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 90; DB 1; Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33B67AF34D0F8583 CRC64;
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(BY
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01-MAR-1989 (Rel. 10, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
15-UND-2002 (Rel. 41, Last annotation update)
Elastase IIIA precursor (EC 3.4.21.70) (Protease E).
                                                                                                                                                                                                                                                                                             CHARGE RELAY SYSTEM
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TISSUE=Pancreas;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.4%;
78.9%;
EMBL; S80379; AAB35830.1; -. EMBL; X59014; CAA41753.1; -. HSSP; P00766; ICHG. MEROPS; S01.157; -.
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nes 15, Conservative
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Elastase 2A precursor (EC 3.4.21.71)
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R EMBL; M18693; AAA66350.1; JOINED.

R EMBL; M18694; AAA66350.1; JOINED.

R EMBL; M18696; AAA66350.1; JOINED.

R EMBL; M18699; AAA66350.1; JOINED.

R EMBL; M26994; ELA3A.

R Genew; HGNC:15944; ELA3A.

R InterPro; IPR001244; Ser protease_Try.

R InterPro; IPR001244; Ser protease_Try.

R PROSITE; PS50240; Tryp.Ser; 1.

R PROSITE; PS60134; TryPESIN LNS; 1.

R PROSITE; PS60135; TRYPESIN LNS; 1.

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MISSING (IN REF. 1)
K -> E (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29474 MW;
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hes 15; Conserv
TISSUE=Prostate;
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EL2A HUMAN
ID EL2A HT
AC P08217,
DT 01-AUG-
DT 15-JUN-
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MEDLINE=881,9076; PubMed=2834346;
Shirasu Y., Yoshida H., Matsuki S., Takemura K., Ikeda N., Shimada Y.,
Cawa T., Mikayama T., Iijima H., Ishida A., Sato Y., Tamai Y.,
Tanaka J., Ikenaga H.;
Tanaka J., Ikenaga H.;
"Molecular clonfing and expression in Escherichia coli of a cDNA
encoding human pancreatic elastase 2.";
J. Blochem. 102:1555-1563(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: ACTS UPON ELASTIN.
-i- CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Met-|-Xaa and Phe-|-Xaa. Hydrolyzes elastin.
-i- SUBSCELDULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: PANCREAS.
-i- TISSUE SPECIFICITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
                                                                                                                                                                                                               MEDLINE=87217962; PubMed=3646943;
Kawashima I., Tani T., Shimoda K., Takiguchi Y.;
"Characterization of pancreatic elastase II cDNAs: two elastase II
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-88107669; PubMed=3427074;
Fletcher T.S., Shen W.F., Largman C.;
"Primary Bruckure of human pancreatic elastase 2 determined by
sequence analysis of the cloned mRNA.";
Biochemistry 26:7256-7261(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomas D.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00113; TRYPSIN HIS; 1.
Hydrolase; Serine protease; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                   mRNAs are expressed in human pancreas.";
DNA 6:163-172(1987).
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InterPro; IPR001254; Ser protease_Try
Pfam; PF00089; trypsin; 1,
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EMBL, AL512883; CAC42421.1; -...
EMBL, AC0707031, AAH07031.1; -...
PIR, A27432, A27432.
PIR, B26823, B26823.
HSSP, P00772; IELG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Pancreas;
                                                                                                               NCBI_TaxID=9606;
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1 IVNGEEAVPGSWPWQVSLQ 19
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57
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206
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227
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P00774;
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                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
MEDLINE-9422022; PubMed=8168476;
Pignol D., Gaboriaud C., Michon T., Kerfelec B., Chapus C.,
Pontecilla-Camps J.C.;
"Crystal structure of bovine procarboxypeptidase A-S6 subunit III,
                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAX SYSTEM (BY SIMILARITY).
CHARGE RELAX SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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15-UND-202 (Rel. 41, Last annotation update)
15-UND-202 (Rel. 41, Last annotation update)
15-OPTOPTORE (Rel. 41, Last annotation update)
111) (Procarboxypeptidase A-S6 subunit III) (PROCPA-S6 III).
111) (PROCPA-S6 III).
112) (PROCPA-S6 III).
113) (PROCPA-S6 III).
114) (PROCPA-S6 III).
115) (PROCPA-S6 III).
116) (PROCPA-S6 III).
117) (PROCPA-S6 III).
118) (PROCPA-S6 III).
119) (PROCPA-S6 IIII).
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                                                                                                                                                                                                                                                                                                                                 Score 86; DB 1; Length 269;
Pred. No. 2.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                         C -> V (IN REF. 3).
A2E05143EFF4987C CRC64;
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-!- TISSUE SPECIFICITY: PANCREAS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 AA
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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EMBO J. 13:1763-1771(1994).
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Interpro; IPRO01314; Chymotrypsin.
Interpro; IRRO01254; Ser protease_Try.
Pfam; PF00089; trypsin; I.
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SEQUENCE OF 1-25.
MEDLINE=91099520; PubMed=2269366;
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Eur. J. Biochem. 157:91-99(1986).
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                                                                                                                                                                                                                                                                      28888 MW;
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78.9%;
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                                                                                                                                                                                                                                                                                                                           Query Match 76.81
Best Local Similarity 78.9<sup>3</sup>
Matches 15, Conservative
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Bovidae, Bovinae, Bos.
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MEROPS; S01.983; -.
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                                                                                                                                                                                                                                                                      269 AA;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116,
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pancreas.";
J. Biol. Chem. 259:14271-14278(1984).
-! FUNCTION: ACTS UPON ELASTIN.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Leu-|-Xaa, Met-|-Xaa and Phe-|-Xaa. Hydrolyzes elastin.
-!- SUBCELLULLAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: PROKREAS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-82182967; PubMed-6918221; MODONAIA R.J., Swain W., Pictet R.L., MODONAIA R.J., Swift G.H., Quinto C., Swain W., Pictet R.L., Nikovits W., Rutter W.J.; "Primary structure of two distinct rat pancreatic preproelastases determined by sequence analysis of the complete cloned messenger ribonucleic acid sequences."; Elochemistry 21:1453-1463(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS0240; TRYPSIN bOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00136; Pancreas; Digestion; 3D-structure.
PROPER PROPERTIES.
PROPERTIES.
PROPERTIES.
                                                                                                                                                                                                                                                                                                             75.9%; Score 85; DB 1; Length 253; 78.9%; Pred. No. 3.2e-05; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                          27337 MW; 24663724D8AE409C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elastase 2 precursor (EC 3.4.21.71).
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EMBL, L00124; AAA98780.1; -.
EMBL, L00116; AAA98780.1; -.
EMBL, L00119; AAA98780.1; JOINED.
EMBL, L00119; AAA98780.1; JOINED.
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MEDLINE=21139112; PubMed=11245484;
Afar D.E.H., Vivanco I., Hubert R.S., Kuo J., Chen E., Saffran D.C.,
Raitano A.B., Jakobovits A.
"Catallytic cleavage of the androgen-regulated TMPRSS2 protease results
in its secretion by prostate and prostate cancer epithelia.";
cancer Res. 61:1686-1692(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21309069; PubMed=11414763;
Teng D.H., Chen Y., Lian L., Ha P.C., Tavtigian S.V., Wong A.K.;
"Mutation analyses of 268 candidate genes in human tumor cell lines.";
Genomics 74:352-364(2001).
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                          SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                         75.0%; Score 84; DB 1; Length 271; 73.7%; Pred. No. 4.7e-05;
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15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transmembrane protease, serine 2 precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=97468144; PubMed=9325052;
Paoloni-Giacobino A., Chen H., Peitsch M.C., Rossier C.,
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CHARGE RELAY SYSTEM (BY SIM:
CHARGE RELAY SYSTEM (BY SIM:
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2; Mismatches 3;
                                                                      HSSP, P00772; IELG.
MEROPS; S01.155; -
InterPro; IPR001314; Chymotrypain.
InterPro; IPR001314; Ser_protease_Try.
Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00020; Tryp SPC.
PROSITE; PS00134; TRYPSIN DOM; I.
PROSITE; PS00134; TRYPSIN HIS; I.
PROSITE; PS00135; TRYPSIN HIS; I.
Hydrolase; Serine protease; Zymogen; Signal.
SIGNAL
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                                                                                                                                                                                                                                              ELASTASE
EMBL, L00121; AAA98780.1; JOINED.
EMBL, L00122; AAA98780.1; JOINED.
EMBL, L00123; AAA98780.1; JOINED.
PIR, A00961; EMTZ.
                                                                                                                                                                                                                                                                                                                                                28885 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                            31 VVGGQEASPNSWPWQVSLQ 49
                                                                                                                                                                                                                                                                                                                                                                                                                             1 IVNGBEAVPGSWPWQVSLQ 19
                                                                                                                                                                                                                                                                                                                                                                                                   14; Conservative
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271
75
123
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224
245
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31 23
123 11
218 2
60
157 2
188 2
214 2
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SEQUENCE
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TMS2 HUMAN
AC 015393,
DT 15-0UT-
DT 15-1UT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21104370; PubMed=11169526; Varianala M.P., Vihko P.T.; Varession of transmembrane serine protease TMPRSS2 in mouse and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC CHAIN.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                   human tissues.";
J. Pathol. 193:134-140(2001).

1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ACTIVATED BY CLEAVAGE AND SECRETED.

1- TISSUE SPECIFICITY: EXPRESSED STRONGLY IN SMALL INTESTINE. ALSO EXPRESSED IN PROSTATE, COLON, STOWACH, AND SALIVARY GLAND.

1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

1- SIMILARITY: CONTAINS I SRCR DOMAIN.

1- SIMILARITY: CONTAINS I LDL-RECEPTOR CLASS A DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CLEAVAGE (POTENTIAL).
BY SIMILARITY.
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BY SIMILARITY.
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BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.

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N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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TRANSMEMBRANE PROTEASE, SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
LDL-RECEPTOR CLASS A.
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CHARGE RELAY SYS
CHARGE RELAY SYS
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EMBL; AF270487; AAX29280.1; -..
HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S01.247; -. Genew; HGNC:11876; TMPRSS2.
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FT VARIANT 449 449 K -> N (IN DBSND:1056602).

FT MUTAGEN 255 255 R->Q:LOSS OF CLEAVAGE.

FT MUTAGEN 441 441 5-A3:LOSS OF ACTIVITY.

FT CONFLICT 160 160 M -> V (IN REF. 3).

FT CONFLICT 329 329 R -> C (IN REF. 1).

FT CONFLICT 489 491 RAD -> KAN (IN REF. 1).

FT CONFLICT 489 491 RAD -> KAN (IN REF. 1).

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FT CONFILCT 481 RAD -> KAN (IN REF. 1).

FT CONFILCT 481 RAD -> KAN (IN REF.
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Search completed: February 12, 2003, 10:23:18 Job time: 3.68657 secs THIS PAGE BLANK (USPTO)

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PRELIMINARY;
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SEQUENCE FROM N.A.
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09w7q4 paralichthy
09w7q4 patalichthy
09pwq6 gadus morhu
09d7t9 mus musculu
09cq52 mus musculu
09psp2 gallus gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0947p8 mus musculu
09eqz8 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9eqz8 rattus norv
Q9er05 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9dc86 mus musculu
Q9d8x8 mus musculu
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Q9d960 mus musculu
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bos taurus
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                                              February 12, 2003, 10:16:06; Search time 14.1493 Seconds (without alignments) 291.248 Million cell updates/sec
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095kw7
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                          671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                OM protein - protein search, using sw model
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0990835
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
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Q9BK47	Q96T73	O9PRR4	0960V5	091039	O9PRR3	O8T4N2	Q8T4N4	QBVHKB	QBVDV1			Q9W7Q2	091674	060491	Q8T4N3	P79343	096286	Q924N9	62Y060			668960			1 090274	096110	08VHJ4	A DROGE6	× .
267 5	492 4	20 13	269 4	270 13	20 13	461 5	298 5	417 11	417 11	249 13		268 13	1524 13		474 5		•	274 1]	310 13		490 11					329 6	417 1	264	
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SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

SEQUENCE TROM N.A.

SEQUENCE TO Pubmed=11217851;

MEDLINE=21085660, Pubmed=11217851;

MARAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

MARAWAI J., Shinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S.,

Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

MA Saito T., Okazaki Y., Gojobori T., Bono H., Kaukawa T., Saito R.,

Macha K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

Machi P., Lewis S., Matsuo Y., Nikaido I., King B., Kochiwa H.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Momberts P.,

Nordone P., Marchionni L., Mashima M., Mame D.A., Kamiya M., Lee N.H.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

Flexicological M., Radotaki S.,

Hayashizaki Y.,

Flexicological M., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL; AK007566; BAB25112.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
96.4%; Score 108; DB 11; Length 263;
Best Local Similarity 90.0%; Pred. No. 2.5e-08;
Matches 18; Conservative 2; Mismatches 0; Indels (
                 HSSP, PROVES, CALLES, CAMEROPS, SOLISS, CAMEROPS, CAMEROPS, CAMEROPS, CAMEROTIS, COMMOTRYPEIN.

InterPro; IPRO01254; Ser_Drotease_Try.

REMINTS, PRO00202; CHYMOTRYPSIN.

REMINTS, PRO00202; TRYPSIN, DOM, 1.

REMOSITE; PS00134; TRYPSIN DOM, 1.

REMOSITE; PS00134; TRYPSIN SER; 1.

REMOSITE; PS00135; TRYPSIN SER; 1.

REMOSITE; PS00135; TRYPSIN SER; 1.

REMOSITE; PS00135; TRYPSIN SER; 1.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
2200008D09Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1913723; 220000BD09Rik.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
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SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
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   EMBL; AK003060; BAB22539.1;
HSSP; P00766; IGCT.
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RM SEQUENCE FROM N.A.

RA Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishli Y.,
RA Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishli Y.,
RA Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishli Y.,
RA Arakawa T., Shinagawa A., Shibata K., Kondo S., Yamanaka I.,
RA Satto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Satto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Aono H., Baldarelli R., Barah G.,
RA Brownstein M.J., Bult C., Pletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Plomann M., Hume D.A., Kamiya M., Lee N. H.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
RA Basaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Wattz C., Whittaker C., Wilming L.,
RA Hayashizaki Y.,
RY "Punctional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
VCBI_TaxID=10090;
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-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS TRYPSIN FAMILY.
                                                                                                      96.4%; Score 108; DB 11; Length 263; 90.0%; Pred. No. 2.5e-08; 1.ve 2; Mismatches 0; Indels C
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Serine protease.
SEQUENCE 263 AA; 27898 MW; C0638FB8F905A92F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
2200008D09Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI.9913723; 2200008D09R1k.
INTERFDO: IPR001314; Chymotrypsin.
INTERPPO: IPR001234; Ser_protease_Try.
PEAN; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PR051TB; PS00240; TRYPSIN DOM; 1.
PR05ITB; PS00134; TRYPSIN DOM; 1.
PR05ITB; PS00134; TRYPSIN JER; 1.
Hydrolase: Serine protease.
SEQUENCE 263 AA; 27822 MM; 28C4487AF1A2.
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EMBL; AK003079; BAB2253.1; --
EMBL; AK007015; BAB25241.1; --
EMBL; AK007015; BAB25241.1; --
EMBL; AK007015; BAB25861.1; --
EMBL; AK008888; BAB25861.1; --
HSSP; P00766; 1GCT.
                                                                                                                                                                                    1 IVNGBEAVPGSWPWQVSLQD 20
                                                                                                                                                                                                         34 IVNGEDAIPGSWPWQVSLQD 53
                                                                                     Query Match
Best Local Similarity 90.08
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PROURINGE FROM N.A.

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REDLINE-21085660, PubMed-117851;

K MEDLINE-21085660, PubMed-117851;

K MEDLINE-21085660, PubMed-117851;

K MEDLINE-21085660, PubMed-117851;

R Arakawa T., Hara A., Fukuniahi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Rasukawa T., Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R., Radoca K., Matsuda H.A., Ashburner M., Batalov S., Casawant T., Radoca K., Matsuda H.A., Ashburner M., Batalov S., Casawant T., Radoca K., Matsuda H.A., Ashburner M., Batalov S., Casawant T., Reischmann M., Gaasterland T., Gissi C., King B., Kochisa H., Reischmann M., Staubii F., Sizukii R., Towackenbush J., Rochim L.M., Staubii F., Sizukii R., Tono H., Baldarelli R., Barsh G., Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sakamoto N., Sakamoto R., Schoenbach C., Seya T., Shibata Y., Storch K.-F., B., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Allanda K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN PAMILY.
EMB1: AKOO19: BAB26029.1; --
HSSP: P00766; 4CHA.
MEROPS; S01.256; --
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukarmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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                                                264 AA
                                      Q9D7PB PRELIMINARY; PRT; 26
C9D7PB; OJUN-2001 (TrEMBLrel. 17, Last sequen
01-JUN-2002 (TrEMBLrel. 17, Last sequen
01-JUN-2002 (TrEMBLrel. 21, Last annota
181004D1SRik protein.
CTRL OR 1810004D1SRIK.
Mus musculus (Mouse)
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01-WAR-2001 (TrEMBLrel. 16, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
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DT 01-MADT 01-MADT 01-UMADT 01-UMADT 01-UMADT 01-UMADT 01-UMADT 00-UMMADT 00-UMMAD
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X Rawain J. Shibata A. Shibata X. Yoshino M., Itch M., Ishii Y., Arawa T., Hara A., Shibata X. Konno H., Adachi J., Fukuda S., Arawa T., Hara A., Shibata Y., Konno H., Adachi J., Fukuda S., Arawa T., Hara A., Shibata Y., Konno H., Kasukawa T., Saito R. Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Beralov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Beralov S., Casavant T., Saito R., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T., Ruhl P., Lewis S., Matsuo Y., Nikaido I., Peeole G., Quackenbush J., Sakami L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T., Bake J., Boffelli D., Bojunga N., Carninci P., Ge Bonaldo M.F., Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima M., Hamme D.A., Kamiya M., Lee N.H., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Schteuki S., Harselawa Y., Kawaji H., Kohteuki S., Harashizaki Y., Walashizaki Y., Kawaji H., Kohteuki S.,
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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96.4%; Score 108; DB 11; Length 263; 90.0%; Pred. No. 2.5e-08; ive 2; Mismatches 0; Indels (
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Last annotation update)
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MGD; MG1.86559; Ctrl.
MGD; MG1.86559; Ctrl.
InterPro; IPR001314; Ser_procease_Try.
InterPro; IPR001254; Ser_procease_Try.
Fram; PR00009; trypāln; J.
SMART; SM00020; Tryp_SPC; 1.
PR0STEE, PS50240; Tryp_SPC; 1.
PR0STEE; PS50240; TryP_SPC; 1.
PR0STEE; PS50240; TRYPSIN DOM; 1.
PR0SITE; PS001135; TRYPSIN HIS; UNKNOWN_1.
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EMBL; AKO07333; BAB24967.1; -.
HSSP; P00766; 4CHA.
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
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                     Query Match
Best Local Similarity 90.0°
Matches 18; Conservative
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CTRL OR 1810004D15RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutnerio
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE
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Rattus norvegicus (Rat). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi; Mammalia, Butheria, Rodentia, Sciurognathi, Muridae; Murinae; Rattus. Last sequence update) Last annotation update)

Best Loca Matches

RESULT 5

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Gaps

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Query Match
Best Local Similarity 95.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9W7Q4;
                                                                                                                                                                                                                                                          Q9W7Q3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9W7Q4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                       RESULT 8
Q9W7Q3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09W7Q4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
                                   SEQUENCE FROM N.A.
TSSUE-RAT PANCREAS;
Sogame Y., Mitsui S., Kataoka K., Kashima K., Kato M., Sakagami J.,
Yamaguchi N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bjoernslett M.;
Subatted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL; ABO16228; BAB20275.1; -.
EMBL; AP235356; 4CHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                       "Molecular cloning of rat chymopasin.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS EMBL; AB020757; BAB20287.1; -.
HSSP; PO0766; 4CHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Mitsui S., Yamaguchi N.;
"Molecular cloning of mouse chymopasin.";
Submitted (UUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                               InterPro; 187001314; Chymotrypain.
InterPro; 187001254; Ser_protease_Try.
InterPro; 187001254; Ser_protease_Try.
InterPro; 187001254; Ser_protease_Try.
PRINTS, PRO0722; CHYMOTRYPSIN.
SWART; SWO0020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
SEQUENCE 264 AA; 28116 MW; F9EDSD210FD3500E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; I.
PRINTS; PR00122; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; I.
PROSITE; PS00134; TRYPSIN DOM; I.
PROSITE; PS00135; TRYPSIN LIS; UNKNOWN I.
PROSITE; PS00135; TRYPSIN SER; I.
Hydrolase; Serine protease.
SEQUENCE 264 AA; 28135 MW; 1D979709A07056C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UON-2002 (TrEMBLrel. 21, Last annotation update)
Chymopasin (Chymotrypsin A CTRA-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.5%; Score 107; DB 11; 95.0%; Pred. No. 3.6e-08; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
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STRAIN~129S6/SVEVTAC; TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVNGEBAVPGSWPWQVSLQD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 IVNGENAVPGSWPWQVSLQD 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; 801.256; -.
MGD; MGI:88558; Ctrl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTRL OR CTRA1.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                    MEROPS; S01.256; -.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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10 PER 05

10 PER 05

10 PER 07

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                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectoidei; Peruronectoidei; Paralichthyidae; Paralichthys.
VCBI_TaxID=8255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suzuki T., Srivastava A.S., Kurokawa T.;
"Japanese flounder mRNA for chymotrpainogen 2.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPEIN FAMILY.
EMBL; ABO29754; BAA82366.1; -.
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       Length 264;
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                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.2%; Score 101; DB 13; Length 90.0%; Pred. No. 2.8e-07; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27793 MW; 9F583044E22F78C0 CRC64;
                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
95.5%; Score 107; DB 11; 95.0%; Pred. No. 3.6e-08;
                                                                                                                                                                                                                                                                   260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S01.152; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001214; Chymotrypsin.
Fam; PR00089; trypsin; I.
PR.NTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; TryPS SR0; I.
PROSITE; PS02040; TRYPSIN DOM; I.
PROSITE; PS00134; TRYPSIN JER; II.
HYGYOLAGE; Serine protesse.
SEQUENCE 260 AA; 27793 MW; 9F583044E22F7
                                             0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 AA
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TISSUE=PANCREAS;
Suzuki T., Srivastava A.S., Kurokawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sed
                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                   Chymotrypsinogen 2.
Paralichthys olivaceus (Flounder).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paralichthys olivaceus (Flounder).
                                                                                                20
                                                                                                                                              53
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                                                                                                                       34 IVNGENAVPGSWPWQVSLQD
                                                                                           1 IVNGEEAVPGSWPWQVSLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 IVNGEEALPHSWPWQVSLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVNGEEAVPGSWPWQVSLQD
                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 90.0 tes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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TISSUE=PANCREAS;
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Q9D7T9

us-10-036-371-6.rspt

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RESULT 11
Q9D7T9
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"Japanese flounder mRNA for chymotrypsinogen 1.";
Submitted (UL-1999) to the EMBL/GenBank/DbBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gadus morhua (Atlantic cod).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microb. Comp. Genomics 5:41-50(2000).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
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MEDLINE=20464334; PubMed=11011764;
Spilliaert R., Gudmundsdottir A.,
"Molecular Cloning of the Atlantic Cod Chymotrypsinogen B.";
                                                                                                                                                                                                                         Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.5%; Score 98; DB 13; Length 263; 94.7%; Pred. No. 7.9e-07; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                    87.5%; Score 98; DB 13; Length 261
90.0%; Pred. No. 7.8e-07;
iive 0; Mismatches 2; Indels
                                                                                                                                                                                               28184 MW; D7090A9D65395B7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 263 CHYMOTRYPSIN B.
263 AA; 28175 MW, EF61B18A34EE5E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                               01-MĀY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Chymotrypsin B precursor (BC 3.4.2.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MERCHES, SULLISSI,
InterPro; PRO01314; Chymotrypsin.
InterPro; IPR001354; Ser protease_Try.
Pfam; PP00089; Lrypsin; 1.
PRINTS; PR00032; CHYMOTRSIN.
SMART; SM00020; Tryp. SPC; 1.
PROSTIE; PS50240; TRYPSIN DOM; 1.
PROSTIE; PS50240; TRYPSIN DOM; 1.
PROSTIE; PS60134; TRYPSIN HIS, UNKNOWN 1.
PROSTIE; PS00135; TRYPSIN SER; 1.
M Hydrolase; Serine protease; Signal.
I SIGNAL
                                                                                 InterPro: IPR001314; Chymotrypsin.
InterPro: IPR001254; Ser_protease_Try.
Pfam: PP00089; Lrypsin: IPR00125, CHYMOTRYPSIN.
SMART; SM00220; Tryp SPC: 1.
PROSITE: PSC0240; TRYPSIN DOM; 1.
PROSITE; PSC0134; TRYPSIN DOM; 1.
PROSITE; PSC0134; TRYPSIN HIS; UNKNOWN_1.
PROSITE; PSC0134; TRYPSIN SER; 1.
PROSITE; PSC0135; TRYPSIN SER; 1.
Pydrolase; Securine protease:
SEQUENCE 261 AA; 28184 MW; D7090A9D6S395
                                                                                                                                                                                                                                                                                                                                                             263 AA.
                                               EMBL; AB029753; BAA82365.1; -.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ242521; CAB43766.1; -. HSSP; P00766; 1CHG.
                                                                                                                                                                                                                                                                    1 IVNGEEAVPGSWPWQVSLQD 20
                                                                                                                                                                                                                                                                                          32 IVNGETAVSGSWPWQVSLQD 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ilarity 94.7%;
Conservative
                                                                                                                                                                                                                                Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                       MEROPS; S01.256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8049;
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Matches
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REDUENCE FROM N.A.

RESULENCE FROM N.A.

RESULENCE-27BL/6J; TISSUE-STOMACH;

RA MARWAR T., HATA A., Shinbara K., Yoshino M., Itoh M., Ishii Y.,

RA ATARWAR T., HATA A., Shinbara K., Yoshino M., Itoh M., Ishii Y.,

RA ATARWAR T., HATA A., Shinbara K., Yoshino M., Itoh M., Ishii Y.,

RA ATARWAR T., HATA A., Shinbara K., Yoshino M., Adachi J., Fukuda S.,

RA ATARWAR T., Rawa M., Nishi K., Kiyoswah H., Kondo S., Yamanaka I.,

RA ATARWAR T., MATUGA H., Ashburnar M., Batalov S., Casavant T.,

Radora K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

Radora K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsud T., Rissic M., Rashida H.,

Rochind L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schrind L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fleetcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Brownstein M., Sato K., Schoenbach C., Sakanto O. N.,

Sasaki H., Sato K., Schoenbach C., Schoata T., Sakanto O. N.,

Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Hynshaw-Boris A., Yoshida K., Rasegawa Y., Kawaji H., Rohtsuki S.,

RA Anshizaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·.
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                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            !- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y., "Function of a full-length mouse cDNA collection.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·.
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Pred. No. 1.1e-06;
1; Mismatches 1; Indels
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                                                  (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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Last annotation update)
   269 AA.
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MGD, MGI.191318; ELABD.
InterPro; IPRO01314; Chymotrypsin.
InterPro; IPRO01314; Chymotrypsin.
Fram; PRO0089; trypsin; 1.
SMART; SMO0202; TrypsPro; 1.
PROSITE; PSO0134; TRYPSIN DOM; 1.
PROSITE; PSO0134; TRYPSIN DOM; 1.
PROSITE; PSO0134; TRYPSIN DOM; 1.
PROSITE; PSO0135; TRYPSIN DOM; 1.
PROSITE; PSO0136; TRYPSIN BSR; 1.
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Q9C052,
G1-JUN-2001 (TERMELrel. 17, Created)
O1-JUN-2001 (TERMELrel. 17, Last seque)
O1-JUN-2002 (TERMELrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AK008858; BAB25932.1; -. HSSP; P05805; 1FON.
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PRELIMINARY;
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ELA3B OR 2310074F01RIK.
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                                                                                                                                                                                                              Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                      01-JUN-2001
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"Affinity purification of chicken pancreas proteinases and their N-
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                                                                                                                                                                         SEQUENCE FROW N.A.

STRAIN-C57BL/60; TISSUB=TONGUE;

KARAIN-C57BL/60; PubMed=11217851;

Kawai J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Jawa M., Nishi X., Kiyosawa H., Kondo S., Yamanaka I., A alawa K., Izawa M., Nishi X., Kiyosawa H., Kondo S., Yamanaka I., Raito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., A saito T., Mashuli F., Baralov S., Casavant T., Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Relischmann W., Gasterland T., King B., Kochiwa H., Saki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Baraki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Butke J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bronstein M.J., Bult C., Fletcher C., Fullta M., Gariboldi M., Auchionni L., Mashima J., Mazzarelli J., Mombarts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Nyashaw-Boris A., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Nawachizaki V.
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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Tluscik F., Polanowski A., Guyonnet V., Long P.L., Travis J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.6%; Score 97; DB 11; Length 269; 89.5%; Pred. No. 1.1e-06; ive 1; Mismatches 1; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28904 MW; C543F76957B2A7CE CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJM-2002 (TrEMBLrel. 21, Last annotation update)
Chymotrypsin C, PI isoform (Fragments).
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1915118; Ela3b.

InterPro; IPR001254; Ser protease_Try.

InterPro; IPR001254; Ser protease_Try.

PERM; PR00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN 1.

PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN 1.

Hydrolase; Serine protease.

SEQUENCE 269 AA; 28904 MW; CS43F76957B2P
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                       ELA3B OR 2310074F01RIK.
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                                                                                                                          NCBI_TaxID=10090;
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

TRYPERITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPERIN FAMILY.

EMBL; AJ000067; CAA03899.1; -.

R HSSP; P05805; IPON.

R HSRPS; 501.154; --

INTERPO; IPRO01314; Chymotrypsin.

R INTERPO; IPRO01314; Ser_protease_Try.

R Pfam; PF00089; trypsin; IF R PF00089; trypsin; IF R Pfam; PF00089; trypsin; IF R PF00089; trypsin; IF R PF00089; trypsin; IF R PF00089; trypsin, IF R PF00089; trypsin, IF R PF00089; trypsin, IF R PROSITE; PS00134; TRYPSIN_EN; I.

R PROSITE; PS00134; TRYPSIN_ERX; I.

R PROSITE; PS00135; TRYPSIN_ERX; I.
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Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                                             Score 95; DB 13; Length 40;
Pred. No. 3e-07;
1; Mismatches 1; Indels
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84.2%; Pred. No. 4.3e-06;
A4.2%; Pred. No. 4.3e-16;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                    4376 MW; 348CPFBFC8C8003D CRC64;
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Last annotation update)
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terminal amino-acid sequences.";
Acta Biochim. Pol. 41:174-177(1994).
HSSP; P00766; 1CHG.
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                                                                            Hydrolase; Serine protease,
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                                                                                                                                                                                                                                                                          17; Conservative
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Matches 16; Conserv
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                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Sziegoleit A.;
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DE Similar to elastase 3, pancreatic (protease E).

S Homo sapiens (Human).

C Enkaryota; Mecazoa; Chordata; Craniata; Verrebrata; Euteleostomi;

C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI TaxID=9666;

RN NII TAXID=9666;

RN NSI TAXID=9666;

RN SEQUENCE FROM N.A.

RC TISSUE-PANCREAS;

RA Straubberg R.;

RL SLDMILLED (MAY-2001) to the EMBL/GenBank/DDBJ databases.

RR SHAL; BC00839; AAH0339.1; -

DR REMEL; BC00839; AAH0339.1; -

DR PROSITE; PS00124; ErrPSIN DOM; 1.

DR PROSITE; PS00124; TRYPSIN DOM; 1.

DR PROSITE; PS00135; TRYPSIN DOM; 1.

DR PROSITE; PS00135; TRYPSIN DOM; 1.

DR PROSITE; PS00135; TRYPSIN DOM; 1.

COMETY MATCH

RA 29446 MW; 946DDBDA694A102E CRC64;

COMETY MATCH

RA 1: | | | | | | | | | | | | |

DD 29 VVHGEBAVPGSWEWQVSLQ 19

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DD 29 VVHGEBAVPGSWEWQVSLQ 47

Search completed; February 12, 2003, 10:27:26

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Sequence 6
Sequence 2
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                                                                                                                                                                                                                                                                Sequence 10, Application US/08278091
Patent No. 2506139
GENERAL INFORMATION:
APPLICANT: LOOSWORE, Sheena M
APPLICANT: VANG, Yan-Ping
APPLICANT: COMEN, Raymond P.
APPLICANT: COMEN, Raymond P.
APPLICANT: APPLICANT: Rejmond P.
APPLICANT: RELEIN, Michel H.
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE AUGURESS.

ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
STATE: Ontario
COUWTRY: Canada
ZIP: MSG 1R7
COMPUTER: EMP PC Compatible
OPERATING SYSTEM: PC-DoS/MS-
COMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PATENTIN Release #1.0, Version #1.25
COMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/278,091
FILING DATE: 21-UUL-1994
CLASSIFICATION: A35
ATTORREY/AGENT INFORMATION:
NAME: STEWART NORMATION:
IREFERENCE/DOCKET NUMBER: 1038-371
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TVPE: amino acids
TVPE: amino acids
TVPE:
ALIGNMENTS
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US-08-278-091-10
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Matches 20;
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Sequence 1, Appli
Sequence 2, Appli
Sequence 57, Appli
                                                               February 12, 2003, 10:18:40; Search time 4.29851 Seconds (without alignments) 136.898 Million cell updates/sec
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Sequence 10, A
Sequence 10, A
Sequence 10, A
Sequence 10, A
Sequence 10, A
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2. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PtrTUS_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PtrTUS_COMB.pep:*
      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-483-859-10
US-08-487-157-10
US-08-487-157-10
US-08-487-167-10
US-08-487-167-10
US-08-266-149-10
US-08-266-149-10
US-09-074-659-10
US-09-074-659-10
US-09-106-468-10
US-09-106-468-10
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US-09-03-44-483-57
US-08-944-483-57
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                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
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1 IVNGEEAVPGSWPWQVSLQD 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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APPLICANT: LOCSMORE, Sheena M.
APPLICANT: LOCSMORE, Sheena M.
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: OWENS, Raymond P.
APPLICANT: OWENS, Raymond P.
APPLICANT: OMENS: 23
CONRESPONDENCE SIME & McBurney
STREET: Sime A McBurney
STREET: Suite A McBurney
STRANDENSES: Suite A McGurney
STRAND
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Batent No. 5665353
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 112; DB 1; Length 228; 100.0%; Pred. No. 1.1e-09; cive 0; Mismatches 0; Indels 0
                                                                                                                                                                  Sequence 10, Application US/08483859
Patent No. 5656436
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IVNGBEAVPGSWPWQVSLQD 20
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1 IVNGEEAVPGSWPWQVSLQD 20
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Best Local Similarity 100.
Matches 20; Conservative
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US-08-483-859-10
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                                                                                                          RESULT 2
US-08-483-859-10
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Reduced Protease Activity
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               ALTIME OF INVESTION:

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSER: Sim & McBurney

STREET: Suite 701, 330 University Avenue

CITY:
COMPUTER SILE 701, 330 University Avenue

CITY:
COMPUTER: Suite 701, 330 University Avenue

CITY:
COMPUTER: Canada

ZIP: M5G 1R7

COMPUTER: READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: DEACHTIN RELease #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,173
FILING DATE: 07-101-1995
CLASSIFICATION NUMBER: US/08/78,091
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/296,149
FILING DATE: 25-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAMME: Stewart, Michael I.
NAMME: Stewart, Michael I.
NAMME: Stewart, Michael I.
NAMME: Stewart, Michael I.
NAMME: Stewart, Michael II.
NAMME: Stewart, Michael II.
NAMME: Stewart, MICHAEL II.
NAMME: STEWENCE/DOCKET NUMBER: 1038-493 MIS:vg
TELECOMMUNICATION INFORMATION:
THERECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LOOSNORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin
TITLE OF INVENTION: Reduced Procease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEB: Sim & McBurney
ADDRESSEB: Sim & McBurney
STREET: Suite 701, 330 University Avenue
FITLE OF INVENTION: Reduced Protease Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08487167; Patent No. 5869302; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (416) 595-1155
TELERAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
SYRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IVNGEEAVPGSWPWQVSLQD 20
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COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , TOPOLOGY: linear
US-08-472-173-10
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CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-08-487-167-10
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APPLICANT: LOSSMORE, Sheena M
APPLICANT: CHONG, Pan-Ping
APPLICANT: COMEN, Raymond P.
APPLICANT: CALEIN, Marchel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
CORRESPONDENCE ADDRESS:
ADDRESSES: 21 & McBurney
                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 112; DB 2; Length 228; Best Local Similarity 100.0%; Pred. No. 1.1e-09; Matches 20; Conservative 0; Mismatches 0; Indels 0
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COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
100.0%; Score 112; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1038-390
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; Sequence IO. Application US/08296149
; Patent No. 593-8297
; GENERAL INFORMATION:
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
                                                                     TELEFAX: (416) 595-1163
| INPORMATION FOR SEQ ID NO: 10:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 228 manno acids
| TYPE: amino acid
| STRANDEDNESS: single
| TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IVNGEEAVPGSWPWQVSLQD 20
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INFORMATION FOR SEQ ID NO: 10
SEQUENCE CARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
                                            (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IVNGEEAVPGSWPWQVSLQD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IVNGEEAVPGSWPWQVSLQD 20
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linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Suite CITY: Toronto STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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US-18-482-18.16.10
US-18-482-18.16.10
US-18-482-18.16.10
US-18-482-18.16
Patent No. 593523
GENERAL INFORMATION:
APPLICANT: COSSONEE, Sheena M
APPLICANT: COMEN. Raymond P.
APPLICANT: COMEN. Analog of Haemophilus Hin47 Protein with Reduced Protease Act
NUMBER OF SEQUENCES: 3
COMERSEOR OF SEQUENCES: 3
COUNTRY: Toronto
CITY: Toronto
CITY: Toronto
CITY: Toronto
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER REABABLE FORM:
MSDIUM TYPE: Floppy disk
COMPUTER PRABABLE FORM:
MSDIUM TYPE: Rloppy disk
COMPUTER: REABABLE FORM:
MSDIUM TYPE: Rloppy disk
COMPUTER: REABABLE FORM:
MSDIUM TYPE: Ratentin Release #1.0, Version #1.25
CURSSIPICATION NUMBER: US/08/482,816
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/228,199
FILING DATE: 26-AUG-1994
ATTORNEY/AGENT NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT NUMBER: US 08/278,091
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100.0%; Score 112; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-494 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1038-508 MIS:vg
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,167
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION MATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGBAT INFORMATION:
NAME: STEWART, MICHAEL II.
NAME: STEWART, MICHAEL II.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-508 M
TELEPHAN: (416) 595-1163
TELEPHAN: (416) 595-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IVNGEBAVPGSWPWQVSLQD 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-08-482-816-10
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APPLICANT: LOOSMORE, Sheena M.
APPLICANT: TANG, Yan-Ping
APPLICANT: COMEN, Real-
APPLICANT: COMEN, Real-
APPLICANT: COMEN, Real-
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SUGURNCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: 61m & McBurney
STREET: 61m & McBurney
STREET: 61m to McBurney
STREET: 61m to McBurney
STREET: 61m to McBurney
STREET: 61m & McGurney
STREET: 61
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                                                                    STREET: Geh Floor, 330 University Avenue
CITY: Toronto
COUNTRY: Canada
JULIA MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,271
FILING DATE: 20-JUN-1996
CLASSIFICATION NUMBER: 1038-580
FLASSIFICATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 1038-580
TELEFONE: (416) 595-1155
TELEFONE: (416) 595-1155
TELEFONE: CHARACTERISICS:
SEQUENCE CHARACTERISICS:
TELEFAX: (416) 595-1163
TELEFAX: (416) 595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 112; DB 2;
Pred. No. 1.1e-09;
                                               3: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,167
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-074-660-10
; Sequence 10, Application US/09074660
; Patent No. 6020183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IVNGEEAVPGSWPWQVSLQD 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-615-271-10
    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
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                                                                                                                                                 APPLICANT: LOOSMORE, Sheena M
APPLICANT: LOOSMORE, Yan-Ping
APPLICANT: VANG, Yele
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease Act
CORRESPONDENCES: 23
ADDRESSES: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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CHONG, Pele
CHONG, Raymond P.
KLEIN, Michel H.
VENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
VENTION: PROTEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 112; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFPLING DATE:

CLASSIFICATION NOMBER: US/UB/BU1,499

FILING DATE:

APPLICATION NUMBER: US 08/482,816

FILING DATE: 07-UN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/296,149

FILING DATE: 26-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/278,091

FILING DATE: 21-UL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-671 MIS:jb

TELEFORMUNICATION INFORMATION:

TELEFORMUNICATION SEQ 1163

INFORMATION POR SEQ 1D NO: 10:

SEQUENCY: CALL SECOND 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                             Sequence 10, Application US/08801499
Patent No. 5962430
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 10, Application US/08615271; Patent No. 5981503
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-801-499-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: LOOSMORE,
APPLICANT: YANG, YAN,
APPLICANT: CHONG, Per,
APPLICANT: COMEN, RAY,
APPLICANT: COMEN, RAY,
ITTLE OF INVENTION: J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Ontario
US-08-801-499-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-08-615-271-10
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APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: Michel H.
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
TITLE OF INVENTION: PROTEASE ACTIVITY
NUMBER OF SECURISCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 112; DB 3; Length 228; Best Local Similarity 100.0%; Pred. No. 1.1e-09; Matches 20; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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STATE: Oncario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTRY: CADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRY: LBM PC compatible
OPERATING SYSTEM: PC-DoS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/09/106,468
FILING DATE:
CLASSIFICATION NUMBER: US/09/106,468
FILING DATE:
CLASSIFICATION NUMBER: US/09/106,468
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US/09/106,468
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US/09/106,468
FILING DATE:
CLASSIFICATION:
ATORNEY/AGENT INFORMATION:
MAME: STEWARY, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-825
TELECOMPUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
'ARRICH TANDAMATION ACIDS
SEQUENCE CHARACTERISTICS:
'ARRICH TANDAMATION ACIDS
'SEQUENCE CHARACTERISTICS:
'ARRICH TANDAMATION ACIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 112; DB 3; Best Local Similarity 100.0%; Pred. No. 1.1e-09; Matches 20; Conservative 0; Mismatches 0;
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6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 10, Application US/09106468
; Patent No. 6114125
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IVNGEEAVPGSWPWQVSLQD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IVNGEEAVPGSWPWQVSLQD 20
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                                                                             INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 228 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                              (416) 595-1163
                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                              ; TYPE: amino acid;
; STRANDEDNESS: sir;
; TOPOLOGY: linear
US-09-074-659-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6th Flo
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-09-106-468-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-106-468-10
                                         TELEFAX:
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US-09-074-659-10
US-09-074-659-10
Sequence 10, Application US/09074659
Fatent No. 6025342
Fatent No. 6025342
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: CHONG, Peale
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 112; DB 3; Length 228; Best Local Similarity 100.0%; Pred. No. 1.1e-09; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,659
FILING DATE: US/09/074,659
FILING DATE: 07-UNN-1995
PRIOR APPLICATION NUMBER: US 08/294,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: US 08/296,149
FILING DATE: 21-UL-1994
PRIOR APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-UL-1994
ATTORNEY/AGRYT INFORMATION:
NUMBER: STORMEY/AGRYT INFORMATION:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-UUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-731 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (146) 595-1155
TELEPHONE: (146) 595-1165
FELEPHONE: (146) 595-1165
FELEPHON
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STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MGS LR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-730 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IVNGEEAVPGSWPWQVSLQD 20
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/600,273
APLING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
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Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 228 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sin
                      STREET: 6th Floc
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
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ADDRESSEE:
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                                                                  Sequence 10, Application US/09106466A

Sequence 10, Application US/09106466A

Patent No. 6147057

GENERAL INFORMATION:
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CLEIN, Michel H.
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
TITLE OF INVENTION: PROTEASE ACTIVITY
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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Perent No. 613580

GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: CHONG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CLEIN, Michel H.
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
TITLE OF INVENTION: PROTEASE ACTIVITY
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 112; DB 4; Length 228; 100.0%; Pred. No. 1.1e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Plany Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,466A
FILING DATE:
CLASSIFICATION DATA:
PRILNG DATE: 20-JUN-1996
CLASSIFICATION: 514514
ATORNEY AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 1038-826
TELEFORME (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: ATORNEY SINGLED ACIDENCY: 1408-1616
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IVNGEEAVPGSWPWQVSLQD 20
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Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-09-106-466A-10
                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-106-467-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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US-08-385-540A-16
Sequence 16, Application US/08385540A
Sequence 16, Application US/08385540A
Sequence 16, Application US/08385540A
Sequence 16, Application US/08385540A
Setent No. 5945102
TITLE OF INVENTION:
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STREET: NJ
COMPUTER: NJ
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM Compatible
COMPUTER: TEM Compatible
COMPUTER: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,540A
                                                           STATE: ORGANIS
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READBLE FORM:
MEDIUM TYPE: FIDADPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PET CATION DATA:
APPLICATION NUMBER: US/09/106,467
FILING DATE:
CLASSIFICATION NUMBER: US/09/106,467
FILING DATE: 20-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US/09/106,467
FILING DATE: 20-JUN-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 1038-824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 10:
SEQUIRACE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 112; DB 4;
100.0%; Pred. No. 1.1e-09;
tive 0; Mismatches 0;
6th Floor, 330 University Avenue
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REGISTRANCE NORMER: 3155

REFERENCE DOCKET NUMBER: 31572-101A

TELECOMMUNICATION INCOMMUNICATION

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97.3%; Score 109; DB 2; Length 20;

Query Match

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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPREBACE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 643, Application US/09925297; Patent No. US20020081659A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IVNGEEAVPGSWPWQVSLQD 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 20; Conservative
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US-09-925-297-643
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Sequence 643, App
Sequence 529, App
Sequence 152, App
Sequence 152, App
Sequence 695, App
Sequence 13, Appli
Sequence 13, Appli
Sequence 334, App
Sequence 934, App
                                                                                                                               February 12, 2003, 10:22:36; Search time 3.04478 Seconds (without alignments) 167.821 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

1: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

3: \cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

4: \cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

7: \cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

9: \cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

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12: \cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

13: \cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

14: \cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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0 US-09-925-297-695

2 US-09-925-297-695

2 US-09-988-975A-1

US-09-988-975A-1

US-09-981-353-23

US-09-981-353-23

US-09-985-791-695

US-09-895-793-4

US-09-895-793-895

US-09-895-814-934

US-09-895-814-934

US-09-822-827-934

US-09-895-814-934

US-09-895-814-934

US-09-895-814-934

US-09-895-814-934

US-09-895-81-895-81-895-81-81-935-81-936-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-895-81-89
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                                                                                        OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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1 IVNGEEAVPGSWPWQVSLQD 20
                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                    Run on:
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Sequence 932, App Sequence 895, App Sequence 895, App Sequence 932, App Sequence 115, App Sequence 1112, App Sequence 130, App Sequence 330, App Sequence 33	PHARMACEUTICAL AND	h 20; s 0; Gaps 0;
	ТНЕІ К	12; Length 10; 0; Indels
0. US-09-895-814-895 0. US-09-895-814-895 0. US-09-759-143-893 0. US-09-759-143-895 0. US-09-759-143-895 0. US-09-759-143-895 0. US-09-759-180-668-993 0. US-09-812-827-893 0. US-09-812-827-893 0. US-09-815-888-6 0. US-09-888-615-111 0. US-00-174-73-73-0 0. US-10-175-73-330 0. US-10-175-73-330 0. US-10-175-73-330 0. US-10-175-73-330	ALIGNMENTS 3036371 INE PROTEINASES AND 10.10.7 11.08 2.7 12.1 2.8 8.8	Score 112; DB Pred. No. 7.8e- 0; Mismatches
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	6-371-6 ce 6, Application US/10036371 L INFORMATION: CANT: BJARNARSON, JON B. OF INFORMATION: COSMETTC USE REFERENCE: 81691/28496 NT FILLING DATE: 1099-10-12 APPLICATION NUMBER: 09/411, 6 FILING DATE: 1999-10-12 APPLICATION NUMBER: 096/49 FILING DATE: 1999-06-18 ROF SEQ ID NOS: 8 ARE: PATENTIN OF SEQ ID NOS: 8 NO 6 FILLING DATE: 1999-06-18	100.0%; larity 100.0%; Conservative
44444444444444444444444444444444444444	6-371-6 Ce 6, Application US/10 No. US2002141987A1 LINFORMATION: CANT: BJARNARSON, JON B OF INVENTION: FISH SER OF INVENTION: FISH SER OF INVENTION: ESHSER OF INVENTION: BJ891/284960 NI APPLICATION NUMBER: 09 PILLING DATE: 1999-10-1 APPLICATION NUMBER: 50 FILING DATE: 1999-6-11 ROF SEQ ID NOS: 8 APPLICATION NUMBER: 50 FILING DATE: 1999-6-11 ROF SEQ ID NOS: 8 APPLICATION NUMBER: 50 FILING DATE: 1999-6-11 NO 6 FILING DATE: 1999-6-11 NO 6 HI 20 FILING BATE: PRESE PATENTIN OF SEQ ID NOS: 8 FILING BATE: PRESE PATENTIN OF SEQ ID NOS: 8 FILING BATE: PRESE PATENTIN OF SEQ ID NOS: 8 FILING BATE: PRESE PATENTIN OF SEQ ID NOS: 8 FILING BATE: PRESE PATENTIN OF SEQ ID NOS: 8 FILING BATE: PRESE PATENTIN OF SEQ ID NOS: 8 FILING BATE: PRESE PATENTIN OF SEQ ID NOS: 8 FILING BATE: PRESE PATENTIN OF SEQ ID NOS: 8 FILING BATE: PATENTIN OF SEQ ID	Similarity O; Conser
01202222222222222222222222222222222222	RESULT 1 US-10-036-371-6 Sequence 6, Application US/10 FRACTA NO. US2002041987A1 GENERAL INFORMATION: APPLICANT: BJARNARSON, JON B TITLE OF INVENTION: FISH SER; TITLE OF INVENTION: FISH SER; TITLE OF INVENTION: FISH SER; CURRENT APPLICATION UNMERR: 0.9 PRIOR PLING DATE: 1999-10-11 PRIOR PLING DATE: 1999-10-11 PRIOR PLING DATE: 1999-10-11 PRIOR FILING DATE: 1999-06-13 PRIOR FILING DATE: 1999-06-13 PRIOR FILING DATE: 1999-06-13 NUMBER OF SEQ ID NOS: 8 SOFTWARE: PATENTING DATE: 1999-06-13 NUMBER OF SEQ ID NOS: 8 SOFTWARE: PATENTING DATE: 1999-06-13 NUMBER OF SEQ ID NOS: 8 SOFTWARE: PATENTING DATE: 1999-06-13 NUMBER OF SEQ ID NOS: 8 SEQ ID NO 6 SEQ I	Query Match Best Local & Matches 20

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APPLICANT: PAGE AND ALL ALL ALL APPLICANT: PAPPLICANT: ALL ALL ALL APPLICANT: ALL JIANGCHUN APPLICANT: KAIOS, MICHAEL D. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER FILE REFERENCE: 2.0012.6.533 CURRENT PILING DATE: 2.001-08-06 NUMBER OF SEQ ID NOS: 155 SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 152 LENGTH: 270
                                                                                                                                     Sequence 529, Application US/09925297

Patent No. US20020081659A1

GENERAL INFORMATION:

APPLICANT: ROSEON et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PAIO5

CURRENT APPLICATION NUMBER: US/09/925,297

CURRENT FILING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2000-03-08

PRIOR PLING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 928

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 529

LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 86.6%; Score 97; DB 10; Length 192; Best Local Similarity 90.0%; Pred. No. 9e-07; Matches 18; Conservative 0; Mismatches 2; Indels
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US-09-925-297-576
US-09-925-297-576
Sequence 576, Application US/09925297
Setent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 152, Application US/09923779
Patent No. US20020076721A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IVNGEEAVPGSWPWQVSLQD 20
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34 IVNGEDAVPGSWPWQVSLQD 53
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Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-09-925-297-529
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US-09-923-779-152
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEX: SITE
LOCATION: (137)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . LOCATION: (143)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-297-643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (130)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                  LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (126)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 97.3%; Score 109; DB 10; Length 146; Best Local Similarity 95.0%; Pred. No. 1.4e-08; Matches 19; Conservative 1; Mismatches 0; Indels
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Patent No. US20020064856A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PLOWENN, GREGORY
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CAENEPEEL, SEAN
APPLICANT: MANNING, GERARD
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
FRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTIN OFF. 2.1
  PRIOR APPLICATION NUMBER: PCT/USO0/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SEQ ID NOS: 928
SEQ ID NO 643
LENGTH: 146
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Best Local Similarity 95.0
Matches 19; Conservative
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; ORGANISM: Homo sapiens
US-09-888-615-96
                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
LOCATION: (94)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
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US-09-888-615-96
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LENGTH: 263
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1 IVNGEEAVPGSWPWQVSLQD 20

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Mismatches
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                                                            1 IVNGEEAVPGSWPWQVSLQ 19
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OTHER INFORMATION: S, P or Y
PEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MOD_RES
LOCATION: (11)
OTHER INFORMATION: S or T
FEATURE:
NAME/KEY: MOD_RES
                  15; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Gadus sp.
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD RES
LOCATION: (20)
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                                                                                                                                                                RESULT 8
US-10-036-371-4
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                  Matches
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                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: SITE
LOCATION: (187)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (187)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: acids
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LOCATION: (213)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-297-576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (220)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (34)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-297-695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Sequence 695. Application US/09925297

Patent No. US2002008165941

SEMERAL INFORMATION:

TITLE OF INVENTION:

FILLE REFERENCE: PAIG

CURRENT APPLICATION NUMBER: US/09/925,297

CURRENT APPLICATION NUMBER: US/09/925,297

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 928

SEQ ID NO 695

LENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 76.8%; Score 86; DB 10; Length 269; Best Local Similarity 78.9%; Pred. No. 4.3e-05; Matches 15; Conservative 1; Mismatches 3; Indels
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/0599
PRIOR PILING DATE: 2000-03-08
PRIOR PAPLICATION NUMBER: 60/124,270
PRIOR PELICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SEQ ID NO ST6
LENGTH: 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 VVGGEEARPNSWPWQVSLQ 52
                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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| Sequence 4, Application US/10036371
| Sequence 4, Application US/10036371
| Patent No. US20020141987A1
| GENERAL INFORMATION:
| APPLICANT: BJARNARSON, JON B.
| TITLE OF INVENTION: COSMETIC USE
| TITLE OF INVENTION: COSMETIC USE
| FILE REPERENCE: 81691/249460
| CURRENT APPLICATION NUMBER: US/10/036,371
| CURRENT APPLICATION NUMBER: 09/411,688
| PRIOR FILING DATE: 1999-10-12
| PRIOR FILING DATE: 1999-06-18
| SOFTWARE: PATENTION NUMBER: 5086/99
| PRIOR FILING DATE: 1999-06-18
| SOFTWARE: PATENTION OF: 2.1
| SEQ ID NO 4
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| Patent No. US20020119531A1
| Patent No. US20020119531A1
| Patent No. US20020119531A1
| APPLICANT: Baly Preeti G.
| TITLE OF INVENTION: PROSTATE-ASSOCIATED PROTEASE ANTIBODY
| FILE REFERENCE: PP.02D7-2 CIP
| CURRENT FILING DATE: 2001-11-19
| NUMBER OF SEQ ID NOS: 8
| SEQ ID NO 1
| ENGTH: 283
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2; Indels
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OTHER INFORMATION: Incyte ID No. US20020119531A1 556016
PEATURE:
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APPLICANT: Foy, Teresa R. Peblicant: Foy, Teresa R. Peblicant: Ranger, Gary R. TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 21012.1.534C2
CURRENT APPLICATION WHERE: US(19/895,793
CURRENT FILING DATE: 2001-06-29
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER PILE REPERBRICE: 210121.427027 CURRENT APPLICATION NUMBER: US/10/012,896 CURRENT FILING DATE: 2001-12-10 NUMBER OF SEQ ID NOS: 1011 SOFTWARE: PastSEQ for Windows Version 3.0 SEQ ID NO 934 LENGTH: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 75.0%; Score 84; DB 9; Length 393; Best Local Similarity 77.8%; Pred. No. 0.00012; Matches 14; Conservative 2; Mismatches 2; Indels
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Pred. No. 0.00012;
2; Mismatches 2; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 934
LENGTH: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 934, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Wi. Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Carig H.
APPLICANT: Variag H.
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
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Best Local Similarity 77.8
Matches 14; Conservative
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CRGANISM: Homo sapiene
US-09-895-793-934
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CRGANISM: Homo sapiens
US-10-012-896-934
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US-09-895-814-934
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US-09-895-793-934
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APPLICANT:
APPLICANT:
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                                                                                        Length 283;
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Pred. No. 0.00012;
2; Mismatches 2; Indels
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; OTHER INFORMATION: Incyte ID No. US20020160382A1 991163CD1
US-09-981-353-23
                                                                                                                            2; Indels
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Pred. No. 8.6e-05;
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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              ; LOCATION: 235
; OTHER INFORMATION: unknown or other
US-09-988-975A-1
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Wantanabe, Yoshihiro
Meagher, Madeleine Joy
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Hepler, William T.
Henderson, Robert A.
Hural, John
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Best Local Similarity 77.8%;
Matches 14; Conservative ;
                                                                                      75.0%;
nilarity 77.8%;
Conservative
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                                                                                          Query Match
Best Local Similarity
Matches 14; Conserv
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US-10-012-896-934
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: CORPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FILE REFERENCE: 10.1021.427.026
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001.06-29
NUMBER OF SEQ ID NOS: 990
SOFTHARE: FASTESEQ for Windows Version 3.0
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Hepler, William T.
Henderson, Robert A.
Hural, John
MCNeill, Patricia D.
Vinals de Bassols, Carlota
Sequence 934, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
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Patent No. US20020022248Al
GENERAL INFORMATION:
                                                                                                          APPLICANT: William APPLICANT: Dillon, Davin C.
APPLICANT: Millon, Davin C.
APPLICANT: Millon, Davin C.
APPLICANT: Millon, Gennifer L.
APPLICANT: Millon, Yugiu
APPLICANT: Retter, Marc M.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: List Samuel
APPLICANT: Carter, Darrick
APPLICANT: List Samuel

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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Suan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
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; ORGANISM: Homo sapiens
US-09-895-814-934
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US-09-759-143-934
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APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Howall, John
APPLICANT: Howalton, Particia D.
APPLICANT: Howalton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND TITLE OF INVENTION: LIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICANTION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 393
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CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FASLSEQ FOR Windows Version 3.0
LENGTH: 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 934, Application US/09780669; Patent No. US20020051977A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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|157 IVGGESALPGAWPWQVSL 174
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                                                                                              ; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-934
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US-09-780-669-934
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US-09-780-669-934
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APPLICANT:
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February 12, 2003, 10:03:55; Search time 2.68657 Seconds (without alignments) 198.395 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                       OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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| SIDSZ/gcgdata/geneseqf/geneseqp-embl/AA1999.DAT:*
| SIDSZ/gcgdata/geneseqf/geneseqp-embl/AA2000.DAT:*
| SIDSZ/gcgdata/geneseqf/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		N-Cerminal polynyd	Peptidase substrat	Peptide component	Ketone analogue nr	Cathenain G inhibi	Chromodenic nentid	Cathenain G inhibi	Aminonaphthalene n	Bacillas alkali ar	Serine protease in	
SUMMAKIES	ID	2 220404669	66404304	AAR04012	AAR10887	AAR11223	AAR29964	AAR34258	AAR38410	AAR44109	AAR52024	AAR46223	
	0.08	-	,	11	12	12	13	14	14	14	15	15	
	Query Match Length DB	4	۳.	4	4	4	4	4	4	4	4	4	
	Query Match	0.001		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
	Score	21	1 3	7.7	21	21	21	21	21	21	21	21	
	Result No.	-		7	m	4	S	9	7	60	6	10	

Sequence of intern Substrate for pept Substrate for pept Porphyromonas ging Cell proliferation Degradable peptide Serine protease-in Substrate peptide Serine protease-in Substrate for seri Proteinse site of Synthetic substrat B. subtilis subtil Synthetic oligopep Indicator for dere Peptide conjugated Alkaline protease Peptide comprising Chymotrypsin enzym Substrate peptide Synthetic Plase s Model substrate pe Protease peptide s Chymotrypsin substr Subtilisin substr Subtilisin substr Subtilisin substrate Model peptide substrate Model	irst entry) hydroxyalkanoyl peptide. moyl peptide; protease; peptidase; prodrug, moyl peptide; protease; peptidase; prodrug, 83FR-0308051. NATIONAL DE LA RECHERCHE SCIENTIFIQUE. yer R; 5/48. minoacid derivs opt. al active gps., e.g. chloroquine, are water-soluble ntiparastitic cpds. and protease targets. 15; 20pp; french. 15; 20pp; french.
AARS1781 AAR72202 AAR722020 AAR722020 AAR722036 AAR722036 AAR722036 AAR857039 AAR857039 AAR857039 AAR857030 AAR85451 AAR85451 AAR85451 AAR861357 AAR861357 AAR86133 AAR86133 AAR86665	- AA. 1 peptide. protease; RECHERCHE 1 peptide 7 e.g. ch ch, anoyl-L-Al
	n; 4 AA /) /anoyl p // // // // // // // // //
	ttry) pptide; 1 00984. 08051. DE LA alkanoy; ve gps. sitic q p; frem
पं पं पं पं पं प प प प प प प प प प प प	tandard; Protein; 4 (first entry) polyhydroxyalkanoyl yalkanoyl peptide; p 5. 4; 84EP-0400984. 3; 83FR-0308051. NTRE NATIONAL DE LA , Mayer R; 296065/48. polyhydroxyalkanoyl erminal active gps., or antiparasitic cp
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	itandard itandard i (fir polyhy, i. i. jolyhy, ii. is. is. is. is. is. is. is. is. is.
	NP40459 st NP40459; NP40459; NOV-1991 Lerminal Jyhydroxy 1126685-A. NOV-1985 MAY-1983 MAY-1983 MAY-1983 MAY-1983 MAY-1983 MAY-1983 MAY-1983 MAY-1983 MAY-1983 MAY-1983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The analogues may be useful in treatment of a variety of disease states. The scissile amide group is replaced with H or a substituted Carbon moiety effectively inhibiting the activity of peptidases such as elastase, plasmin thrombin, urokinase etc.
                                                                                                                                                                                    Gaps
N2-NH- derived from an aromatic amine, eg P-nitro-aniline, alphadaunorubbichion or filoroguine, or it is a gp. which may confer activity, eh H, OH, CH2CLI. When X is the residue of a drug, the cpd. is a prodrug in which the peptide is the substrate for a specific procease secreted by the target cell for the active drug, eg tumour cells or microorganism pathogens, eg Plasmodium falciparum. Due to the polyhydroxy gp., the cpds. are very soluble in water or buffer soln. and are able to bu used at high concon. The cpds. also allow the detection of proteases and peptidases and allow easy determination of the best substrate for a particular
                                                                                                                                                                                                                                                                                                                                                                            Elastase; plasminogen activator; cathepsin; calpain; enkephalinase;
Angiotensin converting enzyme.
                                                                                                                                                                                                                                                                                                                                                     Peptidase substrate analogues having peptidase inhibition activity.
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Terminal modified from -COOH to -COCOR
/note= "R = alkyl group or -H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptidase substrate analogue cpds. - useful as protease inhibitors in treatment of disease states.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 21; DB 11; Length 4; 100.0%; Pred. No. 7.8e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                           100.0%; Score 21; DB 5; Length 4; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                     AAR04012 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angelastro M, Mehdi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RICH ) MERRELL DOW PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88US-0254762.
89EP-0402763.
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                                                                                                                                                                        Local Similarity 100.
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Best Local Similarity
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Sequence
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This peptide is the RI gp. of the cpd. of formula: RINHCH(R2)-COCF2CF3. This cpd. is a peptidase substrate analogue and is a specific enzyme inhibitor for a range of proteases, e.g. serine., carboxilic acid., and metallo-proteases. It is useful in the treatment of rheumatoid arthritis, thrombosis and psoriasis and is also used as a male contraceptive. See also AAR10876-83, AAR10886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel serine-, carboxylic acid-and metallo-proteinase-inhibitors - inhibit range of proteinase(s) in treating rheumatoid arthritis, thrombosis and psoriasis, also is a male contraceptive
                                                                                                                                                                             Protease inhibitor; rheumatoid arthritis; thrombosis; psoriasis; male contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                  Peptide component of pentafluoroethylcarbonyl analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 21; DB 12;
llarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mehdi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ketone analogue protease inhibitor #2
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AAR10887 standard, Protein; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angelastro MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; page 25; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RICH ) MERRELL DOW PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0385624.
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                                                                                          (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AA;
                                                                                                                                                                                                                                                                                                                                                                                         25-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                          10-APR-1991
                                                                                                                                                                                                                                                                                                                                              30-JAN-1991
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                                                                                                                                                                                                                                                                                                 EP410411-A
                                                                                                                                                                                                                                                    Synthetic.
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                                               AAR10887;
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Gaps

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Conservative

Matches

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Best Local Similarity
Matches 4; Conserv.
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                             21-APR-1992;
                                             23-MAY-1991;
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            26-NOV-1992
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AAR34258
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                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                           This peptide is a specific example of a highly generic protease inhibitor useful for medical purposes. The peptide analogues include inhibitors of urokinase, remin, cathepsin D, etc. which can be used as anti-proliferative agents and abortifacients, hypotensives, antiinflammatory and antidemyelinating agents, respectively. See also AAR11222 and AAR11224-R11238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "N-terminal amino acids of the peptides of AAR29963-64 are pref. linked by -C(O)-phenylene-C(O)-, esp. wherein the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cathepsin G; elastase; connective tissue; degradation; protease; gout; rheumatoid arthritis; emphysema; ARDS; adult respiratory distress syndrome; para-phenylene.
                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                        New ketone analogue peptidase and isomerase inhibitors - for inhibition of leukocyte elastase, cathepsin G, thrombin, chymotrypsin, plasmin etc.
                                                                                                                                                                                                                                                                                                                       100.0%; Score 21; DB 12; Length 4; llarity 100.0%; Pred. No. 7.8e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phenylene is a para-phenylene gp."
                                  /label= Methoxysuccinyl-Ala
                                                  /label= Phe-carboxyoxalyl
                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    AAR29964 standard; peptide; 4 AA.
                                                                                                                                                                                                                            Claim 5; Page 26; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cathepsin G inhibiting fragment.
                                                                                                                                      (RICH ) MERRELL DOW PHARM INC
                                                                                                     90EP-0117461
                                                                                                                     89US-0405491
                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-APR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                        WPI; 1991-081980/12.
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                                                                                                                                                       Flynn GA, Bey P;
                                                                                                                                                                                                                                                                                                        4 AA;
                 Key
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                                                                  EP417721-A.
Synthetic.
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                                                                                                                                                                                                                                                                                                        Sequence
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This sequence is an example of a highly generic formula.

Inhibitors of cathepsin G and elastase for preventing connective inhibitors of cathepsin G and elastase for preventing connective tissue degradation are chemically linked inhibitors of the proteases clastase (pref. the peptide of AAR29963, or Lys(2021-pro-Val or Val-pro-Val) and cathepsin G (pref. the peptide of AAR2964, or Val-pro-Phe or Phe).

The N-terminal amino acids of the peptides of AAR2963-64 are pref. Inted by -C(O)-phenylene G(O)-, esp. wherein the phenylene is a para-phenylene gp.

The cpds. have an anti-inflammatory effect useful in the treatment of gout, rhumaroid arthritis and other inflammatory diseases and to prevent elastin mediated tissue damage. They can also be used in the treatment of emphysema and adult respiratory distress syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                               New peptide derivs. used as cathepsin G and elastase inhibitors for treating gout, rheumatoid arthritis, inflammatory disorders, emphysema and adult respiratory distress syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 21; DB 13; Length 4; llarity 100.0%; Pred. No. 7.8e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                     Janusz MJ, Mehdi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chromogenic peptide substrate for peptidase assay.
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/note= "Phe-p-nitroanilide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alkaline protease; detergent; stability
                                                                                                                                                                                                                 Angelastro MR, Bey P, Doherty NS,
Peet NP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13-17; Page 52; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                     (RICH ) MERRELL DOW PHARM INC.
92WO-US03288
                                                                    91US-0704449
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Gaps

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The sequences given in AAR38410-11 are cathepsin G inhibiting peptides which were produced by standard peptide synthesis methods. In the context of the invention one of these peptides may be linked via their N-termini to an elastase inhibiting peptide (see features table). The peptide conjugates may be used to prevent neutrophilmediated connective tissue degradation associated with inflammatory diseases eg. gout and rheumatoid arthritis. They may also be used for preventing elastin-mediated tissue damage in the treatment of emphysema and adult respiratory distress syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5-(N-succinyl-alanyl-alanyl-prolyl-phenylalanyl)aminonaphthalene-1-(N-propyl)sulphamide (Claim 1) and 5-(N-benzyloxycarbonyl-alanyl-alanyl-yptonyl-phenylalanylylaminonaphthalene-1-(N-propyl)sulphamide (Claim 2) are prepared by initially reacting N-benzyloxycarbonyl-phenylalanine with isobutyl chloroformate in tetrahydrofuran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prepn. of new succinyl-alanyl-alanyl-propyl-phenylalanyl-amino-naphthalen-propyl-sulphamide - for use as ansa-substrate in the quantitative determn. of chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Suc-Ala (Claim 1) or 2-Ala (Claim 2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= OTHER
/note= "Phe-NH-(1,5-naphthylene)-SO2NH-C3H7"
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chymotrypsin assay; ansa-substrate; detector group.
                                                                                                                                                                                                                                                                               100.0%; Score 21; DB 14;
100.0%; Pred. No. 7.8e+05;
ttive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aminonaphthalene propyl sulphamide tetrapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1 and 2; Column 8; 4pp; Russian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palaima AI, Yanchene
                                  Claim 13-17; Page 52; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AS LITH BIOCHEM INST.
AS USSR MOLECULAR GENETICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR44109 standard, peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label - OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90SU-4872552.
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                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                            Local Similarity
 tissue degradation
                                                                                                                                                                                                                                                 4 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
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                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                 Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR44109
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                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Linked via a linking chain such as -CO-pienylene-CO- to the N-terminal of a Cathepsin G inhibiting molecule as described in AAR38410-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Way opt. be modified by COCOR, CF2CF3, CF3, CHF2, COOR3, CONHR3, CF2CHR3CONHR, H, alkyl, aryl, aralkyl or COR; where R3 is H, alkyl, phenyl or benzyl and R is OH or alkoxy"
                                                                                                                                                                                                                               The peptide is a chromogenic substrate for use in a peptidase assay to test the peptidase activity of a novel alkaline protease. Detergent was found to interfere with the assay by reducing the protease activity. See also AAR3459-61 and AAR34463-66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inflammatory disease; prevention; rheumatoid arthritis; emphysema; neutrophil-mediated connective tissue degradation; gout; elastase; inhibition; adult respiratory distress syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cathepsin G and elastase inhibitors - prevents connective
                                                                                                                                                                                                                                                                                                                                                        Length 4;
                                                                                                               Alkaline protease produced by bacillus stable in alkaline conditions - used in detergents and bleaches to decompose proteinaceous stains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mehdi S;
                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 21; DB 14;
100.0%; Pred. No. 7.8e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Janusz MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Doherty NS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                          Disclosure, Page 8; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cathepsin G inhibitor peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR38410 standard; Protein; 4 AA
                                                      Lalonde JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RICH ) MERRELL DOW PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92ZA-0003602.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
 CHEMGEN CORP.
VISTA CHEMICAL CO.
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
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                                                      Hsiao H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-197380/24
                                                                                         WPI; 1993-134465/16
                                                                                                                                                                                                                                                                                                                       4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angelastro MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Modified-site
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                                                      DW,
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                                                                                                                                                                                                                                                                                                                         Sequence
   (CHEM-) (
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                                                      Fodge
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Sequence 4 AA;
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Modified-site
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                           04-AUG-1994
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                                                                                        Synthetic.
           AAR46223;
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                                                                      Gaps
followed by reaction with 5-aminonaphthalene-1-(N-propyl)sulphamide. The new compounds are used as detector groups in quantitative determination of chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A novel alkali protease obtained from Bacillus NKG-21 is defined by its physico-chemical properties including substrate specificity for the tetrapeptide AAR52024.
                                                                                                                                                                                                                    Bacillus NKS-21 alkali protease; hydrolysis; thermostable enzyme;
                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                         New alkali protease stable to heat and detergent - useful as industrial enzyme, eg in washing compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 21; DB 15; Length 4; Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                     Length 4;
                                                                    Indels
                                                   Query Match
100.0%; Score 21; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                   Bacillus alkali protease substrate.
                                                                                                                                                 AAR52024 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR46223 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                         /label= OTHER
/note= "Phe-MCA"
                                                                                                                                                                                                                                                                                          /note= "Suc-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 2; 10pp; Japanese
                                                                                                                                                                                                                                                                                  'label= OTHER
                                                                                                                                                                                                                                                                                                                                                                      92JP-0296360.
                                                                                                                                                                                                                                                                                                                                                                                       92JP-0207302.
                                                                                                                                                                                 28-NOV-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       (SHOW ) SHOWA DENKO KK
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-128672/16.
                                                                                                                                                                                                                              detergent stable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 AA;
                                    4 AA;
                                                                                                                                                                                                                                                                Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                      15-MAR-1994.
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                                                                                      1 AAPF 4
                                    Sequence
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                                                                                                                                                                  AAR52024;
                                                    Query Match
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AAR46223
ID AAR462
                                                                                                                                RESULT 9
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic tetra:peptide(s) with an N-terminal blocking gp. and C-terminal enzyme inhibitor - can be formulated into soaps and sprays and used to prevent schistosomal skin penetration
                                                                                          Prevention; schistosomiasis; parasite; infection; prevention; parasitic penetration; skin; cercariae; anti-penetrant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of internal fragment of a chromogenic substrate for cathepsin G.
                                                                                                                                                                                                                                                                                        'note= "PI(protease inhibitor), other than
    chloromethyl ketone, attached"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 21; DB 15; Length 4; larity 100.0%; Pred. No. 7.8e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                 /note= "BG(peptide blocking gp.) attached"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enzyme; cathepsin G; protease; chromogenic substrate
                                              Serine protease inhibitor tetrapeptide
                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      91US-0798565.
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cohen FE, McKerrow JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-056364/07.
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Modified-site
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To measure the activity of E. coli PPlase-alpha (peptidyl prolyl c trans isomerase alpha), the PPlase and CsA (cyclosporine A) are added in the cell and mixed for 1 minute. Then, this peptide is added and incubated, and chymotrypsin added to start the reaction. The effect of CSA on the inhibition of the PPlase activity can be detected by varying the amt. of the CsA added. The inventors are claiming a PPlase-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli, protein conformation, folding, acceleration, PPIase-alpha, peptidyl prolyl cia trans isomerase alpha, catalysis, isomerisation, prolyl peptide bond.
                                                                                                                                                                          New E.coli peptidyl prolyl cis trans isomerase beta - used accelerate the folding of proteins, partic. for activation
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Substrate for peptidyl prolyl cis trans isomerase alpha.
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                                                                                                              Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21; DB 16;
Pred. No. 7.8e+05;
0; Mismatches 0;
                                                                                                          Suzuki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "N-succinyl-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Phe-MCA (sic)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR72876 standard; Peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                          inactive recombinant proteins
                                                                                                            Maki N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89JP-0184738.
89JP-0260244.
89JP-0344705.
                               89JP-0260244.
89JP-0344705.
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                89JP-0184738
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                            Hayano T, Katou S,
                                                                                                                                            WPI; 1995-140756/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-140755/19
                                                                            (TOFU ) TONEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                     4 AA;
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                                              29-DEC-1989;
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                19-JUL-1989;
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06-OCT-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Protease inhibitory profiles of the Kunitz inhibitors were determined for a variety of proteases using a variety of conceases using a variety of chromogenic substrates and compared to the inhibitory activity shown by the Kunitz-type inhibitor domain of the amyloid protein precursor and bovine aprotinin. The substrate AAR53780 was tested using the protease leukocyte elastase.
                                                                                                                                                                                                                                                                                                                                  New human Kunitz type protease inhibitor and related DNA - for treating pancreatitis and other disorders involving serine protease, also new amyloid protein precursor homologues including the inhibitor in its sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 21; DB 15;
llarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "N-succinyl-Ala"
/note= "Succinyl group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Phe-MCA (sic)"
                                              /note= "p-nitroanil"
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                                                                                                                                                                                                                                                                        Sprecher CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 63; 70pp; English.
                              /label= Phe-pNA
                                                                                                                                            93WO-US11696.
                                                                                                                                                                          92US-0985692,
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                                                                                                                                                                                                                       (NOVO ) NOVO-NORDISK AS. (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                         Norrie K,
                                                                                                                                                                                                                                                                                                       WPI; 1994-200265/24.
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                                                                                                            09-JUN-1994
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Gaps

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100.0%; Score 21; DB 16;
ilarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
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                                                                                                                               AAR77196 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                              94EP-0120406
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                                                                                 To measure the activity of E. coli PPIase-alpha (peptidy) prolyl cistrans isomerase alpha), the PPIase and C8A (cyclosporine A) are added in the cell and mixed for 1 minute. Then, this peptide is added and incubated, and chymotrypsin added to start the reaction. The effect of C8A on the inhibition of the PPIase activity can be detected by varying the amt. of the C8A added. The inventors are claiming the PPIase-alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An enzyme originated from a periodontal disease pathogenic microbe and an antibody against the enzyme, for the determination of the progress and activity of the disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR77315 is a target substrate for a Porphyromonas gingivalis (a periodontal disease pathogenic microbe) protease. An antibody raised against the enzyme can be used to diagnose the presence and progress of a periodontal disease, caused by a pathogenic microbe.
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              New E.coli peptidyl prolyl cis trans isomerase alpha - used to accelerate the folding of proteins, partic. for activation of inactive recombinant proteins
                                                                                                                                                                                                                                                                                                                                                                                                                         Protease; periodontal disease; pathogenic microbe; diagnosis;
                                                                                                                                                                                                 h Similarity 100.0%; Score 21; DB 16; Length 4; Similarity 100.0%; Pred. No. 7.8e+05; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Porphyromonas gingivalis protease substrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                             Disclosure; Page 5; 85pp; English.
                                                                                                                                                                                                                                                                                                                                AAR77315 standard; Protein; 4 AA
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Matches 4; Conserv
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                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       substrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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stimulates cell proliferation and has macrophage chemotactic action
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell proliferation enzyme proteinase activity substrate peptide #1.
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larity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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2: pir2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

subesophageal gang hypothetical prote cytochrome-c oxida hypothetical prote cytochrome-c oxida cytochrome-c oxida hypothetical prote hypothetical prote probable metal-bin hypothetical prote fill probable metal-bin hypothetical prote male accessory gla Mst26Ab protein -hypothetical prote probable cell surf hypothetical prote hypothetical prote PE family protein probable PE protein hypothetical prote hypothetical prote protein T17H7.7 [i probable transcrip anti-SS-A/Ro 60K p anti-SS-A/Ro 60K p hypothetical prote flagellar biosynth male accessory gla Mst26Ab protein -Description SUMMARIES JS0319 843963 843963 AD377 808083 AB2778 C96953 E90905 P97429 P97429 S330412 S330412 S330412 S330413 S330413 S36174 B865774 B866774 H70898 H75397 PC4279 PC4280 C83501 * Query Match Length DB 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 Score Result Š.

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ADD6605 AB3048 AD28864 A71334 A71334 I377408 I379498 C36196 S76285 F75297 A714330 A714330 A714330 A714330 A714330 A71489	ALIGNMENTS RESULT 1 US0319 Subesophageal ganglion pentapeptide - house cr Sibectes: Achteta domesticus (house cricket) C.Patcession: JS0319 R.Wicker, C. C. Micker, C. Comp. Biochem. Physiol. C 88, 185-187, 1987 A.Title: Isolation and structure of a peptide A.Accession: JS0319 A.Molecule type: protein A.Residues: 1-5 cMIC>	. Σ. Ο,
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U U U U U U U U U U U U U U U U U U U	RESULT 1 US0319 Subseophageal ganglion pentapeptide C;Species: Achter domesticus (house C;Date: 07-Sep-1990 #sequence_revisis C;Accession: US0319 R;Wicker, C; Wicker, C. Comp. Biochem. Physiol. C 88, 185-18 A;Title: Isolation and structure of A;Reference number: US0319 A;Accession: JS0319 A;Residues: 1-5 cWIC>	Query Match Best Local Matches

'n 1 AAPF 4

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Abgolis 2

Apporthetical protein (clone pR57) - Rhizobium sp. (strain NGR234) (fragment)

C;Bocices: Rhizobium sp.

A;Variety: strain NGR234

C;Date: 20-Oct-1994 #sequence_revision 23-Feb-1996 #text_change 21-Aug-1998

C;Accession: 843963

C;Accession: 843963

A;Title: Subtraction hybridisation and shot-gun sequencing: a new approach to identify s)

A;Reference number: 843961; MUID:94248027; PMID:8190622

A;Reference number: 843963

A;Reference number: stayel: MUID:94248027; PMID:8190622

A;Reference number: stayel: DNA

A;Reference number: scrain NGR234

C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology

Gaps ·, h 100.0%; Score 21; DB 2; Length 42; Similarity 100.0%; Pred. No. 1e+02; 4; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches

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10 AAPF 13

1 AAPF 4

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RESULT 3 PN0607

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RiTsukihara, T.; Aoyama, H.; Yamashita, E.; Tomizaki, T.; Yamaguchi, H.; Shinzawa-itoh, Fabinakited to the Brookhaven Protein Data Bank, April 1996
A;Reference number: A67451; PDB:10CC
A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 17-63
R;Tsukihara, T.; Aoyama, H.; Yamashita, E.; Tomizaki, T.; Yamaguchi, H.; Sinzawa-Itoh, K. Science 272, 1136-1144, 1996
A;Title: The whole structure of the 13-subunit oxidized cytochrome c oxidase at 2.8 angst A;Contents: annotation; X-ray crystallography, 2.8 angstroms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Genome: nuclear
C;Complex: part of a 13 chain complex spanning the inner mitochondrial membrane and consilese PIR:CABO), VD (see PIR:CABO), VD (see PIR:CABO), VD (see PIR:CABO), VD (see PIR:CABO), VIC (see C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribuse, G.; Steffens, G.J. Chem. 359, 1005-1009, 1978
httppe-Seyler's Z. Physiol. Chem. 359, 1005-1009, 1978
A;Title: Studies on cytochrome c oxidase, II. The chemical constitution of a short polype
A;Reference number: A00498; MUID:79046803; PMID:213363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S10303
R;Akamatsu, M.; Grossman, L.I.
Nucleic Acids Res. 18, 3645, 1990
A;Title: Nucleotide sequence of a CDNA for mouse cytochrome c oxidase subunit VIIc.
A;Reference number: S10303; MUID:90301494; PMID:2163523
                                                                                                                                                                                                                                                                                                                                                     A, Accession: A00498
Molacule type: protein
A;Residues: 17-63 <BUS>
A;Experimental source: heart
A;Experimental source: heart
B;Ananmura, W; Zhangy, Y.Z.; Takamiya, S.; Capaldi, R.A.
Biochemistry 27, 4909-4914, 1988
A;Ittle: Tissue-specific differences between heart and liver cytochrome c oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytochrome-c oxidase (EC 1.9.3.1) chain VIIc - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                     A;Molecule type: mRNA
A;Residues: 1-63 <AQU2>
A;Crose-references: EMBL:X15725; NID:g277; PIDN:CAB57793.1; PID:g6015488
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C;Superfamily: cytochrome-c oxidase chain VIIc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: H29968
A,Molecule type: protein
A,Residues: 17-42 <YAN>
A,Experimental source: liver
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Matches 4; Conserv
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A; Molecule type: mRNA
A; Residues: 1-63 <AKA>
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OSBOBA
Cytochrome-c oxidase (EC 1.9.3.1) chain VIIC precursor [validated] - bovine
NyAlternate names: cytochrome-c oxidase chain VIIIa
C;Species: Bos primigenius tautus (cattle)
C;Species: Bos primigenius tautus (cattle)
C;Date: 31-May-1979 #sequence revision 31-Dec-1992 #text_change 15-Sep-2000
C;Accession: JH0473; S06597; Ā00498; H29968; S18834
C;Accession: JH0473; S06597; Ā00498; H29968; S18834
A;Attle: Characterization and expression of a cDNA specifying subunit VIIc of bovine cyt
A;Reference number: JH0473; MUID:92009215; PMID:1655579
A;Accession: JH0473
A;References: GB:X58823
A;Accession: JH0473
A;References: GB:X58823
A;Accession: JH0473; MII:; Schon, E.A.; Grossman, L.I.
A;Cross-references: GB:X58823
A;Attle: Acidas Res. 17, 8376, 1989
A;Teile: Ancleotide sequence of a cDNA for bovine cytochrome c oxidase subunit VIIc.
A;Reference number: S06597; MUID:90045968; PMID:2554257
cytochrome-c oxidase (BC 1.9.3.1) chain VIIc - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
B;Sillard, R. Joenvall, H.; Mutt, V.
Biochem. Blophys. Res. Commun. 195, 746-750, 1993
A;Title: Characterization of porcine intestinal cytochrome c oxidase subunit VIIc, purif
A;Reference number: PNO607; MUID:93384597; PMID:8396926
A;Molecule type: protein
A;Residues: 1-47 KSIL-
A;R
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AD3575
C;Accession: AD3575
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
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A,Readduas: 1-50 «KUB»
A,Readduas: 1-50 «KUB»
A,Cross-references: Strain 16M
A,Experimental source: strain 16M
C,Genetics:
A,Gane: BMSI10525
A,Map position: II
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100.0%; Score 21; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Score 21; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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A; Status: preliminary
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probable metal-binding protein [imported] - Clostridium acetobutylicum C;Species: Cs. Species: Cs. Spe
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A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Retues: prefilminary
A;Molecule type: DNA
A;Residues: 1-86 cHAy
A;Reperimental source: strain 0157:H7, substrain RIMD 0509952
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Skonth, D. N., Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; J.; Smith, D. N.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; J. Oliu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. Altitle: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Restaus: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA

A;Residues: 1-79 a/MTH

A;Experimental source: strain Delta H

A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001
A;Authore: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Atu1639 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A,Reference number: AB2577; PMID:11743193
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-75 < kTNS
A;Cross=references: GB:AE008688; PIDN:AAL42640.1; PID:g17740071; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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                                                                                             Length 63;
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                                                                              Query Match
100.0%; Score 21; DB 2; Length 63
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
C; Keywords: mitochondrion; oxidoreductase
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A,Gene: MTH206
A,Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                        50 AAPF 53
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A, Molecule type: DNA

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1 AAPF 4

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RiAguade, M.; Miyashita, N.; Langley, C.H.
Senetics 132, 752-770, 1992
A;Title: Polymorphism and divergence in the Mst26A male accessory gland gene region in D:
A;Reference number: S30407; MUID:93106377; PMID:1361475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AjAccession: S30410
AjStatus: preliminary; nucleic acid sequence not shown; translation not shown
AjMoleoule type: DNA
AjMoleoule type: DNA
AjMoleoule type: DNA
AjKesidues: 1-79, VV, 81-90 <AG3>
AjCross-references: EMBL:X70889; NID:g3402846; PIDN:CAA50235.1; PID:g8237
AjExperimental source: allele NC2
AjNote: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
                                                                                                                                                                                                                                                                                A, Experimental source: allele NC5
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
A,Accession: $30420
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C;Superfamily: male accessory gland secretory protein 26Ab
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-90/Product: male accessory gland secretory protein 26Ab #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Experimental source: allele NC7; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993; Accession: 630426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: allele NC10
A;Note: the nucleotide seguence was submitted to the EMBL Data Library, January 1993
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
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A;Residues: 1-63, "H' 65-90 <AG4>
A;Cross_references: EMBL:X70896; NID:g3406838; PIDN:CAA50249.1; PID:g8258
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession: S30428
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-90 < AGU>
A; Cross-references: EMBL: X70898; NID: 98261; PIDN: CAAS0253.1; PID: 98263
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                                                                               A.Scatus: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-90 <AGW> A; Residues: 1-90 <AGW> A; Cross_references: EMBL:X70892; NID: 98244; PID: 98246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-90 <AGA> A; Residues: 1-90 <AGA> A; Cross_references: EMBL; X70897; NID: 98259; PID: 98260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: DNA
Residues: 1-90 <AGF>
.Cross-references: EMBL:X70894; NID:g8250; PID:g8252
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A,Cross-references: FlyBase:FBgn0002856
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A;Cross-references: FlyBase:FBgn0012495
A;Introns: 11/1
A; Experimental source: allele NC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: S30424
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802854
male accessory gland secretory protein 26Ab precursor - fruit fly (Drosophila melanogast NALernate names: male accessory gland secretory protein msP355b; male paragonial prote (;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jul-2000
C;Accession: 802854; 830408; 830416; 830426; 830410; 830424
R;Monsma, S.A.; Wolfner, M.F.
R;Monsma, S.A.; Wolfner, M.F.
A;Title: Structure and expression of a Drosophila male accessory gland gene whose produc
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#AG2647
#AG2640
#AG2
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A;Anclecule type: DNA
A;Anclecule type: DNA
A;Anclecule: 1-90 <MONN>
A;Cross-references: EMBL:Y00219; NID:g8264; PIDN:CAA68367.1; PID:g8266
A;Cross-references: Extrain Canton-S
B;Aguade, M.; Miyashita, N.; Langley, C.H.
Genetics 132, 755-770, 1992
A;Title: Polymorphism and divergence in the Mst26A male accessory gland gene region in A;Reference number: $30407; WUID:93106377; PMID:1361475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Reference of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A, Accession: A22647 A, Accession: A22647 A, Status: preliminary A, Andecule type: DNA A, Residues: 1-88 cKUR> A, Residues: 1-88 cKUR> A, Residues: 1-88 cKUR> A, Cross-reference
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                                       A;Residues: 1-88 «KUR»
A;Cross-references: GB:AE007869; PIDN:AAK86391.1; PID:g1515521; GSPDB:GN00169
C;Genetics:
A;Gene: AGR C 1023
A;Map positIon: circular chromosome
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A;Experimental source: strain C58 (Dupont)
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C,Genetics: A,Gene: fliQ A,Map position: circular chromosome

65 AAPF 68

1 AAPF 4

ઠે a A; Molecule type: DNA A; Residues: 1-90 <AGU>

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Maid accessory gland secretory protein 26Ab precursor (variant 1) - fruit fly (brosophil male accessory gland secretory protein 355b; Met26Ab protein (Species: Drosophila melanosaster and accessory gland secretory protein 355b; Met26Ab protein (Species: Drosophila melanosaster and accessory pland secretory protein 355b; Met26Ab protein (Species: Drosophila melanosaster (Species: Drosophila melanosaster (Spid) (S
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F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-90/Product: male accessory gland secretory protein 26Ab #status predicted <MAT>
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                                                                                                                                                                                  Gaps
                                                                                                                                                                              0;
                                                                                Query Match 100.0%; Score 21; DB 2; Length 90; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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C; Superfamily: male accessory gland secretory protein 26Ab
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A;Cross-references: FlyBase:FBgn0002855
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bacillus su saccharomyc caenorhabdi caenorhabdi

09780 h 09781 c 09781 c 014049 s 094175 h 005220 h 004019 s 009596 c 009596 c 009596 c 009596 p 0095156 c

bacillus ha arabidopsis escherichia

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Suboesophageal ganglion pentapeptide.
Acheta domesticus (House cricket).
Bukaryota, Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera;
Gryllidae; Gryllinae; Acheta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUL-1986 (Rel. 01, Created)
01-JUL-1986 (Rel. 23, Last sequence update)
01-JUL-1902 (Rel. 24, Last sequence update)
Cytochrome c oxidase polypeptide Viic, mitochondrial precursor (EC 19.3.1) (VIIIA)
COX7C OR COX7CPI.

Bos taurus (Bovine)
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90045968; PubMed=2554257; Aqua M.S., Lomax M.I., Schon E.A., Grossman L.I.; "Nucleotide sequence of a cDNA for bovine cytochrome c oxidase subunit VIIc."; Nucleic Acids Res. 17:8376-8376 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 21; DB 1; Length 5; 100.0%; Pred, No. 1.1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                         (Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                             5 AA.
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                  ACD2_CLOAB
RS8A_SCHPO
YD99_HAEIN
YWRF_BACSU
YM80_YEAST
GR88_CAEEL
GR88_CAEEL
RY88_CAEEL
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SEQUENCE FROM N.A.
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2 AAPF 5
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01-FEB-1991
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308.768 Million cell updates/sec
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                                                                                                        February 12, 2003, 10:04:45; Search time 0.537313 Seconds
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARDINE-22009115; PubMed-1655579;
Aqua M.S., Bachman N.J., Lomax M.I., Grossman L.I.;
Aqua M.S., Bachman N.J., Lomax M.I., Grossman L.I.;
"Characterization and expression of a cDNA specifying subunit VIIc of bovine cytochrome c oxidase.";
Gene 104:211-217(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE=96216288; PubMed=8638158;
TSUKINE=1., Royama H., Yamashita E., Tomizaki T., Yamaguchi H.,
Shinzawa Itoh K., Nakashima R., Yaono R., Yoshikawa S.;
"The whole structure of the 13-subunit oxidized cytochrome c oxidase
                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=97248578; PubMed=9092564;
Seelan R.S., Grosman L.I.;
Structural organization and promoter analysis of the bovine
cytochrome c oxidase subunit VIIC gene. A functional role for YYI.";
J. Biol. Chem. 272:10175-10181(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLUTAR LOCATION: Mitochondrial inner membrane.
-1- TISSUB SPECIFICITY: LIVER, HERAT, MUSCLE AND BRAIN, CONTAIN THE SAME ISOFORM OF COX VIIC, BUT AT DIFFERENT CONCENTRATIONS.
-1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
                                                                                                                                                                                                                                                                                                     Buse G., Steffens G.J.; "Studies on cytochrome c oxidase, II. The chemical constitution of short polypeptide from the beef heart enzyme."; Hoppe-Seyler's Z. Physiol. Chem. 359:1005-1009(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89000697; PubMed=2844245; Yanamura W., Zhang Y.-Z., Takamiya S., Capaldi R.A.; Thang Y.-Z., Takamiya S., Capaldi R.A.; "Tissue-specific differences between heart and liver cytochrome c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99190827; PubMed=10089392;
MIONIZEAKI T., Yamashita E., Yamaguchi H., Aoyama H., Tsukihara T., Shinzawa-Itoh K., Nakashima R., Yaono R., Yoshikawa S.;
"Structure analysis of bovine heart cytochrome c oxidase at 2.8 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acta Crystallogr. D 55:31-45(1999).
                                                                                                                                                                                                                                                                            TISSUE=Heart;
MEDLINE=79046803; PubMed=213363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 27:4909-4914(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at 2.8 A.";
Science 272:1136-1144(1996).
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 17-42.
                                                                                                                                                                                                                                                        SEQUENCE OF 17-63.
SEQUENCE FROM N.A.
                 TISSUE-Heart;
                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                resolution.
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-1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHOUBLAL ELECTRON TRANSPORT.

-1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + 0(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BALB/c; TISSUE-Heart;
MEDLINE=9031494; PubMed=2163523;
Akamatsu M., Grossman L.I.;
"Nucleotide sequence of a cDNA for mouse cytochrome c oxidase subunit
                                                                                                                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                                     CYTOCHROME C OXIDASE POLYPEPTIDE VIIC. MITOCHONDRIAL MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathl; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-UDN-2002 (Rel. 41, Last annotation update)
Cytochrome c oxidase polypeptide VIIc, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                          Oxidoreductase; Mitochondrion, Transit peptide; 3D-structure;
Inner membrane; Transmembrane.
                                                                                                                                                                                                                                                                                                           100.0%; Score 21; DB 1; Length 63; 100.0%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                      MITOCHONDRIAL INTERMEMBRANE
                                                                                                                                                                                                                                                                                      C6A2AD5CC4E63C0B CRC64;
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InterPro; IPR004202; COX7C.
Pfam; PC02935; COX7C, 1.
Oxidoreductase; Mitochondrion; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 AA
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                                                                                                                                                                                                           MITOCHONDRION
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       EMBL, X15725; CAB57793.1; --
EMBL, X5823; CAA4127.1; --
EMBL, U58653, AAC48719.1; --
EMBL, 1040473; OSBOGA,
PDB; 10CC; 07-DEC-96.
PDB; 10CC; 13-JAN-99.
PDB; 10CC; 22-JUL-99.
PDB; 10CZ; 22-JUL-99.
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                                                                                                                                                                                                                                                                                      7331 MW;
                                                                                                                                                InterPro, IPR004202, COX7C.
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63
63
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Best Local Similarity
Matches 4; Conser
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DOMAIN
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COXO_MOUSE
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region in Drosophila.
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                                                                                    NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mode by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
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                                                                       Gaps
                                                                                                                                                                                    01-FBB-1994 (Rel. 28, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Accessory gland specific peptide 26Ab precursor (Male accessory
gland secretory protein 355B).
ACP26AB OR MSTSAB.
Drosophila mauritiana (Fruit [ly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Perrygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Robertson C340;
MEDLINE=3106377; PubMed=1361475;
Aguade M., Miyashita N., Langley C.H.;
"Polymorphism and divergence in the Mst26A male accessory gland gene region in Drosophila.";
Genetics 132:755-770(1992).
                                                                                                                                                                                                                                                                                                                                                                                                       -:- FUNCTION: THIS PROTEIN IS TRANSFERRED FROM MALE TO FEMALE DURING MATING AND MAY AFFECT EGGLAYING AND BEHAVIOR AFTER MATING.
-:- SUBCELLULAR LOCATION: Extracellular.
-:- TISSUE SPECIFICITY: MAIN CELLS OF THE ACCESSORY GLANDS OF MALES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
             CYTOCHROME C OXIDASE POLYPEPTIDE VIIC. C6A2AD4ABFEB2C7B CRC64;
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0
                                           100.0%; Score 21; DB 1; Length 63; 100.0%; Pred. No. 82; tive 0; Mismatches 0; Indels
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                                                                                                                                                                      90 AA.
   MITOCHONDRION
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lyBase; FBgn0012495; Dmau\Acp26Ab.
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1 16
17 63
63 AA; 7333 MW;
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                                                                   Conservative
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Best Local Similarity
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                                                                                                            50 AAPF 53
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**REDINE=2019606; PubMed=10731132;

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SERAIM-MOI, NC3, NC3, NC4, NC5, NC6, NC7, NC8, NC9, and NC10;
MEDLINE-93106377; Pubmed=1361475;
Aguade M., Miyashita N., Langley C.H.;
"Polymorphism and divergence in the Mst26A male accessory gland gene
Accessory gland-specific peptide 26Ab precursor (Male accessory gland secretory protein 355B).
ACPSCAB OR NST26AB OR NST355B OR CG9024.
Drosophila melanogaster (Fruit fly).
Bukaryora, Merazoa, Arthropda, Mandibulata, Pancrustacea; Hexapoda; Insecta; Pterygota, Neoptera; Endoprerygota; Diptera; Brachycera; Muscomorpha; Ephydroidea, Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE-89033045, PubMed=3142802, Monama S.A., Wolfner M.F.; Structure and expression of a Drosophila male accessory gland gene "Structure and expression of a prosophila male accessory gland gene whose product resembles a peptide pheromone precursor."; Genes Dev. 2:1063-1073(1988).
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STRAIN-MOJSA, MOJ3A, MO47A, MO79B, MO80B, LA25, LA46, and LA108;
MEDLINE=99016087; Pubmed=9799260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Various strains;
MEDLINE=98364843; PubMed=9718731;
Tsauz S.-C., Ting C.-T., Wu C.-I.;
"Positive selection driving the evolution of a gene of male reproduction, Acp26Aa, of Drosophila: II. Divergence versus polymorphism.";
Mol. Biol. Evol. 15:1040-1046(1998).
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Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Strong R., Sun H. T., Spier B., Stradling A.C., Stapleton M., Strong R., Sun K., San S., Shan S., Yang Z.-Y., Wassarman D.A., Weinstock G.M., Weisenbach J., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weisenbach J., A. Willams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., A. Zheng X.H., Zhong F.N., Zhong W., Zhon G., Zhao Q., Zhao G., Shith H.O., Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

Science 287:2185-2195(2000).

HATING AND MAY AFFECT EGGLAYING AND BEHAVIOR AFTER MATING.

MATING AND MAY AFFECT EGGLAYING AND BEHAVIOR AFTER MATING.

SUBSCELLULAR LOCATION: Extracellular.
                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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APO52471, AAC27996.1;
APO52472, AAC28000.1;
APO52473, AAC28000.1;
APO52474, AAC28000.1;
APO52474, AAC28000.1;
APO52476, AAC28000.1;
APO52477, AAC28010.1;
APO52477, AAC28010.1;
APO52478, AAC28010.1;
APO52478, AAC28010.1;
APO52480, AAC28012.1;
APO52480, AAC28016.1;
APO52481, AAC28016.1;
APO52481, AAC28016.1;
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AAC28825.1;
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POTENTIAL.

POTENTIAL.

ACCESSORY CLAND-SPECIFIC PEPTIDE 26AB.

AFG, AFT, AFB, AF9, AF10, AU4, AU7, AU8,

AF6, AF7, AF8, AF9, AF10, AU4, AU7, AU8,

NC3, NC4, NC6, NC8, NC9, NY2, NY3, NY4,

NY5, TW1, TW2, TW5, TW6, TW7, TW8, TW10

AND TW11).

P - R (IN STRAIN TW9).

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NC8, NY2, NY4, TW2, TW4, TW5, TW8, TW10

AND TW11).
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01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 28, Last annotation update)
16-OCT-2001 (Rel. 28, Last annotation update)
16-OCT-2001 (Rel. 28, Last annotation update)
18-OCT-2001 (Rel. 28, Last annotation upd
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EMBL, AP053276; AAC28843.1; --
EMBL, AJ231354; CAB37201.1; --
EMBL, AJ231356; CAB37201.1; --
EMBL, AJ231356; CAB37201.1; --
EMBL, AJ231359; CAB3721.1; --
EMBL, AJ231359; CAB3721.1; --
EMBL, AJ231372; CAB3723.1; --
EMBL, AJ231372; CAB3725.1; --
EMBL, AJ31317; --
EMBL, AJ
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Best Local Similarity 100.
Matches 4; Conservative
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99 AAPF 102
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01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Accessory gland secretory protein 355B).
ACP26AB OR MSTSAB.
Drosophila simulans (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Perrygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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"Polymorphism and divergence in the Mst26A male accessory gland gene
region in Drosophila.";
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ACCESSORY GLAND-SPECIFIC PEPTIDE 26AB.
99CFC4EE69B7782E CRC64;
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                        or send an email to license@isb-sib.ch).
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FlyBase; FBgn0012778; Dsec\Acp26Ab.
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PIR, S30430; S30430.
FlyBase; FBgn0012821; Dsim\Acp26Ab.
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MEDLINE=93106377; PubMed=1361475;
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RESULT 8

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Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Enthartoideae, Oryzeae, Oryza,
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris E Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Deviln K., Feltwell T., Gentles S., Hamin N., Hoiroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
"Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.",
Nature 393:537-544 (1998).
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                                                                                                                                                                                                                                                                                                                     STRAIN=CV. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 100.0%; Score 21; DB 1; Length 102; Similarity 100.0%; Pred. No. 1.3e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE UPF0185 (BM-002) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l protein.
102 AA; 10362 MW; 1B8F85B27F371159 CRC64;
                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein P0483G10.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein RV1386 precursor.
RV1386 OR MT1430 OR MTCY21B4.03.
     102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AP003263; BAB63621.1; -
InterPro; IPR005375; UPF0185.
Pfam; PF03671; UPF0185; 1.
STANDARD;
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                                                                                                                                                     (Rice)
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Best Local Similarity
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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25 AAPF 28
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CONFLICT
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PEPTIDE
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  SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alband D., Eisen J.A., Haft D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                   Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CALZ HUMAN STANDARD; PRT; 127 AA.
P10092; QSUCN9;
D10092 (ABCN9);
D10092 (ABCN 10, Created)
D1-MAR-1989 (Rel. 10, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
Calcitonin gene-related peptide II precursor (CGRP-II) (Beta-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure and expression of the human calcitonin/CGRP genes."; FEBS Lett. 209:97-103(1986).
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MEDLINE=85180007; PubMed=2985435;
Steenbergh P.H., Hoeppener J.W.M., Zandberg J., Lips C.J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=87105923; PubMed=3492393; Steenbergh P.H., Hoeppener J.W.M., Zandberg J., Visser A., Lips C.J.M., Jansz H.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 102 HYPOTHETICAL PROTEIN RV1386.
102 AA; 9862 MW; 8165F09DBDB9D752 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGE, MI1430; -.
Tuberculist; M71430; -.
Tuberculist; Rv1386; -.
InterPro; IPR000004; PE_region.
Pfan; PP00934; PE; 1.
Hypothetical protein; Signal; Complete proteome.
Hypothetical protein; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 21; DB 1; I
100.0%; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE007014; AAK45695.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z80108; CAB02191.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 AAPF 34
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                                                                                                                                     Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Matsuo H., Bto T.; "Isolation and characterization of peptides which act on rat platelets, from a pheochromocytoma."; Biochem Biophys. Res. Commun. 185:134-141(1992).

1. FUNCTION: CGRP induces vasodilatation. It dilates a variety of vessels including the coronary, cerebral and systemic vasoulature. It abundance in the CNS also points toward a neurotransmitter or
PARTIAL SEQUENCE OF 82-108.

MEDINE-8710542; Whedea3492492;

MEDINE-8710542; Born W., Chang J.Y., Fischer J.A.;

"Identification in the human central nervous system, pituitary, and thyroid of a novel calcitonin gene-related peptide, and partial amino acid sequence in the spinal cord.";

J. Biol. Chem. 262:542-545(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
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G -> S (IN REF. 3).
BOA71A063CD5ACE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          "Isolation, purification and characterization of beta-hCGRP from human spinal cord.";
                                                                                                                                                                                                                                                                             TISSUE=Spinal cord;
MEDLINE=90211348; PubMed=2322288;
Wimalawansa S.J., Morris H.R., Etienne A., Blench I., Panico M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALCITONIN GENE-RELATED PEPTIDE II
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Cleavage on pair of basic residues; Amidation; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 1; Length 127; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 167:993-1000(1990)
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InterPro; IPR001693; Calcitonin-like.
InterPro; IPR002163; Calcitonin B.
Pfam; PF00214; Calc CGRP IAPP; I.
SMRTT; SM00113; CALCITONINB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, X04855, CAC05295.1; --
EMBL, X04857; CAC05295.1; JOINED.
EMBL, X04861, CAC05295.1; JOINED.
EMBL; BC008428; AAH08428.1; --
EMBL; X02404; CAA26249.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Pheochromocytoma;
MEDLINE=92287083; PubMed=1318039;
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                                                                                                                                                                                                                                                SEQUENCE OF 82-86 AND 104-117.
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Conservative 0
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PIR; A34565; A34565.
PIR; B26142; B26142.
Genew; HGNC:1438; CALCB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuromodulator role.
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127
88
118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 82-104.
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us-10-036-371-7.rsp

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MEDLINE=85166259; PubMed=3872459;
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SETAIN=Nichols:
MEDLINE=98332770; PubMed=9655876;
Frast C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodesgren E., Hardham J.M., McLeed M.P., Salzberg S., Petersson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
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MEDLINE=89386053; PubMed=2571128;
Broad P.M., Symes A.J., Thakker R.V., Craig R.K.;
"Structure and methylation of the human calcitonin/alpha-CGRP gene.";
Nucleic Acids Res. 17:6999-7011(1989).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALL HUMAN STANDARD; PRT; 128 AA.
01-JAN-1998 (Rel. 06, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
calcitonin gene-related peptide I precursor (CGRP-I) (Alpha-type
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 21; DB 1; Length 127;
llarity 100.0%; Pred. No. 1.6e+02;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete proteome.
SEQUENCE 127 AA; 14526 MW; 18848EF0DAC4ADC4 CRC64;
                                                                                                                                                                                                                                             pirochaetales; Spirochaetaceae; Treponema.
                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
Hypothetical protein TP0355.
                                                                            127 AA.
                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spirochete.";
Science 281:375-388(1998);
                                                                            STANDARD;
                                                                                                                                                                                                                      Freponema pallidum.
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SEQUENCE FROM N.A.
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NCBI_TaxID=9606,
                                                                                                                                                                                                                                             Bacteria, Spirod
NCBI_TaxID=160,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter J.C.;
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                                                  Y355 TREPA
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PARTIAL SEQUENCE OF 83-117.

MEDINIE-87109142; PubMed-1492492;

Petermann J.B., Born W., Chang J.Y., Fischer J.A.;

"Identification in the human central nervous system, pituitary, and thyroid of a novel calcitonin gene-related peptide, and partial amino acid sequence in the spinal cord.";

J. Biol. Chem. 262:542-545(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IISSUE=Thyroid carcinoma;
MEDLINE=84240176; PubMed=6610687;
Steenbergh P.H., Hoppener J.W., Zandberg J., de Ven W.J., Jansz H.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 77-128 FROM N.A.
MEDLINE-8721335; PubMed=3034287;
Craig R.K., Riley J.H., Edbrooke M.R., Broad P.M., Foord S.M.,
Al-Kazwini S.J., Holman J.J., Marshall I.,
"Expression and function of the human calcitonin/alpha-CGRP gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Matsuo H., Eto T., "Isolation and Characterization of peptides which act on rat
Jonas V., Lin C.R., Kawashima E., Semon D., Swanson L.W.,
Mermod J.-J., Evans R.M., Rosenfeld M.G.,
"Alternative RNA processing events in human calcitonin/calcitonin
gene-related peptide gene expression.",
Proc. Natl. Acad. Sci. U.S.A. 82:1994-1998(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 49-128 FROM N.A. MEDINE-85230541; PubMed=240883; Edbrooke M.R., Parker, Mevey J.H., Riley J.H., Sorenson G.D., Pettengill O.S., Czaig R.K.; "Expression of the human calcitonin/CGRP gene in lung and thyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H
                                                                                                                                                                                             SEQUENCE OF 48-119 FROM N.A.
MEDLINE-85022523; PubMed=6148938;
Nelkin B.D., Rosenfeld K.I., de Bustros A., Leong S.S., Roos B.A.
Baylin S.B.;
                                                                                                                                                                                                                                                                                                                                                               "Structure and expression of a gene encoding human calcitonin and calcitonin gene related peptide.";
Biochem. Blophys. Res. Commun. 123:648-655(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation and characterization of human calcitonin gene-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91105142; PubMed=1988044; Berzez A.L., Harvey T.S., Bazzo R., Campbell I.D., Selvez A.L., Harvey T.S., Bazzo R., Campbell I.D., Solution structure of human calcitonin gene-related peptide by NMR and distance geometry with restrained molecular dynamics."; Biochemistry 30:575-582(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quence is conserved
thyroid carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 83-119.
MEDLINE-84191466; PubMed*6609312;
Morris H.R., Panico M., Etienne T., Tippins J., Girgis S.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Calcitonin gene related peptide coding sequence
human genome and is expressed in medullary thyroi
J. Clin. Endocrinol. Metab. 59:358-360(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              platelets, from a pheochromocytoma.";
Biochem. Biophys. Res. Commun. 185:134-141(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Soc. Symp. 52:91-105(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE #92287083; PubMed = 1318039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NWR OF CGRP. MEDLINE=91248117; PubMed=2039456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 83-108, AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 77-128 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 308:746-748(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR OF CGRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO J. 4:715-724 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Pheochromocytoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 health and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.

BY SIMILARITY.

CALCITONIN GENE-RELATED PEPTIDE II.

BY SIMILARITY.

BY SIMILARITY.

AMIDATION (G-121 PROVIDE AMIDE GROUP) (BY SIMILARITY).
                                                                                                                                                                                                                                                       alpha and beta genes.";

DNA Seq. 12:131-135(2001).

-!- FUNCTION: CGRP induces vasodilatation. It dilates a variety of vessels including the coronary, cerebral and systemic vasculature. Its abundance in the CNS also points toward a neurotransmitter or neuromodulator rote (By similarity).

-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae; Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                      Thomas P.M., Nasonkin I., Zhang H., Gagel R.F., Cote G.J.; "Structure of the mouse calcitonin/calcitonin gene-related peptide
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALCITONIN; 1.
basic residues; Amidation; Hormone; Signal.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Small inducible cytokine B5 precursor (CXCL5) (Cytokine LIX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
Kelner G.S., Maciejewski-Lenoir D., Lee E.D., Maki R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97299244E8F6C536 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IRR000443; Amylin.
InterPro; IRR001693; Calcitonin-like.
InterPro; IRR001693; Calcitonin_B.
Pfam; PR00214; Calc CGRP IAPP; I.
PRINTS; PR00817; CALCITONINB.
RRINTS; PR00818; ISLETANYLOID.
SMART; PR00013; CALCITONIN; 1.
PROSITE; PS00258; CALCITONIN; 1.
Cleavage on pair of basic residues; Amic
                                                                                                                                                        STRAIN=129/Sv;
MEDLINE=21604266; PubMed=11761712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF325526; AAK16431.1; -.
EMBL; AF325524; AAK16431.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 AA; 14623 MW;
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                                                    NCBI_TaxID=10090;
                                                                                                                          SEQUENCE FROM N.A.
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      SOCCOCCETTITITES
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                                          Price N.C.;
"Solution structures of calcitonin-gene-related-peptide analogues of
"Solution structures of calcitonin-gene-related peptide and amylin.";
Biochem. J. 275:788.1991).
-!- FUNCTION: CGRP induces vasodilatation. It dilates a variety of
vessels including the coronary, cerebral and systemic vasculature.
Its abundance in the CNS also points roward a neurotransmitter or
neuromodulator role. It also elevates platelet cAMP.
-!- ALTERNATIVE PRODUCTS: 3 ISOPORMS; I (AC P01258), 2 (AC P01258) AND
-!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Cleavage on pair of basic residues; Amidation; Alternative splicing;
Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMIDATION (G-120 PROVIDE AMIDE GROUP)
R -> V (IN REF. 4)
R -> V (IN PER. 4)
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CALZ MOUSE STANDARD;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calcitonin gene-related peptide II precursor (CGRP-II) (Beta-type CGRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
            Hubbard J.A.M., Martin S.R., Chaplin L.C., Bose C., Kelly S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CALCITONIN GENE-RELATED PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 21; DB 1; Length 128;
Pred. No. 1.6e+02;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A003A1069260D9B8 CRC64;
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InterPro: IPR002163; Calcitonin B.
Pfan, PF00214; Calc CGRP IAPP; I.
PRINTS; PR00817; CALCITONINB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M12664; AAAS1914.1; JOINED.
M12665; AAAS1914.1; JOINED.
K03512; AAAS2011.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, MI2665, AAA51914.1; JOINE
EMBL, M28637, AAA52011.1; --
EMBL, M28637, AAA52012.1; --
EMBL, M26094, AAA51912.1; --
PIR, B22716; TCHUR.
PIR, A22949; A22949.
PIR, A26142; A26142.
PIR, S07644; S07644.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA51914.1; -.
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80
119
128
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Best Local Similarity
4, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X02330;
M12667;
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Gaps

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MOD RES

CALCB

SCEEDAGE

MOUSE

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SIGNAL

EMBL;

SOLUTION TO THE STATE OF STATE

EMBL;

InterPro; IPR000276; GPCR_Rhodpsn.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
mitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
FUNCTION: MAY PRATICIPATE IN THE RECRUITMENT OF INFLAMMATORY CELLS
BY INJURED ONE INFECTED TISSUB (BY SYMILARITY).
SIMILARITY: BELONGY TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
C-X-C) (CHEMOKINE CXC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang A.S., Chang S.M., Schilling W.P.;
"Identification of multiple P2 purinergic receptor subtypes in bovine aortic endothelial cells (BABCg).";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that activate a phosphatidylinositol-calcium second messenger system (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SMALL INDUCIBLE CYTOKINE BS.
BY SIMILARITY.
BY SIMILARITY.
COOF6B3605524F4E CRC64;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
P2Y purinoceptor 2 (P2Y2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 AA.
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InterPro; IPR001811; Chemokine_IL8.
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PRINTS; PR00437; SMALLCYTKCXC.
SMART; SM00199; SCY; 1.
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Matches 4; Conserv
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SIGNAL 1
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DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                   4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                               PEAM; PROGOTISTY TEM 1, 1.

PROSITE; PSO127; G PROTEIN RECEP_F1_2; 1.

G-PROTEIN PRECEP_F1_2; 1.

G-PROTEIN COUPLED CO
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Search completed: February 12, 2003, 10:23:20 Job time : 2.53731 secs

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us-10-036-371-7.rspt

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P70957;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
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                                                                                                            February 12, 2003, 10:16:06; Search time 2.82985 Seconds (without alignments) 291.248 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Q9TCK3
Q9YSV3
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Q9ABQ2
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	JGNMENTS 1. 41 AA. sed) sequence update) annotation update untagonist/calory phyta; Embryophy hicoryledons; cor aceae; Brassica. I., Polya G.M.; ultiple forms of dulin antagonist tinase."; (11996).	e 21; DB . No. 3.2e smatches	45 AA.
Q8S4B6 Q8S4B4 Q8S4B4 Q8S4B7 Q8S4B7 Q8S4B6 Q9S30B Q9J1W6 Q9J1W6 Q9DKP9 Q9DKP9 Q9DKP9 Q9DKP9 Q9DKP9 Q9DKP9 Q9TSD9 Q9TSD9 Q9TSD9 Q95NY3 Q95NY3 Q97185 Q97185 Q97185 Q97185 Q97185 Q97185 Q97185 Q97186 Q9	ignn i, i, intage phyt icot intage inta	Score 2 Pred. N 0; Misma	PRT;
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CATAIN-16M, ATCC 23456 / BIOTYPE 1;

MEDLINE-20020109; PubMed=11756689;

MEDLINE-20020109; PubMed=11756689;

A DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

DelVecchio V.G., Kapatral V., Berala N., Barnal A., Mazur M., Goltsman E.,

A Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

A Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

A Haselkorn R., Kyrpides N., Overbeek R.;

The genome sequence of the facultative intracellular pathogen

Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).

R EMBL, AROSS88; AALSJ671; -

R Hypotherical procein; Complete proteome.

SQUENCE SO AA; 5208 MW; 8DES59A82243EFC17 CRC64;
                                                                                                        Chang Y.M., Lin S., Liao T.H.; "Bovine pancreatic focusing, peptide "Bovine pancreatic deoxyribonuclease F: isoelectric focusing, peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Brucellaceae, Brucella.
NCBI_TaxID=29459;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Lecithin-cholesterol acyltransferase (EC 2.3.1.43) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 21; DB 16; Length 50; 100.0%; Pred. No. 3.88+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    Length 47;
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100.0%; Pred. No. 3.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                           mapping and primary structure.";
Biotechnol. Appl. Biochem. 19:129-140(1994).
HSSP; P00639; 3DNI.
Interpro; IPR001582; DNase_I.
PRINTS; PR00130; DNASEI.
ProDom; PD005408; DNase_I; 1.
SEQUENCE 47 AA; 4937 MW; D757A9F441095799 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein BMEI10525.
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                                                                                  MEDLINE=94183469; PubMed=8136077;
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Matches 4, Conservative
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Bovidae, Bovinae, Bos.
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Matches 4; Conserv
                 NCBI_TaxID=9913;
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QBYCK3;
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PÉRM: PF02935; COX7C; L. SEQUENCE 47 AA; 5457 MW; E1IE89CFBC18B5D7 CRC64;
                                                                                                                                                                                   MEDLINE=91092499; PubMed=2265757;
Jorgensen P.L., Hansen C.K., Poulsen G.B., Diderichsen B.;
Jorgensen P.L., Hansen C.K., Poulsen G.B., Diderichsen B.;
"In vivo genetic engineering: homologous recombination as a tool for plasmid construction.";
plasmid construction.";
Gene 96:37-41(1990).
EMBL; M62638; AAA22242.1; -.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Deoxyribonuclease F (Fragment).
Booxyribonuclease F (Fragment).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cytochrome C oxidase subunit VIIC (Fragment).
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                          Bacillus stearothermophilus.
Bacteria, Firmicutes; Bacillus/Clostridium group, Bacillales;
Geobacillus.
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35 >45 POTENTIAL.
45 45 45
45 Aa, 5119 MW, 192F623EA13E6DA6 CRC64;
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Alpha-amylase precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 AA.
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Best Local Similarity
                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                              NCBI_TaxID=1422;
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SEQUENCE
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RESULT 3
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coelicolor A3(2).";
Nature 417:41-147(2002).
EMBL; AL589708; CAC33946.1; -.
Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus.
                                                                                                                                                                 Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 AAPF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 AAPF 8
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29DWS-4
ID 09DWS-
DT 01-MAD
DT 01-MAD
DT 01-DR

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EMBL. AFINSINB, AAF655552.1; -.
                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum aestivum (Wheat).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0TM-2001 (TrEMBLrel. 17, Created)
01-0TM-2001 (TrEMBLrel. 17, Last sequence update)
01-0TM-2001 (TrEMBLrel. 17, Last sequence update)
01-0TM-2002 (TrEMBLrel. 21, Last annotation update)
4 procherical protein SCG101.
SCG6101 OR SCBACIA6.25C
Streptomyces coelicolor.
Streptomyces coelicolor.
Actinomycetales, Streptomycineae; Streptomyces.
                                                      SEQUENCE FROM N.A.

OJ JF., SAKU K., Liao Y.L., Jimi S., Jin W.J., Arakawa K.;

OA U.JF., SAKU K., Liao Y.L., Jimi S., Jin W.J., Arakawa K.;

OA novel missense variant Thrl3Met in the lecithin: cholesterol
acyltransferase (LCAT) gene associated with fish eye disease.";

EMBL, ALTAGOS1, AAD28484.1;

Acyltransferase, Transferase.

Acyltransferase, Transferase.

NON_TER S1 S1 NON_TER S1 NON_TER
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                                                                                                                                                                                                                                                                                     Ouery Match 100.0%; Score 21; DB 4; Length 51; Best Local Similarity 100.0%; Pred. No. 3.9e+02; Matches 4; Conservative 0; Mismatches 0; Indels
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 AA; 6085 MW; E35F7AC99E250F78 CRC64;
                                                                                                                                                                                                                                              51 AA; 5666 MW; EB511439A5129965 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCT-2001 (TrEMBLrel. 19, Last annotation update)
MFP1 attachment factor 1 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Dest Local Similarity 100.00
Dest Local 4; Conservative
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STRAIN=A3(2) / M145;
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                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                  22 AAPF 25
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NON_TER
SEQUENCE
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Q9ADG2
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Q9M7N1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MEC-2001 (TrEMBLrel. 19, Last amontation update)
Genome polyprotein [Contains: envelope glycoprotein El (GP32) (GP35)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Croin A., Fraser A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Marten S., Taylor M., Marren T., Mietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBL_TaxID=11103;
                                                                                                                                                                                                                                                                                                           "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0854B7;
01-JUN-2002 (TEMBLrel. 21, Created)
01-JUN-2002 (TEMBLrel. 21, Last sequence update)
01-JUN-2002 (TEMBLrel. 21, Last annotation update)
Adenosine kinase (Fragment).
Amblystegium humiles (Fragment).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 21; DB 16; Length 59; 100.0%; Pred. No. 4.5e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in Amblystegium.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF465020; AAL96441.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 69
69 AA; 7793 MW; BICIC22B4EAC30AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 AA; 6387 MW; 885755E65DB6C9EF CRC64;
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                                                                                                                                         STRAIN-CHINESE AND PHILIPPINE STRAINS;
STRAIN-CHINESE AND PHILIPPINE STRAINS;
MEDLINE-971014915; PubMed=8946393;
HOOKER C.W., Brindley P.J.;
"Cloning and characterisation of strain-specific transcripts encoding triosephosphate isomerase, a candidate vaccine antigen from Schistosoma japonicum.";
MOL. Biochem. Parasitol. 82:265-269(1996).
BNBL: 1057557; AAC47394.1; -..
HSSP; P00940; TITM.
InterPro; IPR000652; Triophos_ismrse.
Prodom; P00121; TIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=21608550; PubMed=11743193;

Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmeira A.,

Ruyyavin T., Levy R., Li M.-J., McClelland E., Romero P., Gordon D.,

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Nester E.W.,

The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                  scniatosoma japonitoma (Blood tluke).
Eukaryota: Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidas; Schistosoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 21; DB 5; Length 73; Best Local Similarity 100.0%; Pred. No. 5.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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73 73 73
73 AA; 7982 MW; 6BlODB35855F5A33 CRC64;
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EMBL, AE003121; AAL42640.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 75 AA, 8397 MW; B3B9D20CE8EE82DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Atul639.
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 AA.
                     Triosephosphate isomerase (Fragment)
                                             Schistosoma japonicum (Blood fluke)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                        NCBI_TaxID=6182;
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                   STRAIN=VE3216;
MEDLINE=20394384; PubMed=10935993;
Argentin C., Detrori S., Villano U., Guadagnino V., Infantolino D.,
Dentico P., Coppola R.C., Rapicetta M.;
"Molecular characterisation of HCV genotype 4 isolates circulating in
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Archosauria, Aves, Neognathae, Passeriformes, Passeroidea,
Fringillidae, Emberizinae, Certhidea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and reciprocal recombination.";
(In) Kasahara M. (eds.);
Major histocompatibility complex:
evolution, structure, and function, pp.518-541, Springer-Verlag,
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                                                                                                                                         J. Med. Virol. 62:84-90(2000).
-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1
EMBL, AJS50216; CAC16883.1; -.
Pfan: PRO1539; HCV env.
Pfam: PRO1539; HCV env.
Coat protein; Envelope protein; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                          Query Match

100.0%; Score 21; DB 12; Length 70;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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70 70
70 AA; 7698 MW; BD360B7B1C3BF80F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
MHC class IIB antigen (Fragment).
Certhidea olivacea.
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Last sequence update)
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EMBL, AF164163; AAF36225.1; ...

InterPro; IPR000353; MHC II beta.

Pfam; PF00969; MHC II beta; 1.

ProDom; PD000329; MHC II beta; 1.
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01-NOV-1996 (TEMBLrel. 01,
01-NOV-1996 (TEMBLrel. 01,
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
SEQUENCE 20082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Matanabe A. Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuti Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
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                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 12). Last annotation update)
01-UTN-2002 (TrEMBLrel. 12). Last annotation update)
Formyltetrahydrofolate dehydrogenase (Fragment).
6111folthys mirabilis (Long-Jawed mudsucker).
8ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Percomorpha; Perciformes; Gobioidei;
Gobiidae; Gillichthys.
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDGINE=21117151; PubMed=11172064;
Gracey A.Y., Troll J.V., Somero G.N.;
Gracey A.Y., Troll J.V., Somero G.N.;
Gracey A.Y., Troll J.V., Somero G.N.;
Gillichthys mirabliss.";
Proc. Natl. Acad. Sci. U.S.A. 98:1993-1998(2001).
Broc. Natl. Acad. Sci. U.S.A. 98:1993-1998(2001).
HSSP, P05091; JCH.
HSSP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 21; DB 13; Length 76; Best Local Similarity 100.0%; Pred. No. 5.7e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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SEQUENCE 77 AA; 8189 MW; 8A2BF074E4C16806 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 098L67;
01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein msril58.
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DNA Res. 7:331-338(2000).
EMBL; AP002996; BAB48596.1; -.
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SEQUENCE FROM N.A.
TISSUE=LIVER;
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Search completed: February 12, 2003, 10:27:29
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; Sequence 1, Application US/07973335
; Patent No. 5338547
; GENERAL INFORMATION:
; APPLICANT: Kennedy and Szuhaj
; TITLE OF INVENTION: No. 5338547el Bowman-Birk Inhibitor
; TITLE OF INVENTION: Product For Use As An Anticarcinogenesis Agent
; VUMBER OF SEQUENCE: 1
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5338547is
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
US-08-751-070B-4
US-09-06-9823-2
US-09-076-460-1
US-08-950-618-31
US-08-950-618-31
US-08-120-36-101
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US-09-147-502A-11
US-09-313-56-25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,335
FILING DATE: 19921102
CLASSIFICATION: 4.24
PROOF APPLICATION TATA:
APPLICATION NUMBER: 824,719
FILING DATE: January 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 679,155
FILING DATE: September 6, 1990
ATTORNEY/AGENT INFORMATION:
ANAME: Jane Massey Licata
REFERENCE/POCKET NUMBER: 32,527
REFERENCE/POCKET NUMBER: 32,527
REFERENCE/POCKET NUMBER: 32,527
REFERENCE/POCKET NUMBER: 32,527
REFERENCE/POCKET NUMBER: 126,527
REFERENCE/POCKET NUMBER: 126,537
RELEPHONE: (215) 568-3100
TELLEPHONE: (215) 568-3100
TELLEPHONE: POR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
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2: /cggg_6/ptodata/l.iaa/5B_COMB.pep:*
3: /cgg_6/ptodata/l.iaa/6A_COMB.pep:*
4: /cggg_6/ptodata/l.iaa/6A_COMB.pep:*
5: /cgg_6/ptodata/l.iaa/pcgg.*
6: /cgg_6/ptodata/l.iaa/pcgg.*
6: /cgg_6/ptodata/l.iaa/packfilesl.pep:*
        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-276-936A-2

US-08-34-936A-2

US-08-34-14AA-3

US-08-34-14AA-3

US-08-34-14AA-3

US-08-44-02-19

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US-08-43-959-6

US-08-434-959-5

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US-08-434-959-5

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US-08-434-959-6

US-08-434-959-5

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US-08-434-959-6

US-08-434-959-6

US-08-434-959-6

US-08-434-959-6

US-08-438-568-56

US-08-722-268-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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-08-698-575E-2
-08-424-017B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                            US-10-036-371-7
21
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Match Length
                                                                                                                                                                                                                                                                                                                                  1 AAPF 4
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                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
No.
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1 AAPF 4
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COTHER INFORMATION: /label= ALA-1

OTHER INFORMATION: /label= ALA-1

OTHER INFORMATION: with a succinyl group"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1..4

OTHER INFORMATION: /label= Phe-4

OTHER INFORMATION: /note= "Carboxyl-terminal phenylalanine resudue is OTHER INFORMATION: capped with p-nitroanil..."
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                                                                                                                                                                                                                                                                                               | Sequence 19, Application US/08155331 | Patent No. 5441931 |
| Patent No. 5441931 | GENERAL INFORMATION: Foster, Donald C | APPLICANT: Foster, Cindy | APPLICANT: Sprecher, Cindy | APPLICANT: No. 5441931ris, Kjeld | TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR | TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR | TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR | NUMBER OF SEQUENCES: 19 | CORRESPONDENCE ADDRESS: | ADDRESSE: ZymoGenetics, Inc. | STREET: 4225 Roosevelt Way, N.E. | CITY: Seattle | STREET: M. | ADDRESSE: | CITY: Seattle | STREET: M. | ADDRESSE: | CITY: Seattle | CITY: CITY: Seattle | CITY: CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 21; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 2e+05; Matches 4; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDERR: US 07/985,692
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: PARKET, GATY B
REGISTRATION NUMBER: 92-21C1
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 maino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                            RESULT 2
US-08-155-331-19
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RESULT 3

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Sequence 2, Application US/08004643C

Patent No. 540079

GREATIAL INFORMATION:

ONDERSON SEGURCES:

ONDERS
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NAME/KEY: Modified peptide used for enzyme activity assay
OTHER INFORMATION: Peptide is modified with n-terminal
OTHER INFORMATION: Succinyl group and c-terminal p-nitroanilide group
PUBLICATION INFORMATION:
AUTHORS: Del Mar. B. G.
AUTHORS: Largman, C.
AUTHORS: Largman, C.
AUTHORS: Broderick, J. W.
TITLE: A Sensitive New Substrate for Chymotrypsin
VOLUME: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-08-407-000-6

US-08-407-000-6

Sequence 6, Application US/08407000

Patent No. 5578324

GENERAL INFORMATION:

APPLICANT: Dohl, Mashiko

APPLICANT: Makino, Yuji

TITLE OF INVENTION: PEPTIDE PROTEINACEOUS DRUG NASAL

TITLE OF INVENTION: PEPTIDE PROTEINACEOUS DRUG NASAL

TITLE OF INVENTION: PEPTIDE COMPOSITION

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSE: SUGHBUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; DB 1; Length 4; larity 100.0%; Pred. No. 2e+05; Conservative 0; Mismatches 0; Indels
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RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 4
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MEDIUM TYPE: Floppy Disk
COMPUTER: ISM PC compatible
APPLICATION NUMBER: US/08/407,000
FILING DATE: 29-MAR-1995
PRIOR APPLICATION NUMBER: PCT/JP94/01257
FILING DATE: 29-JUL-1994
APPLICATION NUMBER: JP-A-5-206922
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Giblin, James A.:
REGISTRATION NUMBER: 25772
REFERENCE/DOCKET NUMBER: MSB-7214
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510)705-7910
TELEPHONE: (510)705-7904
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single strand
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
DESCRIPTION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAGES: 316-329
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                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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Sequence 1, Application US/08282860

Patent No. 5561108

APPLICANT: Tasy, Grace C.
APPLICANT: Cheung) Neal K. H.
APPLICANT: Cheung) Neal K. H.
APPLICANT: Bettencourt, Jeffrey D.
ITITLE OF INVENTION: Preparation of Alpha-1 Antichymotrypsin NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
ADDRESSE: Bayer Corporation
STREET: P. O. Box 1986
CITY: Berkeley
STREET: P. O. Box 1986
CITY: Berkeley
STATE: California
COUNTRY: USA
COUNTRY: USA
MEDIUM FIREL Diskette, 3.50 inch, 1.44Mb Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
                                             COUNTRY: USA

ZIP: 45.15-63.00

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/462,456
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/342,999
FILING DATE:
APPLICATION NUMBER: US/08/22,552
FILING DATE:
APPLICATION NUMBER: US/07/987,587
FILING DATE:
APPLICATION NUMBER: US/07/704,499
FILING DATE:
APPLICATION UMBER: APPLICATION U
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COMPUTER: 1SM
COPERATING SYSTEM: DOS
SOFTWARE: WOAGBETECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,860
FILING DATE: 07/29/94
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 214320
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-462-456-5
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAPF 4
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/07890422B
Patent No. 5602102
GENERAL INFORMATION:
APPLICANT: THIRLE, DWAIN L.
APPLICANT: HIPSKY, PETER E.
TITLE OF INVENTION: DIPEPTIDYL PEPTIDASE-I
TITLE OF INVENTION: INHIBITORS AND USES THEREOF
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSE:
ADDRESSES: ARROLD, WHITE & DURKEE
STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210
COMPUTE: IBM PC COMPATIBLE
CORPUTES: IBM COMPATION:
NAME: MAYELELD, DENIER L.
REGISTRATION NUMBER: 33,732
REGISTRATION NUMBER: 33,732
RELEPHONE: 512-320-7200
TELEPHONE: 512-320-7207
TELEPHONE: 512-340-7577
TELEPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                   APPLICATION NUMBER: JP-A-5-235841
FILING DATE: 30-AUG-1993
APPLICATION NUMBER: JP-A-6-1644
FILING DATE: 12-JAN-1994
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTER.ISTICS:
LENGTH: 4 amino acida
TYPE: amino acid
STRANDEDNESS: @ingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 amino acid residues
       30-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-407-000-6
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Best Local Similarity
Matches 4; Conserv
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FILING DATE:
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US-07-890-4228-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-890-422B-28
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Sequence 10. Statistication US/0226936A
September No. Scillatation US/0226936A
TITLE OF INVENTION: Recombinant Settine Processes Inhibitors and Uses of These Number OF SURGENCE INTERNATION: Recombinant Settine Processes Inhibitors and Uses of These Number OF SURGENCE INTERNATION: Recombinant Settine Processes Inhibitors and Uses of These Number OF SURGENCE INTERNATION: Recombinant Settine Processes Inhibitors and Uses of These Number OF SURGENCE IN SURGENCE SUR
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Sequence 9, Application US/08397602A
Patent No. 564604
Patent NorMATION:
APPLICANT: Wilson, Charles R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear _
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΡA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: P. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-397-602A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 21; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 2e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3. Application US/08541143A
Patent No. 5646028
GENERAL INFORMATION:
TITLE OF INVENTION:
THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1100
CITY:
CALIFORNIA
CALIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 21; DB 1; Length 4; larity 100.0%; Pred. No. 2e+05; Conservative 0; Mismatches 0; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
IN APPLICATION NUMBER: US/08/345,820B
SEQUENCE FOR SEQ ID NO: 2:
SEQUENCE CHARACTER.STICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-4121
CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATER: Parent: PC-DOS/MS-DOS
SOFTWARE: Parent: Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 17-0CT-1995
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: de RURIZ, K. Alison
REGISTRATION NUMBER: 37,119
REFERENCE/DOCKET NUMBER: 0409.054US3
TELECHOME: 415-362-5556
TELEPHONE: 415-362-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-362-5418
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                      STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-345-8208-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity
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US-08-397-602A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAPF 4
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Gaps
APPLICANT: Tang, Maria R
APPLICANT: Berger, Harald
APPLICANT: Christianson, Peresa M
APPLICANT: Christianson, Peresa M
APPLICANT: Hansen, Dieter
TITLE OF INVENTION: Expression Systems for the Production
TITLE OF INVENTION: of Target Proteins in Bacillus
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-437-029-5
US-08-437-029-5
Sequence 5, Application US/08437029
Sequence 5, Application US/08437029
Sequence 5, Application US/08437029
Sequence 5, Application US/08437029
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Inhibiting Elastase
NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 1; Length 4; 100.0%; Pred. No. 2e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Ploppy disk
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA: US/08/397,602A
FILING DATE: 02-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jaeschke, Wayne C
REGISTRATION NUMBER: 11,062
REFERENCE/DOCKET NUMBER: 12,062
REFERENCE/DOCKET NUMBER: 09969/M4828
TELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: A amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                 ADDRESSEE: Herkel Corporation Law Department STREET: 140 Germantown Pike, Suite 150 CITY: Plymouth Meeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1
OTHER INFORMATION: /note= "N-SUCCINYL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
COATION: 4
OTHER INFORMATION: /note=
OTHER INFORMATION: "P-NITROANILIDE"
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NAME/KEY: Modified-site
LOCATION: 1..4
OTHER INFORMATION: /label= Phe-4
OTHER INFORMATION: /note= "Carboxyl-terminal phenylalanine resudue is
OTHER INFORMATION: capped with p-nitroanil..."
                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site
LOCATION: 1..4
OTHER INFORMATION: /label= ALA-1
OTHER INFORMATION: /note= "Amino terminal alanine residue is capped
OTHER INFORMATION: with a succinyl group"
FEATURE:
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Sequence 10, S719041
GENERAL INFORMATION:
APPLICANT: Lazarus, Robert A.
APPLICANT: Dennis, Mark S.
APPLICANT: Ulmer, Jana S.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING TITLE OF INVENTION: ECOTIN AND HOMOLOGS THEREOF NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 11-MAY-1995
CLASSIFICATION NUMBER: 08/319501
FILING DATE: 104-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/319501
FILING DATE: 04-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/319501
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISCHATION NUMBER: 36,575
REGISCHATION NUMBER: 36,575
REGISCHATION NUMBER: 36,575
TELEPHONE: 415/252-8228
TELEPHONE: 415/252-8288
TELEPHONE: 415/252-8288
TELEPHONE: 415/252-8288
TELEFAX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 21; DB 1;
100.0%; Pred. No. 2e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
STATE: California
COUNTY: USA
ZIP: 94080
                              19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
206-548-2329
                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                              amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAPF 4
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US-08-439-534-10
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US-08-424-022-19

i Sequence 19, Application US/08424022

j Sequence 19, Application US/08424022

j Sequence 19, Application US/08424022

j Setence 19, Application General Canada C
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                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/437,029
FILING DATE: 08 May 95
CLASSIFICATION: 514
ATTONENY/AGENT INFORMATION:

NAME: Dow, Karen B: REGISCTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 29,684
RETERRENCE/DOCKET NUMBER: 017066-000620
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 5:
SEQUENCE CHRARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,692
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-684
REPERNEK/DOCKET NUMBER: 92-21C2
TELEPHONE: 206-547-8080 ext 322
                                                               ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY; linear; MOLECULE TYPE: protein US-08-437-029-5
          California
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SEQUENCE CHANCTERISTICS:

INCOLOGY: Inter

US-08-499-514-10

US-08
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100.0%; Score 21; DB 1; Length 4;

Query Match

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Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAPF 4

Db 1 AAPF 4

Search completed: February 12, 2003, 10:30:11
Job time: 1.8597 secs
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6

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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserv
US-09-757-908A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
Sequence 10, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 10, Appl
Sequence 1, Appl
Sequence 38169, Appl
Sequence 48747, Appl
Sequence 566, Appl
Sequence 566, Appl
Sequence 622, Appl
                                                                                          (without alignments)
167.821 Million cell updates/sec
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                                                                           February 12, 2003, 10:22:36 ; Search time 0.608955 Seconds
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                                                                                                                                                                                                                                                                                                                                    Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USOF_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/USOF_PUBCOMB.pep:*
         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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0 US-09-75-7908A-15
0 US-09-315-744-1
2 US-10-090-624-33
2 US-10-090-624-33
2 US-10-091-655-10
2 US-10-013-526-1
2 US-10-013-526-1
2 US-10-013-526-1
2 US-10-013-526-1
2 US-10-013-526-1
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0 US-09-178-178-189-0
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                                                                                                                                                                                                           140259 seqs, 25548876 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    OM protein - protein search, using sw model
                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
                                                                                                                     US-10-036-371-7
21
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65:
74:
110:
111:
14:
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Perfect score:
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Maximum DB seq
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                                                                             Run on:
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1 AAPF 4
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US-10-036-371-7
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    SEQ ID NO 1
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Sequence 2, Application US/09117380B

Patent No. US20020119917A1

GENERAL INFORMATION:

APPLICANT: FRIDKIN, Matityahu

APPLICANT: YAVIN, Eran J.

TITLE OF INVENTION: ANTI-INPLAMMATORY PEPTIDES DERIVED FROM C-REACTIVE

TITLE OF INVENTION: PROTEIN

FILE REPERBNCE: PRIDKIN=1

CURRENT FILING DATE: 1999-01-27

PRIOR PILING DATE: 1999-01-27

PRIOR PLING DATE: 1999-01-27

PRIOR PLING DATE: 1999-01-27

PRIOR PLING DATE: 1996-01-31

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2
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Patent No. US20020137118A1

GENERAL INRORMATION:
APPLICANT: Shinde, Ujwal
APPLICANT: Shinde, Ujwal
APPLICANT: Shinde, Ujwal
TITLE OF INVENTION: Bloogically Active Protein Folding Intermediates
FILE REFERENCE: 266/223
CURRENT APPLICATION UNDER: US/09/935,744

CURRENT FILING DATE: 2001-08-24

NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: The N-terminal Ala residue is modified with a OTHER INFORMATION: succinyl group; the C-terminal Phe residue is OTHER INFORMATION: modified with a nitroanilide group.
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 09/326,039
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: US 60/088,136
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-757-908A-15
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Matches 4, Conserva
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US-09-117-380B-2
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US-09-935-744-1
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LENGTH: 4

JENGTH: 4

JENGTH: A

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: The sequence is part of a synthetic peptide that is used as a sub-
OTHER INFORMATION: atrate for determining the activation time of a stable crosslinke
OTHER INFORMATION: d intermediate conformer.

NAME/KEY: MISC_FEATURE

J. OCTHER INFORMATION: Sequence is preceded by N-succinyl and followed by p-nitroanilide
US-09-935-744-1
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Patent No. US20020141987A1
GENERAL INFORMATION:
APPLICANT BJARNARSON, JON B.
TITLE OF INVENTION: FISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND TITLE OF INVENTION: COSMETIC USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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; OTHER INFORMATION: Residue 4 is modified by a p-nitroaniline group.
US-10-090-624-33
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SUBLEAU INCOMENTION,
APPLICANT: MORISHITA, Mio
APPLICANT: MORISHITA, Mio
APPLICANT: MORISHITA, Mio
APPLICANT: ASADA, VIONORO
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAKURA-6
CURRENT FILING DATE: 2002-03-06
FRIOR APPLICATION NUMBER: 09/445,472
PRIOR PILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 151969/1997
PRIOR APPLICATION NUMBER: 151969/1997
PRIOR PILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PACHELIN VERSION 3.0
SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Residue 1 is modified by a succinyl group.
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Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 4; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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us-10-036-371-7.rapb

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SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-994-927-1
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US-10-033-526-4
                                           SEQ ID NO 1
LENGTH: 4
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US-10-036-371-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: peptide substrate
US-10-040-655-10
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| Parent No. US200201479991
| GRNERAL INFORMATION US/200201479991
| APPLICANT: Robert W. Mahley | APPLICANT: Robert W. Mahley | APPLICANT: Yadong Huang | TITLE OF INVENTION: APOE | TITLE OF INVENTION: APOE | FILE REPERENCE: UCALLT | CURRENT APPLICATION NUMBER: US/10/033,526 | CURRENT FILING DATE: 2001-11-02 | PRIOR FILING DATE: 2001-11-03 | PRIOR FILING DATE: 2001-11-03 | PRIOR FILING DATE: 2000-11-03 | NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 21; DB 12; Length 4; Best Local Similarity 100.0%; Pred. No. 1.2e+05; Matches 4; Conservative 0; Mismatches 0; Indels
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FILE REFERENCE: 81691/284960
CURRENT APPLICATION NUMBER: US/10/036,371
CURRENT FILING DATE: 2002-01-07
PRIOR PLILING DATE: 1999-10-12
PRIOR FLILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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US-10-040-655-10
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US-10-033-526-1
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parent No. US20020120203
; Sequence 1, Application US/09994927
; Patent No. US20020120203
; GENERAL INCORMATION:
    APPLICANT: Guilford Pharmaceuticals Inc.
    APPLICANT: Garadov, Sergei
    APPLICANT: Hamilton, Gregory
    APPLICANT: Was, Ling
    APPLICANT: Was,
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ORGANISM: Artificial Sequence
PERATURE
OTHER INFORMATION: Model substrate for measuring rotamase inhibition activity
NAME/KEY: MISC FEATURE
LOCATION: (1)...(1)
OTHER INFORMATION: Xaa at position 1 is N·succiny1
NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
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                                                                                                                                                                                                                                                                                             Length 4;
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Patent No. US200201479991
APPLICANT: Neobert W. Mahley
APPLICANT: Yadong Huang
TITLE OF INVENTION: Methods of Treating Disorders Related to
TITLE OF INVENTION: APPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 21; DB 10; Length 6; Best Local Similarity 100.0%; Pred. No. 1.2e+05; Matches 4; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Xaa at position 6 is p-nitroanilide US-09-994-927-1
                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 21; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                               ; OTHER INFORMATION: synthetic peptide US-10-033-526-1
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-664-761-38169
US-09-664-761-38169
US-09-664-761-38169
PRECENT NO. USSO200468-0531
PRECENT NO. USSO200468-0531
PRECENT NO. USSO200468-0531
APPLICANT: RAILE, DAVId R.
APPLICANT: RAILE, DAVId R.
APPLICANT: RAILE, DAVId R.
APPLICANT: RAILE, DAVID R.
ITITLE OF INVENTION: HIPMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITITLE OP INVENTION: HIPMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITITLE OP INVENTION: HIPMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL SOUTH OF THE STATE 
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ilarity 100.0%; Pred. No. 18;
Conservative 0; Mismatches 0;
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PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Optimized Abl substrate US-09-985-157-11
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 60/046,727
PRIOR FILING DATE: 1997-05-16
PRIOR FILING DATE: 1997-05-07
PRIOR FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
LENGTH: 12
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial sequence
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Matches 4; Conserva
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Patent No. US20020146797A1

GENERAL INFORMATION:

APPLICANT: SHOWATION:

TITLE OF INVENTION: Engineered Protein Kinases Which Can Utilize Modified Nucleotide

TITLE OF INVENTION: Triphosphate Substrates

FILE REFERENCE: 51538-5002-03

CURRENT APPLICATION NUMBER: US/09/985,157

CURRENT PILING DATE: 2002-03-13

PRIOR PLING DATE: 1999-11-17

PRIOR APPLICATION NUMBER: PCT/US98/02522
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| Patent No. US20020156123A1 |
| GENERAL INFORMATION: DELIGNAL JEAN-LUC |
| APPLICANT: PERON, OLIVIER |
| TITLE OF INVENTION: NOVEL PHARMACEUTICAL COMPOSITIONS FOR MODULATING |
| TITLE OF INVENTION: NOVEL PHARMACEUTICAL COMPOSITIONS FOR MODULATING |
| TITLE OF INVENTION: NOVEL PHARMACEUTICAL COMPOSITIONS FOR MODULATING |
| TITLE OF INVENTION: NOVEL PHARMACEUTICAL COMPOSITIONS FOR MODULATING CURRENT PAPLICATION NUMBER: US/10/068,965 |
| CURRENT FILING DATE: 2000-08-09 |
| PRIOR FILING DATE: 2000-08-09 |
| PRIOR FILING DATE: 1999-08-09 |
| NUMBER OF SEQ ID NOS: 86 |
| SOFTWARE: PATENTING UPT: 2.1 |
| SEQ ID NO 4 |
| LENTH: 10 |
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OTHER INFORMATION: Description of Artificial Sequence: Caveolin
OTHER INFORMATION: binding motif
US-10-068-965-4
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100.0%; Score 21; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 4; Conservative 0; Mismatches 0;
                    CURRENT APPLICATION NUMBER: US/10/033,526
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 60/245,737
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PARCERQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: synthetic peptide US-10-033-526-4
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-068-965-4
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Best Local Similarity 100.0%; Score 21; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 4; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.91
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.95
US-09-684-761-38169
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 38169
LENGTH: 25
TYRE: PAT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 335, Application US/09974879
Sequence 335, Application US/09974879
GENERAL INFORMATION:
APPLICANT: Rosen et al.
ITILE OF INVENTION: 125 Human Secreted Proteins
FILIE REFERENCE: PZ020p2
CURRENT APPLICATION NUMBER: US/09/974,879
CURRENT FILING DATE: 2001-10-13
FRIOR APPLICATION NUMBER: US 09/318,683
FRIOR FILING DATE: 2001-01-32
FRIOR PELING DATE: 1990-11-04
FRIOR PELING DATE: 1990-11-04
FRIOR APPLICATION NUMBER: US 09/305,736
FRIOR PELING DATE: 1997-11-07
FRIOR APPLICATION NUMBER: US 00/064,911
FRIOR PELING DATE: 1997-11-07
FRIOR FILING DATE: 1997-11-17
FRIOR FILING DATE: 1997-11-17
FRIOR FILING DATE: 1997-11-07
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FRIOR FILING DATE: 1997-11-07
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US-09-974-879-335
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Sequence 48747, Application US/09664761

Sequence 48747, Application US/09664761

Sequence 48747, Application US/09664761

Sequence 48747, Application US/09664761

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Application Wensheng

TITLE OF INVENTION: HURAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                      .
                                                                                                                                                                                                                 Gaps
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                                                                                                             Query Match 100.0%; Score 21; DB 9; Length 31; Best Local Similarity 100.0%; Pred. No. 48; Matches 4; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: EXPRESSED IN PLACEMTA, SIGNAL = 2.8
; OTHER INFORMATION: SWISSPROT HIT: P15772, EVALUE 8.20e+00
US-09-664-761-48747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THERE OF INVALICATION CARE EXPRESSION ANALYSIS BY MICRO)
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
FRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PELING DATE: 2000-02-04
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-06
PRIOR PELING DATE: 2000-09-04
PRIOR PELING DATE: 2000-09-04
PRIOR PELING DATE: 2000-09-07
PRIOR PELING DATE: 2000-09-07
PRIOR PELING DATE: 2000-09-07
PRIOR PELING DATE: 2000-09-07
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-0
; ORGANISM: Homo sapiens
US-09-974-879-335
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ORGANISM: Homo sapiens
FEATURE:
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Query Match 100.0%; Score 21; DB 10; Length 45; Best Local Similarity 100.0%; Pred. No. 71; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps දි දි

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1 AAPF 4 ||||| 39 AAPF 42

Search completed: February 12, 2003, 10:31:07 Job time : 1.60896 secs

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GenCore version 5.1.3
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February 12, 2003, 10:03:55 ; Search time 13.4328 Seconds	(without alignments)	198.395 Million cell updates/sec
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Title: Perfect acore:	US-10-036-371-1
Sequence:	
Scoring table: BLOSUM62	BLOSUM62
	Gapop 10.0 , Gapext 0.5

908470 seqs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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		/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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	13;	/SIDS2/gcgdata/geneseq/genesecp-embl/AA1992 DAT: *
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	15:	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
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	22:	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
	23:	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	N-Toyanasa A-	N-towning of 11	N-terminal of atla	/ Atlantia of Atla	(Actancte con nyaro)	Atlantic cod colt	Atlantic cod multi	Atlantic cod multi	Attailer cod I mul	Actanulo con 11 mu N-terminal of an a
SUMMARIES	ID	AAY93937	AAE07943	AAE07944	AAY33347	AAY3334R	AAB22966	AAB22967	AACCICA	AA021359	AAY93946
	DB	21	22	22	20	20	21	21	23	23	21
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	Query Match	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7
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Atlantic cod multi Amino acid seguenc Engraulis japonicu Atlantic cod hydro Salmon enzyme i mu N-terminal of an a	N-terminal of slam Salmon enzyme i mu Engraulis japonicu Human amyloid beta Amino terminal seq Canine anionic try	e anionic ne trypsin inogen-lik spleen try pancreati trypsin s	Human trypsin seri Human TRYI trypsin Human trypsinogen. Human panorearic t Human protease PRT N-terminus of bovi Amino terminal seq	54 · O O S · M C
23 AAO213 22 AAB315 23 ABB046 20 AAY333 21 AAB229	22 AAE0794 23 AA02135 23 ABB0464 19 AAW6426 22 AAB3157 21 AAY7897	0 H H O H C C	2011881100	2.0 AAM1767 2.1 AAK59973 2.1 AAK53637 2.2 AAK53638 2.2 AAV91926 2.2 AAV91926 2.3 AAB8053 2.3 ABB83322
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11 12 12 12 12 12 12 12 12 12 12 12 12 1	\ B B B B B B B B	2 2 2 2 2 2 2 4 5 4 5 5 5 5 5 5 5 5 5 5		

ALIGNMENTS

RESULT 1 AAY93937	AAY93937 standard; peptide; 23 AA.	AAY93937;	03-OCT-2000 (first entry)	N-terminal of an atlantic cod hydrolase enzyme.
AA AA	ΩX	AX X	77	E E

Transplantation rejection; hydrolase; graft versus host disease; cell surface adhesion molecule; immune reaction; inflammation; shock; tumour metastasis; autoimmune disease; Krill derived multifunctional enzyme. Gadus sp.

(PHAI-) PHAIRSON MEDICAL INC. 99WO-US30818. 98US-0114147. WO200038708-A1. 24-DEC-1998; 23-DEC-1999; 06-JUL-2000.

Preventing or ameliorating transplantation rejection reactions using hydrolase enzymes

Franklin RL, St Pierre Y; WPI; 2000-452301/39.

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Ameliorating, preventing or treating immune rejection reactions, such as graft versus host disease, autoimmune disease, asthma, cancer, by extra-corporeally treating donor tissue with hydrolase such as a
     Disclosure; Page 26; 66pp; English
                                                                                                                                                                                                                                                     AAE07943 standard; peptide; 23 AA.
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95US-0486820.
96US-0600273.
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                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                      Query Match
Best Local Similarity 85.0
Matches 17; Conservative
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                                                                                                                                                        23 AA;
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07-JUN-1995;
08-FEB-1996;
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                                                                                                                                          invention
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The present invention relates to a method for ameliorating transplantation rejection reaction. The method comprises treating extra-corporeally donor tissue or donor source of immune cells with a rejection ameliorating effective amount of a hydrolase enzyme. The method is useful for ameliorating, treating or preventing immune rejection reactions such as graft versus host diseases, organ or tissue risansplantation rejection, autoimmune disease and associated conditions, microbial infection, immune disorder, cystic fibrosis, chronic obstructive pulmonary disease (COPD), atherosclerosis, cancer, asthma, septic shock, toxic shock syndrome, conjunctivitis, reperfusion injury and pain in humans. The present sequence is the Niterminal peptide of atlantic cod I serime multifunctional hydrolase, used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multifunctional hydrolage; rejection reaction; extra-corporeal; therapy, graft versus host disease; transplantation rejection; autoimmune disease; microbial infection; immune disorder; cytostatic; cytostatic; atherost obstructive pulmonary disease; COPD; atherosclerosis; cancer; asthma; septic shock; toxic shock syndrome; conjunctivitis; reperfusion injury; pain; immunosupressive; antibacterial; vasotropic; atlantic cod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ameliorating, preventing or treating immune rejection reactions, such as graft versus host disease, autoimmune disease, asthma, cancer, by extra-corporeally treating donor tissue with hydrolase such as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal of atlantic cod II serine multifunctional hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         94.7%; Score 90; DB 22;
85.0%; Pred. No. 1.2e-08;
iive 0; Mismatches 3;
Disclosure, Column 15-16, 27pp, English.
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                                                                                          transplantation rejection reactions for transplantation of immune cells or other tissues. The method comprises treating a source of immune cells or other tissues. The method comprises treating a source of immune cells with a hydrolase or hydrolase mixture and administering the treated immune cells to a recipient animal. The hydrolase especially has a preference for removing destroying, inactivating or disabling at least one of CD4. CD5. CD28 ICAM-1 (CD54). CD182, an integrin, CD14, CD40 and CD80 in contrast to removing, destroying, inactivating or disabling TCR. The methods are useful for preventing graft versus host disabling TCR. The methods are useful for preventing graft versus host concuses which are involved in triggering the immune reactions involved in the diseases. The methods are used for treating or preventing in the diseases. The methods are used for treating or preventing cell-cell or cell-virus adhesion syndrome comprising inflammation, shock, tumour metastases, autoimmune disease, transplantation rejection recations or microbial infections. The present sequence represents the remainal of a hydrolase, which may be used in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multifunctional hydrolage; rejection reaction; extra-corporeal; therapy; graft versus host disease; transplantation rejection; autoimmune disease; microbial infection; immune disease; cytostatic; cytostatic; cytostatic fibrosis; chronic obstructive pulmonary disease; COPD; atherosclerosis; cancer; asthma; septic shock; toxic shock syndrome; conjunctivitis; reperfusion injury; pain; immunosuppressive; antibacterial; vasotropic; adjantic cod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                specification describes a method for preventing or ameliorating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal of atlantic cod I serine multifunctional hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.7%; Score 90; DB 21; Length 23; 85.0%; Pred. No. 1.2e-08; ive 0; Mismatches 3; Indels
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The present invention relates to a method for ameliorating transplantation rejection reaction. The method comprises treating extra-corporeally donor tissue or donor source of immune cells with

Disclosure; Column 15-16; 27pp; English.

protease

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Gaps

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a rejection ameliorating effective amount of a hydrolase enzyme. The method is useful for ameliorating, treating or preventing immune rejection reactions such as graft versus host diseases, organ or tissue transplantation rejection, autoimmune disease and associated conditions, obstructive pulmonary disease (COPD), atherosclerosis, chronic septic shock, toxic shock syndrome, conjunctivitis, reperfusion injury and pain in humans. The present sequence is the N-terminal peptide of atlantic cod II serine multifunctional hydrolase, used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multifunctional enzyme; treatment; acne; eczema; chymotrypsin; trypsin; collagenses; elastase; exopeptidase; cell surface receptor; anti-acne; antiseborrheic; dermatological; anti-eczema; adhesion molecule; ICAM-1; CD54; ICAM-2; VCAM-1; CD1, CD8; CD28; CD28; CD31; CD44; CD49; CD62L; CD102; GM1 ceramide; krill; atlantic cod.
                                                                                                                                                                          Note: The sequence is stated as being the same as that shown as SEQ ID NO 19 (see AAE07951) in column 31-32 of the specification, However the sequences differ at several positions.
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating acne and eczema using a krill-derived multifunctional enzyme
                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                     94.7%; Score 90; DB 22; Length 23;
85.0%; Pred. No. 1.2e-08; "Minnarches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Atlantic cod hydrolase N-terminal fragment II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Faire JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Column 21-22, 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY33347 standard; peptide; 25 AA.
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                                                                                                                                                                                                                                                                                                                                                                                1 IVGGYECTRHSQAHQVSLNS 20
                                                                                                                                                                                                                                                                                                                                                           1 IVGGYXCXXHSQAHQVSLNS 20
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95US-0385540.
95US-0486820.
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                                                                                                                                                                                                                                                                                                      Local Similarity 85.0
les 17; Conservative
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                                                                                                                                                                                                                                                      23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USS958406-A.
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                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY33347;
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                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multifunctional enzyme; treatment; acne; eczema; chymotrypsin; trypsin; collagenses; elastase; exopetidase; cell surface receptor; anti-acne; antiseborrheic; dermatological; anti-eczema; adhesion molecule; ICAM-1; CD54; ICAM-2; VCAM-1; CD4 CD8; CD29b; CD31; CD44; CD54; CD62L; CD102; GM1 ceramide; krill.
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                                                                                                                                                                                              Gaps
  an atlantic cod (Gadus sp.) hydrolase which is used to describe the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Krill-derived multifunctional enzyme N-terminal fragment 3.
                                                                                                                              94.7%; Score 90; DB 20; Length 25; 85.0%; Pred. No. 1.3e-08; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 25,
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85.0%; Pred. No. 1.3e-08;
Live 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                           AAY33348 standard, peptide; 25 AA.
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                                                                                                                                                                                                                                1 IVGGYXCXXHSQAHQVSLNS 20
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95US-0385540.
95US-0486820.
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                                                                                                                                                                                17; Conservative
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Best Local Similarity 85.0
Matches 17, Conservative
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                                                                                                                        Query Match
Best Local Similarity
                                                                              25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 AA;
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07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-NOV-1994;
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                                                                           Sequence
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1 IVGGYECTRHSQAHQVSLNS 20
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AAB22966 standard; peptide; 25 AA

AAB22966;

(first entry) 10-JAN-2001 Atlantic cod multifunctional hydrolase I peptide

protease activity; chymotrypsin; trypsin; collagenase; elastase; wound healing; corneal ulcer; internal trauma; internal surgical wound; nerve; tendon; sheath; adhesion formation inhibition; opthalmological; vulnerary. Multifunctional hydrolase; multifunctional protein;

Gadus morhua

WO200049991-A2.

31-AUG-2000

99WO-US14751. 29-JUN-1999;

99US-0256484. 23-FEB-1999; (PHAI-) PHAIRSON MEDICAL INC

Cowling D, Hubbell JA;

Franklin R,

WPI; 2000-587120/55.

Use of microgel comprising crosslinked polyanionic polymer and optionally proteclytic enzyme in treatment of corneal wounds e.g. ulcers and abrasions and internal trauma e.g. surgical wounds and treating implants to reduce adhesions

Disclosure, Page 25; 85pp; English.

The invention relates to use of a microgel comprising a crosslinked polyamical compositions for treatment of an area affected by a trauma selected from corneal wounds and internal trauma. The compositions further comprise a multifunctional procease having activities selected from two of chymotrypsin activity, trypsin activity, collagenase activity and elsetase activity. In particular, the procease compositions of six isoforms of white shrimp (Penseus vannamei) antifunctional hydrolase (AAB22947-B22952), or a multifunctional enzyme comprising one of the peptide sequences given in AAB2951-B22967.

Compositions of the peptide sequences given in AAB2951-B22967.

Compositions of the invention may be used to treat corneal ulcer. (Including infected ulcers), or abrasions or a chemical or physical insult to the cornea that are likely to give rise to a corneal ulcer. They are also used to treat internal traumas selected from an internal organ or tissue or the cavity in which one or more internal internal organ or tissue or the cavity in which one or more internal organs or tissues reside, with the membrane being selected from the peritoneum, the pericardium, the epicardium and the pleura and a peritoneum, the pericardium, the epicardium and the pleura and a corneal enternal sheath, where the trauma is to a tendon, tendon sheath, a nerve cor a nerve sheath, where the trauma is susceptible to givining rise to a reduce formation or reformation of adhesions, and the composition can be used to treat an implant to reduce formation of adhesions, and the composition of squences AAB22951-B22967 represent peptide sequences from a variety of squences AAB22951-B22967 represent peptide sequences from a variety of these sequences are claimed for use in compositions of the invention.

25 AA; Sequence

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Gaps ö Length 25; 3; Indels Query Match

94.7%; Score 90; DB 21;
Best Local Similarity 85.0%; Pred. No. 1.3e-08;
Matches 17; Conservative 0; Mismatches 3.

AAB22967 standard; peptide; 25 AA.

AAB22967;

(first entry) 10-JAN-2001 Atlantic cod multifunctional hydrolase II peptide.

protease activity; chymotrypsin; trypsin; collagenase; elastase; wound healing; corneal ulcer; internal trauma; internal surgical wound; nerve; tendon; sheath; adhesion formation inhibition; opthalmological; vulnerary. Multifunctional hydrolase; multifunctional protein;

Gadus morhua.

WO200049991-A2.

31-AUG-2000.

99WO-US14751. 29-JUN-1999;

99US-0256484. 23-FEB-1999;

(PHAI-) PHAIRSON MEDICAL INC.

Cowling D, Hubbell JA;

WPI; 2000-587120/55.

Franklin R,

Use of microgel comprising crosslinked polyanionic polymer and optionally proteolytic enzyme in treatment of corneal wounds e.g. ulcers and abrasions and internal trauma e.g. surgical wounds and treating implants to reduce adhesions -

Disclosure; Page 25; 85pp; English.

control in the comparison of the comparison of an area affected by polyamionic polymer in compositions for treatment of an area affected by a trauma selected from corneal wounds and internal trauma. The compositions further comprise a multifunctional procease having activity, trypsin activity, collagenase activity and elastese activity. In particular, the procease collagenase activity and elastese activity. In particular, the procease collagenase activity and elastese activity. In particular, the procease (collagenase activity and elastese activity. In particular, the procease comprising one of the peptide sequences given in AAB22953.B22967.

Compositions of the invention may be used to treat corneal ulcers (including infected ulcers), or abrasions or a chemical or physical (including infected ulcers), or abrasions or a chemical or physical ulcer. They are also used to treat internal traumas selected from an internal organ or tissue or the carity in which one or more internal organ or tissue or the carity in which one or more internal organ or tissues reside, with the membrane being selected from the periconeum, the pericardium, the epicardium and the pleura and a periconeum, the parthal trauma is to a tendon, tendon sheath, a nerve meninges. The internal trauma is to a tendon, tendon sheath, a nerve cor a nerve sheath, where the trauma is susceptible to giving rise to a reduce formation or reformation of adhesions, and the composition of albesions. The amount of microgel administered is sufficient to prevent or sequences AAB225951-B22967 represent poptide sequences from a variety of multifunctional hydrolases. Multifunctional hydrolases comprising one of these sequences are claimed for use in compositions of the invention. The invention relates to use of a microgel comprising a crosslinked

25 AA; Sequence

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AAO21359 standard; Peptide; 25 AA.

RESULT 9

AA021359;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for treating corneal wounds or internal trauma. The method provides administration of a composition comprising a polyamionic polymer. The method is useful for treating corneal wounds, including corneal ulcers. Corneal abrasions or injuries which may give treat to corneal ulcers. The method is also useful for treating internal organ, tissue or cavity or trauma likely to give rise to occurs an entrance of the method is useful for treating covers an further method is useful for treating coveries and sorder, endometricosis, pelvic inflammatory disease, adhesive peritonitis, appendicitis, peridentitis, pericarditis and pleuritis or multifunctional hydrolase peptide regresents the atlantic cod I polymers of the invention.
                                                 Gaps
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   94.7%; Score 90; DB 21; Length 25; 85.0%; Pred. No. 1.3e-08; 1.ve 0; Mismatches 3; Indels
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(BIDG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cowling DSP, Hubbell JA,
                                                                                                                                                                                          AAO21358 standard; Peptide; 25 AA.
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                                                                              20
                                                                                                   1 IVGGYECTRHSQAHQVSLNS 20
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                                                                                                                                                                                                                                                                     (first entry)
                                                                       1 IVGGYXCXXHSQAHQVSLNS
Query Match
Best Local Similarity 85.0
Matches 17, Conservative
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                                                                                                                                                                                                                                                               05-AUG-2002
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                                                                                                                                                                                                                            AA021358;
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Tranquiliser; vulnerary; cytostatic; gynaecological; antiinflammatory; corneal wound; internal trauma; polyanionic polymer; corneal ulcer; corneal abrasion; surgical wound; organ membrane trauma; tissue; cavity; adhesion; cervical spondylosis; cumulative trauma disorder; appendicitis; endometriosis; polvic inflammatory disease; adhesive peritonitis; peridantitis; peridantitis; pleuritis; inflammatory disease; multifunctional protein; hydrolase; enzyme; atlantic cod.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for treating corneal wounds or internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trauma. The method provides administration of a composition comprising a polyanionic polymer. The method is useful for treating corneal unders, corneal abrasions or injuries which may give inset to corneal ulcers. The method is also useful for treating internal trauma, including surgical wounds, trauma to a membrane that covers an organ, tissue or cavity or trauma likely to give rise to adhesions. A trauma disorder, endometriosis, pelvic inflammatory disease, adhesive perifontis, appendicitis, peridentics, pericarditis and pleuritis or other inflammatory diseases. This sequence represents the atlantic cod II polymers of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment of corneal wounds, internal trauma or inflammatory diseases comprises administration of a polyanionic polymer
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Van De Wetering P;
                                                             Atlantic cod II multifunctional hydrolase peptide region.
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(EIDG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Cowling DSP, Hubbell JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 24; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY93946 standard; peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.7%;
85.0%;
                                                                                                                                                                                                                                                                                                                         23-AUG-2000; 2000WO-US23072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IVGGYXCXXHSQAHQVSLNS 20
                                                                                                                                                                                                                                                                                                                                                           23-AUG-2000; 2000WO-US23072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IVGGYECTRHSQAHQVSLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-425632/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 AA;
                                                                                                                                                                                                                                                            WO200215913-A1.
                                                                                                                                                                                                                          Gadus morhua.
                                   05-AUG-2002
                                                                                                                                                                                                                                                                                            28-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Franklin R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY93946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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ID AAY9
XX
AC AAY9
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DT 03-0
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Gaps

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94.7%; Score 90; DB 23; Length 25; 85.0%; Pred. No. 1.3e-08; ive 0; Mismatches 3; Indels

1 IVGGYECTKHSQAHQVSLNS 20

1 IVGGYXCXXHSQAHQVSLNS 17; Conservative

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Query Match Best Local Similarity Matches 17; Conserv

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The specification describes a method for preventing or ameliorating cransplantation rejection reactions for transplantation of immune cells crother tissues. The method comprises treating a source of immune cells with a hydrolase or hydrolase mixture and administering the treated immune cells to a recipient animal. The hydrolase especially has a preference for removing, destroying, inactivating the treated of CD4. CD8, CD2, CD2, CD2, CD2, CD2, an integrin. CD154, cone of CD4. CD8, CD25, CD24 in CD152, an integrin. CD154, CD40 and CD80 in contrast to removing, destroying, inactivating or disabling rCR. The methods are useful for preventing graft versus host molecules which are involved in triggering the immune reactions involved in the disease by using hydrolase enzymes to remove the cell surface adhesion collection cells. The methods are used for treating or preventing or cell-cell or cell-virus adhesion syndrome comprising inflammation, shock, tumour metasteses, autoimmune disease, transplantation rejection reservance or microbial infections. The present sequence represents the remaind of a trypsin hydrolase, which may be used in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tranquiliser; vulnerary; cytostatic; gynaecological; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                    Transplantation rejection; hydrolase; graft versus host disease; cell surface adhesion molecule; immune reaction; inflammation; shock; tumour metastasis; autoimmune disease; krill derived multifunctional enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preventing or ameliorating transplantation rejection reactions using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Atlantic cod multifunctional hydrolase N-terminal peptide region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.7%; Score 90; DB 21; Length 37; 85.0%; Pred. No. 2e-08; ive 0; Mismatches 3; Indels
     N-terminal of an atlantic cod trypsin hydrolase enzyme.
                                                                                                                                                                                                       /note= "any amino acid"
                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 26; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAO21360 standard; Peptide; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IVGGYQCEAHSQAHQVSLNS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IVGGYXCXXHSQAHQVSLNS 20
                                                                                                                                                                                                                                                                                                                                                                                  (PHAI-) PHAIRSON MEDICAL INC
                                                                                                                                                                                                                                                                                                              99WO-US30818.
                                                                                                                                                                                                                                                                                                                                                 98US-0114147.
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                                                                                                                                                                                                                                                                                                                                                                                                                  St Pierre Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-452301/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hydrolase enzymes
                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the invention.
                                                                                                                                                                                                                                             WO200038708-A1
                                                                                                                                                                                                                                                                                                                                                                                                                       Franklin RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-AUG-2002
                                                                                                                                                                                                                                                                                                                23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                   24-DEC-1998;
                                                                                                                                                                                                                                                                                06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                      Gadus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
EXEXEXEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis, inflamed joint, bursitis, osteoarthritis, septic arthritis, rheumation, dringmed joint, bursitis, osteoarthritis, septic arthritis; rheumatoid arthritis; fibromyalgia; systemic lupus erythematosus; pilebitis; tendinitis; rash; psoriasis; acne, eczema; facial seborrheic eczema; foreskin infection, athlete's foot; fistulae infection, ulcer; navel infection; wrinkle; scar, kelloid; boil; wart; allergic itch; hemorrhoid; wound; fungal infection; autoimmune disease.
corneal wound; internal trauma; polyanionic polymer; corneal ulcer; corneal abrasion; surgical wound; organ membrane trauma; tissue; cavity; adhesion; cervical spondylosis; cumulative trauma disorder; appendicitis; andometriosis; pelvic inflammatory disease; adhesive peritonitis; peridantitis; pericarditis; pleuritis; inflammatory disease; multifunctional protein; hydrolase; enzyme; atlantic cod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment of corneal wounds, internal trauma or inflammatory diseases comprises administration of a polyanionic polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.7%; Score 90; DB 23; Length 37;
85.0%; Pred. No. 2e-08;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Cowling DSP, Hubbell JA, Van De Wetering P;
                                                                                                                                                                                                                                                                                                                                    PHAIRSON MEDICAL INC.
BIDGENOESSISCHE TECH HOCHSCHULE ZUERICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of cod trypsin isozymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB31579 standard; peptide; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 24; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IVGGYXCXXHSQAHQVSLNS 20
                                                                                                                                                                                                                                                               23-AUG-2000; 2000WO-US23072.
                                                                                                                                                                                                                                                                                                    23-AUG-2000; 2000WO-US23072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IVGGYQCEAHSQAHQVSLNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.0
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-425632/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 AA;
                                                                                                                                                                                       WO200215913-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                    Franklin R,
                                                                                                                                                     Gadus morhua
                                                                                                                                                                                                                               28-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                              (PHAI-)
                                                                                                                                                                                                                                                                                                                                                                  (EIDG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
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'note= "Xaa is any amino acid or absent"
                                                                                                                                                                                                                                                                                                                                                                                                label= Met, Val, Cys
                            Location/Qualifiers
                                                    label= Lys, Arg
                                                                                                                                   label= Asp, Gln
                                                                                                                                                                                                                                label= Asp, Asn
                                                                                                                                                              label= Tyr, Phe
                                                                                /label= Tyr, Phe
                                                                                                                                                                                                                                                                                    label= Ala, Asp
                                                                                                                                                                                                                                                            label= Lys, Glu
                                                                                                                                                                                                                                                                                                                                           label= Asn, Ser
                                                                                                                                                                                                                                                                                                                                                                      label= His, Asn
                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Asn, Ser
                                                                                                        label= Lys,
                                                                                                                                                                                      label= Ile,
                                                                                                                                                                                                                                                                                                                 label= Val,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2000; 2000WO-IS00005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  991S-0005086.
                                                                                                                                                                                                                                                                                                Misc-difference 136
                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 212
                                                                                                                                                                                                                                                                                                                                                    Misc-difference 204
                                                                                         Misc-difference 32
                                                                                                                    Misc-difference 33
                                                                                                                                              Misc-difference 64
                                                                Misc-difference 24
                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 22.
                                   Misc-difference 9
Gadus callarias.
                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200078332-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-2000
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(BJAR/) BJARNASON J B.

Bjarnason JB;

Fish serine proteinase, useful as a cosmetic, medicament for treating eczema, psoriasis, arthritis, and in the manufacture of the medicament for treating, preventing pathogenic diseases involving receptor mediated binding

Disclosure; Page 13; 38pp; English.

The specification describes a fish serine proteinase. The proteinases are useful as medicaments, for treating and preventing a disease in a numan nor an animal such as pain, acute inflammation, chronic remainal such as pain, acute inflammation, chronic rehumatoid arthritis, inflamed joints, burstis, osteoarthritis, fibromyladia, systemic lupus erythematosus, phibitis, tendinitis, rash, psoriasis, acne eczema, facial seborrheic cezema, eczema of the hands, infections, acne eczema, facial seborrheic cezema, eczema of the hands, infections, wounds from burst, infections in newborns, wrinkles, scars, infections, wounds from burst, fungal infections and immunological and skin from otherwise healthy skin, and for treating or preventing a disease. They are also useful for removing dead or peeling disease in which pathogenesis is caused by bacteria, virus, funga, the present sequence represents the amino acid sequence of cod trypsin

225 AA; Sequence

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The present sequence represents a trypsinogen, which is a protease (I) isolated from Engraulis japonicus (also called Engraulis japonica or Japanese anchowy). The present invention also describes: (I) a DNA encoding (I), or encoding a protease consisting of an amino acid sequence in which part of the amino acid residue is replaced, inserted or deleted in the amino acid sequence encoded by the above DNA and thaving a bio-activity substantially same as (I); (2) an expression vector in which the above DNA is recombined; (3) producing a sardine-containing substantially no other protein derived from fish; and containing substantially no other protein derived from fish; and containing substantially no other protein derived from fish; and containing substantially no other protein derived from fish; and the generation of an unpleasant small compared to a case where the protease prepared by the above method is not added in which at least cone of a fish or a shellfish selected from the group consisting of clupeidae order is immersed in an aqueous solution containing salts in a short naving a short mathod is added to it and fermented for about it to II and the protease prepared to a containing salts in the part of the group consisting as the protein a short protein a short protein containing salts in the preparation of a fish sauce in a short protein containing salts in the preparation of a fish sauce in a short protein containing salts in the preparation of a fish sauce in a short protein containing salts in the preparation of a fish sauce in a short protein and                                                                 0
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                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease; trypsinogen; sardine; Japanese anchovy; fish sauce
     94.7%; Score 90; DB 22; Length 225; 90.0%; Pred. No. 1.4e-07; 1ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 240;
                       / Match
Local Similarity 75.0%; Pred. No. 1.2e-05;
length 24(
No. 1.2e-05;
les 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Engraulis japonicus trypsinogen (aTry I) SEQ ID NO:1.
                                                                                                                                                                                                                                                        ABB04644 standard; Protein; 240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 7; 32pp; Japanese.
                                                                                                                                      1 IVGGYECTXHSQAHQVSLNS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-2000; 2000JP-0084302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAR-2000; 2000JP-0084302.
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                                                                                             1 IVGGYXCXXHSQAHQVSLNS
Query Match
Best Local Similarity 90.03
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                        04-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IVGGYXCXXHSQAHQVSLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-078276/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Engraulis japonícus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A new DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABA04345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP2001269173-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-2001.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel method for treating acne and eczema using a krill-derived multfunctional enzyme (1) which comprises 2 or more of the activities of chymotrypsin, trypsin, collagenase, elastase or exopeptidase and is reactive with cell surface receptors such as proteins or glycoproteins. The product of the invention have antiseborrheic, anti-acne, dermachological and anti-eczema activity.
(1) removes or inactivates cell surface receptors (proteins and glycoproteins) and adheaion molecules such as ICAM-1 (i.e. CD54), UCAM-1, CD4, CD8, CD29, CD31, CD44, CD49, CD61, CD102 and the asialo GM, ceramide. This sequence represents the N-terminal fragment of an atlantic cod (Gadus sp.) hydrolase which is used to describe the
                                                                                                          Multifunctional enzyme; treatment; acne; eczema; chymotrypsin; trypsin; collagenase; elastase; exopeptidase; cell surface receptor; anti-acne; antiseborrheic; dermatcological; anti-eczema; adhesion molecule; ICAM-1; CD54; ICAM-2; VCAM-1; CD8; CD8; CD8; CD91; CD11; CD44; CD49; CD62L; CD102; GM1 ceramide; krill; atlantic cod.
                                                                                                                                                                                                                                                                                                                                                                         Treating acne and eczema using a krill-derived multifunctional enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.1%; Score 78; DB 20; Length 25; 75.0%; Pred. No. 1.6e-06; Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multifunctional hydrolase; multifunctional protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmon enzyme 1 multifunctional hydrolase peptide.
                                                                                                                                                                                                                                                                                                                                  De Faire JR;
                                                                                          Atlantic cod hydrolase N-terminal fragment I.
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Column 21-22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ż
                                                                                                                                                                                                                                                                                                                                    Kay J, Franklin RL,
                           AAY33346 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB22965 standard; peptide; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IVGGYXCXXHSQAHQVSLNS 20
                                                                                                                                                                                                                                                                                                              (PHAI-) PHAIRSON MEDICAL INC.
                                                                                                                                                                                                                                                                               95US-0385540.
95US-0486820.
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Best Local Similarity 75.0
Matches 15; Conservative
                                                                      29-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              method of the invention
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07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                     Lindblom R,
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          RESULT 14
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The invention relates to use of a microgel comprising a crosslinked polyanionic polymer in compositions for treatment of an area affected by polyanionic polymer in compositions for treatment of an area affected by compositions further comprise a multifunctional protease having conjugations further comprise a multifunctional protease having collagenase activity and elastase activity. In particular, the protease only in a six isoforms of white shrimp (Penaeus vannamei) and internal by a six isoforms of white shrimp (Penaeus vannamei) on pritaing one of the invention may be used to treat corneal ulcers of insult to the cornea that are likely to give rise to a corneal ulcer. Compositions of the invention may be used to treat corneal ulcer. Compositions of the invention may be used to creat corneal ulcer. Insult to the cornea that are likely to give rise to a corneal ulcer. Compositions or tissue or the random selected from an internal surgical wound, or a trauma selected from an internal organ or tissue or the cavity in which one or more internal organ or tissue or the cavity in which one or more internal organ or tissue or the cavity in which one or more internal organ or tissue or the cavity in which one or more internal organ or tissue or the remains the perioardium, the epicardium, the pelangement or meninges. The internal trauma is to a tendon, tendon sheath, an areveen meninges. The internal trauma is to a tendon, tendon sheath, an or reduce formation or reformation of adhesions.

The absolvant of microgel administered is sufficient to giving rise to a reduce formation or reformation of adhesions.

The absolvant of microgel administered is sufficient to giving one of multifunctional hydrolases. Multifunctional hydrolases comprising one of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of microgel comprising crosslinked polyanionic polymer and optionally proteolytic enzyme in treatment of corneal wounds e.g. ulcers and abrasions and internal trauma e.g. surgical wounds and treating implants to reduce adhesions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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protease activity; chymotrypsin; trypsin; collagenase; elastase; wound healing; corneal ulcer; internal trauma; internal surgical wound; nerve; tendon; sheath; adhesion formation inhibition; opthalmological; vulnerary.
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75.0%; Pred. No. 1.6e-06;
iive 2; Mismatches 3.
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February 12, 2003, 10:22:36; Search time 34.2537 Seconds (without alignments)
167.821 Million cell updates/sec
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1158
1 IVGGYECTXHSQAHQVSLNS......GVYAKVXVLSGWVRDTMAAYY
GenCore version 5.1.3
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140259 segs, 25548876 residues Searched:

140259

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:*

| cgn2_6/ptodata/1/pubpaa/USOB NEW PUB.pep:*
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SUMMARIES

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ALIGNMENTS

Sequence 8, Application US/10036371

Fatent No. US2002014199741

FAPLICATION: COSMETIC USE

TITLE OF INVENTION: FISH SERINE PROTEINASES AND THEIR PHARMACEUTICAL AND TITLE OF INVENTION: COSMETIC USE

FILE REPEREBREE: 81691/284960

CURRENT APPLICATION NUMBER: US/10/036,371

PRIOR APPLICATION NUMBER: 096411,688

PRIOR PELING DATE: 1999-10-12

PRIOR PELING DATE: 1999-10-12

PRIOR PELING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 8

LENGTH: 225

LENGTH: 225

FEATURE:
NAME/KEY: MOD_RES
LOCATION: (9)
CTHER INFORMATION: K or
FEATURE: TYPE: PRT ORGANISM: Gadus sp.

NAME/KEY: MOD RES LOCATION: (24) OTHER INFORMATION: Y OF F FEATURE: O NAME/KEY: MOD RES LOCATION: (32) OTHER INFORMATION: K or D or or FEATURE:
NAME/KEY: MOD RES
LOCATION: (33)
OTHER INFORMATION: D

FEATURE:
MANE/KEY: MOD RES
LOCATION: (64)
OTHER INFORMATION: Y OF FEATURE:

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Jequence 154, Application US/09923779

Jequence No. US20020076721A1

GENERAL INFORMATION:

Jequence No. US20020076721A1

GENERAL INFORMATION:

APPLICANT: Pyle Ruth A.

APPLICANT: Kalos, Michael D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF PANCREATIC CANCER

FILE REFERENCE: 210121.553

CURRENT FILING DATE: 2001-08-06

NUMBER OF SEQ ID NOS: 155

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 154

LENGTH: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 271;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
COMPUTER: IEB PC compatible
COMPUTER: IEB PC compatible
COMPUTER: DESCRIPTION DATE:
APPLICATION DATE: U-Dec-2001
CLASSIFICATION AUMBER: U5/10/021,368
FILING DATE: 12-Dec-2001
CLASSIFICATION AUMBER: 09/201,038
FILING DATE: CURKNOWN>
PRIOR APPLICATION NUMBER: 09/201,038
APPLICATION NUMBER: 09/201,038
FILING DATE: CURKNATION:
APPLICATION NUMBER: 01/201
REGISTRATION NUMBER: 00398/100002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBRANCE: 017/542-8906
TELEBRANCE: 0005540
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71.1%; Score 823.5; DB 12; Length
Best Local Similarity 63.4%; Pred. No. 7.7e-74;
Matches 168; Conservative 16; Mismatches 38; Indels
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-021-368-10
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STRANDEDNESS: not relevant
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SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
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Sequence 10, Application US/10021368
Batent No. US20020106367A1
GENERAL INFORMATION:
APPLICANT: Band, Vimla
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
    NAME/KEY: MOD_RES
LOCATION: (71)
OTHER INFORMATION: I or unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                  NAME/KEY: MOD RES
LOCATION: (136)
OTHER INFORMATION: V or C
                                                                                                                                                                                                                                                                                                                                                                                                                                      C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: MOD_RES
LOCATION: (212)
OTHER INFORMATION: M, V
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LOCATION: (224)
CTHER INFORMATION: N or
US-10-036-371-8
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                                                                                                                                                                                                                                                             LOCATION: (129)
OTHER INFORMATION: A OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ION: (204)
INFORMATION: H
                                                                                                                                                                             LOCATION: (92)
OTHER INFORMATION: K
                                                                              NAME/KEY: MOD RES
LOCATION: (82)
OTHER INFORMATION: N
                                                                                                                                                                                                                                                                                                                                                                  Olher
FEATURE:
NAME/KEY: MOD RES
                                                                                                                               PEATURE:
NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                          NAME/KEY: MOD_RES
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US-10-021-368-10
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84 NMMTRYARINVLEGNEQFVDSAKIIRHPNYNSWTLDNDIMLIKLASPVTLMMTRYARNAR 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 GPGMITQSMFCAGYLEGGKDSCQGDSGGPVVCNGVLQGVGVVSWGY-----GCAERDX 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IVGGY------ECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEH 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 IVGGYMATRYARTCRESSVPYQVSLNAGYHFCGGSLINDQWVVSAAHCYKYRIQVRLGEH 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 H-----IRVNEGTEQXISSSVXRHPNYSSYNIXNDIMLIKLTXPATL-----NQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 VASVPLPSSCAPAGTQCLISGWGNTLSNGVNNPDLLQCVDAPVLPQAMMTRYARDCEASY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 281;
                                                                                                                  DNA, AND RELATED
                                                                                                                                                                                                                                                                        COMPURRY: USA

ZIP: 02110-2804

ZIP: 02110-2804

COMPUTER READABLE FORM:

WONDIN TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/021,368
FILING DATE: 12-Dec-2001

CLASSIFICATION: CURROWN-
PRIOR APPLICATION: CURROWN-
APPLICATION NUMBER: 09/201,038
FILING DATE: CURROWN-
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162

REFERENCE DOCKET NUMBER: 30,162

REFERENCE DOCKET NUMBER: 30,162

TELECHOWEN: 617/642-6070

TELEPHONE: 617/642-6070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%; Score 661.5; DB 1
52.9%; Pred. No. 7.2e-58;
tive 27; Mismatches 56
                                                                       APLICANT: Band, Vimla
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DN
MOLECULES AND METHODS
                                                                                                                                                 NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                     ; Sequence 7, Application US/10021368
; Patent No. US20020106367A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-021-368-8 Sequence 8, Application US/10021368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 PGVYAKVXVLSGWVRDTMA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| || || || || || || || || || || PGVYTKVCNYVDWIQNTIA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
US-10-021-368-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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APPLICANT: Alkawa, Selichi
APPLICANT: Alkawa, Selichi
APPLICANT: Matsuzawa, Funiko
ITILE OF INVENTION: Method and Apparatus for Extracting and Evaluating Mutually Simil
ITILE OF INVENTION: Structures of Molecules
FILE REFERENCE: 522.1921D2
CURRENT APPLICATION NUMBER: US/09/910,071
CURRENT FILING DATE: 2001-07-23
                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3,
                                                                                                                                                                                                                                       61 TEQXISSSSVARHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
                                                                                                                                                                                                                                                                   WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                   1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
                                                                                                                                                                                              24 IVGGYICEENSVPYQVSLNSGYHFCGGSLISEQWVVSAGHCYKSRIQVRLGEHNIEVLEG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 WGNTMSS-VXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 ;
                                                                  61.3%; Score 710; DB 10; Length 247; Conservative 31; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.6%; Score 702; DB 10; Length 223; 60.3%; Pred. No. 5.7e-62; 1ve 29; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                             203 PVVSNGELQ--GIVSWGYGCAQKNRPGVYTKVYNYVDWIKDTIA 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: amino acid sequence of trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION UNMBER: US 08/014,867
PRIOR FILING DATE: 1993-02-08
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/09910071
Patent No. US20020116146A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 60.39
Matches 135; Conservative
  ; ORGANISM: Homo sapiens
US-09-923-779-154
                                                                                     Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 223
TYPE: PRT
ORGANISM: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-910-071-14
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                                                                  Query Match
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TELEPHONE: 617/542-50
TELEFAX: 617/542-8906
                                                          NUMBER OF SEQUENCES: 11
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Matches 121; Conservative
                                                                                                                           CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 QYVHAVALPTECAADATMCTVSGWGNTMSSVXD-GDKLQXLXLPILSHA-----DCA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 H-----IRVNEGTEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATL-----N 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IVGGYECTXH-----SOAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEH 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 299;
                                                                 DNA, AND RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56; Indels
                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION UMBER: US/10/021,368
FILING DATE: 12-Dec-2001
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: 09/201,038
FILING DATE: «UNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/100002
TELECHANING INFORMATION:
TELEPHONE: 617/542-6970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
53.5%; Score 619.5; DB 1
Best Local Similarity 50.2%; Pred. No. 1.1e-53;
Matches 132; Conservative 32; Mismatches 56
Patent No. US20020106367A1
GENERAL INFORMATION:
APPLICANT: Band, Vimla
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DN
MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: INC RELEVANT

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-021-368-8
                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 WKNRPGVYTKVYNYVDWIKDTIA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 ERDXPGVYAKVXVLSGWVRDTWA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
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US-10-021-368-9
, Sequence 9, Application US/10021368
, Patent No. US20020106367A1
, GENERAL INFORMATION:

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145 NSKVSTIPLÞQYCPTAGTECLVSGWGVLKFGFESPSVLQCLDAPVLSDSRNTRYPVBVCH 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IVGGYB------CTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 İVĞGYRNTRYPVBTCQEHSVPYQVSLNAĞSHICĞGSLİTDQMVLSAAHCYHPQLQVRLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12; Length 286;
APELICANT: Band, Vimla
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
MOLECULES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 NQYVHAVALPTECAADATMCTVSGWGNTMSSVXDGDKLQXLXLPILSHAD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.5%; Score 549.5; DB 12; Length
46.0%; Pred. No. 7.8e-47;
tive 22; Mismatches 77; Indels
                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 0210-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/021,368
FILING DATE: 12-Dec-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/201,038
PLING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/100002
TELECOMMUNICATION:
                                                                                                                             Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: Linear MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-10-021-368-9
                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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US-09-808-615-90
US-09-808-615-90
Patent No. US20020064856A1
GENERAL INFORMATION
APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHYTE, DAVID
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APPLICAT....
PILING DATE: 1997-10-2>
APPLICATION NUMBER: 60/063735
R FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063738
OR APPLICATION NUMBER: 60/063738
                                                   PRIOR FILING DATE: 1997-09-17
PRIOR PELICATION NUMBER: 60/05912
PRIOR PELICATION NUMBER: 60/05912
PRIOR PELICATION NUMBER: 60/05926
PRIOR PELICATION NUMBER: 60/05926
PRIOR PELICATION NUMBER: 60/05926
PRIOR PELICATION NUMBER: 60/05926
PRIOR PELICATION NUMBER: 60/05926
PRIOR PELICATION NUMBER: 60/05926
PRIOR PELICATION NUMBER: 60/05226
PRIOR PELICATION NUMBER: 60/05236
PRIOR PELICATION NUMBER: 60/05314
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PRIOR PELI
                                                           FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059122
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APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 GAESCEGDSGGPLVCGGILQ--GIVSWGDVPCDNTTKPGVYTKVCHYLEWIRETM 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.7%; Score 494; DB 10; Length 320;
44.7%; Pred. No. 2.6e-41;
Live 27; Mismatches 87; Indels 16;
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: MANNING, GERARD
THE CAFTER OF INVENTION: NOVEL PROTEASES
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/13.
CURRENT APPLICATION NUMBER: US/9/88,615
CURRENT FILING DATE: 2001.06-26
PRIOR FILING DATE: 2000.06-26
PRIOR FILING DATE: 2000.06-26
SOFTWARE: PATENTIN VUMBER: 10.05
SOFTWARE: PATENTIN VOICE: 15.0
SOFTWARE: PATENTIN VOICE: 1.0
SEQ ID NO 90
TYPE: RAT
CORGANISM: HOMO SADIENS
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CURRENT FILING DATE: 2011-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/05974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PLING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 506, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
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Wood, William
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Matches 105; Conservative
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Filvaroff, Ellen
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TITLE OF INVENTION:
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1G17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTEQXISSSSVXRHPNYS----SYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATM 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 CTVSCWGNTMS-SVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IVGGYECTXHSQAHQVSL-NSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 IIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHCLKPRYIVHLGGHNLQKEE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 GDSGGPVVCNGVLQGVGVVSWGYG-CAERDXPGVYAKVXVLSGWVRDTM 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.9%; Score 451; DB 9;
41.0%; Pred. No. 3.3e-37;
tive 38; Mismatches 87
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR PEDITORION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-29
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090459
PRIOR APPLICATION NUMBER: 60/090459
PRIOR APPLICATION NUMBER: 60/090459
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR APPLICATION NUMBER: 60/091360
PRIOR APPLICATION NUMBER: 60/091360
PRIOR PILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-121-049-506
Sequence 506, Application US/10121049
Publication No. US20030022239A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stewart, Timothy A
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Goddard, Audrey
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Watanabe, Colin K
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Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
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Best Local Similarity 41.0
Matches 94; Conservative
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND THE SAME
FILE REPERBACE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
SEQ ID NOS: 550
                                                           116 CTVSGWGNTMS-SVXDGDKLQXLXLPILSHADCANSYGPGMITOSMFCAGYLEGGKDSCQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 GTEQXISSSSVXRHPNYS----SYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATM 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 CTVSGWGNTMS-SVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQ 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IVGGYECTXHSQAHQVSL-NSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNE 59
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                                                                                                            GDSGGPVVCNGVLQGVGVVSWGYG-CAERDXPGVYAKVXVLSGWVRDTM 222
                                                                                                                                    38.9%; Score 451; DB 9; Length 250; ilarity 41.0%; Pred. No. 3.3e-37; Conservative 38; Mismatches 87; Indels
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VS-10-175-746-506
Sequence 506, Application US/10175746
Publication No. US20030027270A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
                                                                                                                                                                                                                                                 Sequence 506, Application US/10140470
Publication No. US20030022331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Gerritsen,Mary E.
Goddard,Audrey
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Beresini, Maureen
DeForge, Laura
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Wood, William
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Filvaroff, Ellen
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) ORGANISM: Homo Sapien
US-10-140-470-506
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US-10-140-470-506
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C3
CURRENT TAPLICATION NUMBER: US/10/123,904
CURRENT TAILNED AFFE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
                                                                                                                                                                                                                                                                                                      82 GCEQTRIATESPHPGFNNSLPNKDHRNDIMLVRVAASPVSITWAVRPLTLSSRCVTAGIS 141
                                                                                                                                                                                                                                                                                                                                                   116 CTVSGWGNTMS-SVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQ 174
                                                                                                                                                                                                                                                                                                                                                                                 142 CLISGWGSTSSPQLRLPHTLRCANITIIEHQRCENAY-PGNITDIWVCASVQEGGKDSCQ 200
                                                                                                                                                                  Gaps
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                                                                                                                                                                  10;
                                                                                                                           Length 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 GDSGGPLVCNQSLQ--GIISWGQDPCAITRKPGVYTKVCKYVDWIQETM 247
                                                                                                                                                                87; Indels
                                                                                                                   38.9%; Score 451; DB 9;
41.0%; Pred. No. 3.3e-37;
tive 38; Mismatches 87
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Publication No. US20030022328A1
GENERAL INFORMATION:
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
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Stewart, Timothy A.
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Wood, William
                                                                                                                                  Best Local Similarity 41.09
Matches 94; Conservative
                                                         ; ORGANISM: Homo Sapien
US-10-121-049-506
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; ORGANISM: Homo Sapien
US-10-123-904-506
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LENGTH: 250
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APPLICANT:
APPLICANT:
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C288
CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT PILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
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41.0%; Pred. No. 3.3e-37;
tive 38; Mismatches 87; Indels
           CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO SG ED
LENGTH: 250
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Watanabe, Colin K
Wood, William
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Best Local Similarity 41.0%
Matches 94; Conservative
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Goddard, Audrey
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Filvaroff, Ellen
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Best Local Similarity 41.0%
Matches 94; Conservative
FILE REFERENCE: P3330R1C382
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CORGANISM: Homo Sapien
US-10-176-921-506
                                                                                                                                                TYPE: PRT
CORGANISM: Homo Sapien
US-10-176-918-506
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APPLICANT: Wood, William
APPLICANT: Zhang, Zemer
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                     APPLICANT: Zhang, Zemin TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACLOS ENCODING THE SAME FILE REFERENCE: P3330R1C353 CURRENT APPLICATION NUMBER: US/10/175,746 CURRENT FILING DATE: 2002-06-19 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
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38.9%; Score 451; DB 9; Length 250;
Best Local Similarity 41.0%; Pred. No. 3.3e-37;
Matches 94; Conservative 38; Mismatches 87; Indels
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Publication No. US20030027275A1
GENERAL INFORMATION:
APPLICANT: Baker, Keyin P.
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Gurney, Austin L.
Sherwood, Steven
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Stewart, Timothy A.
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Wood, William
                            Desnoyers, Luc
Filvaroff, Ellen
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                                                                           Gao, Wei-Qiang
             DeForge, Laura
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ORGANISM: Homo Sapien
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US-10-176-918-506
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LENGTH: 250
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Search completed: February 12, 2003, 10:31:08 Job time: 35.2537 secs

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Q9w65 dissostichu
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017086 anopheles s
09v1f5 drosophila
09cv76 mus musculu
09qyn3 mus musculu
09dqn3 mus musculu
09ddel brachydanio
063275 rattus norv
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091036.
01.NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 21, Last sequence update)
01.JUN-2002 (TrEMBLrel. 21, Last sequence update)
01.JUN-2002 (TrEMBLrel. 21, Last annotation update)
Trypsinogen I (Fragment).
Gadus morhua (Atlantic cod)
Gadus morhua (Aclantic cod)
Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ONG T.L., Armstrong R.F., McNamara P., Buckley L.J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.5%; Score 932.5; DB 13; Length 219; Best Local Similarity 87.6%; Pred. No. 1.1e-90; Matches 176; Conservative 5; Mismatches 17; Indels 3;
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HSSP; P00763; 1DPO.
MEROPS; 301.125; 301.125; 301.125; 301.125; InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pram; PR00089; trypsin; 1.
PRINTS; R00020; trypsin; 1.
PROSITE; PS50240; TRYPSIN DM; 1.
PROSITE; PS00134; TRYPSIN DM; 1.
PROSITE; PS00135; TRYPSIN DM; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                      Q9QCPN7
Q9W6K0
Q9W6K0
Q9W6C3
Q9Z046
Q9Z046
Q9KRQ0
Q6KRQ0
Q6KRQ0
Q6Z7761
Q9RR47
Q9RR47
Q9RR47
Q9RR47
Q9RR47
Q9RR47
Q9RR47
Q9RY18
Q9CV76
Q9CV76
Q9CV76
   Q9Z1R9
Q9CPN9
Q9D7Y7
     [1]
SEQUENCE FROM N.A.
 $\text{0.000} \text{0.000} \tex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8049;
729
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659.5
640
581.5
563.5
560.5
548.5
498
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467.5
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438.5
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à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91036 gadds morhu
Q94727 paralichthy
O93266 pseudopleur
Q91515 fugu rubrip
Q92099 paranocothe
Q94766 paralichthy
Q98th0 engraulis j
Q98tg9 engraulis j
Q86tg9 engraulis j
Q86tg9 engraulis j
Q81259 petromyzon
Q42168 petromyzon
Q42168 petromyzon
Q42168 mus musculu
Q90tk9 mus musculu
Q90tb9 mus musculu
                                                                                                         February 12, 2003, 10:16:06; Search time 159.179 Seconds (without alignments) 291.248 Million cell updates/sec
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                                                                                                                                                                                                    1158
1 IVGGYECTXHSQAHQVSLNS......GVYAKVXVLSGWVRDTMAXY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
     GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                              671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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0987Q7
093266
091215
092099
098TG9
098TG9
042159
042159
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Q9R0T7
093594
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sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
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sp_virus:*
sp_vertebrate:*
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Gapop 10.0 , Gapext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_rvirus:*
sp_bacteriap:*
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1: sp_archea:*
2: sp_bacteria:*
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Maximum DB seq length: 2000000000
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sp_human:*
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Match Length
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898.7
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740.5
737.5
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121 WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 TEGFVSSSRVIRHPNYDSWNIDNDIMLIKLSKPATLNQYVKTVALPSSCAPAGTMCKVSG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trypsinogen (Fragment).
Rogu rubitpes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Precomorpha; Pleuronectiformes; Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 IVGGYECTPHSQAHQVSLNSGYHFCGGSLVNSNWVVSAAHCYKSRVEVRMGEHKIRVNEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Mar. Biotechnol. 0:0-0(1998).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS TRYPSIN FAMILY.
                                                                                                                                                                         Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. TISSUE AND PANCREAS; TISSUE=INTESTINE, PYLORIC CAECA, AND PANCREAS; Douglas S.E., Gallant J.W.; Isolation of conset for Trypsinogen from the Winter Plounder, Pleuronectes americanus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.6%; Score 910.5; DB 13; Length
75.6%; Pred. No. 2.7e-88;
ive 15; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 VICHGELQ--GVVSWGYGCAERGNPGVYAKVCLFNDWLESTWASY 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08D2A834FB289080 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Trypsinogen (Fragment).
                                                                                ol-wowlays (TrEMBLrel. 08, Last agguence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Trypsinogen 2 precursor (EC 3.4.21.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; DR001254; Ser protease_Try.
InterPro; IPR001254; Ser protease_Try.
Pfam; PR00089; trypain; I.
SMART; SM00020; Trypain; I.
PR0SITE; PS50240; TRYPSIN, DOM; I.
PR0SITE; PS00134; TRYPSIN, DOM; I.
PROSITE; PS00135; TRYPSIN, ER; III, WIQUOMN_I.
Hydrolase; Serine protease; Signamin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRYPSINGEN 2.
                                   242 AA
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                                                                            Created)
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                                      PRT;
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HSSP; P00763; 1DPO.
MEROPS; S01.125; -.
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Best Local Similarity 75.64
Matches 170; Conservative
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                                   093266 PRELIMINARY;
093266,
01-NOV-1998 (TEMBLrel. 0
01-NOV-1998 (TEMBLrel. 0
01-JUN-2002 (TEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242
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                                                                                                                                                                                                        americanus)
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Q91515;
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RESULT
093266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 IVGGYECTPYSQPHQVSLANSGYHFCGGSLVNENWVVSAAHCYKSRVEVRMGEHHIKINEG 80
                                                                                      1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
                                                               TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=PANCREAS;
Suzuki T., Srivastava A.S., Kurokawa T.;
"Japanese flounder mRNA for trypsinogen 1.";
"Japanese flounder mRNA for trypsinogen 1.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
EMBL; AB022975; BAA82362.1; -.
HSSP; P00763; 1DPO.
140 WGNIMSSVADGDKLQCLNLFILSHADCSNSY-PGMITQSMPCAGYLEGGKDSCQGDSGGP
                                                                                                                                             WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.1%; Score 915.5; DB 13; Lengum
76.4%; Pred. No. 7.9e-89;
U. mmatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEANCE'S SOLICES, SOLICES, Chymotrypain.
InterPro; IPR001254; Ser protease_Try.
Pfam; PF00089; trypain; 1.
PRINTS, PR00722; CHYMOTRYPSIN.
SMART; SM00320; TRYPSIN.
PROSITE; PS00130; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Serine protease.
SEQUENCE 242 AA; 26548 MW; 6DA722C80BC194AZ CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVCNGELQ--GVVSWGYGCAERDHPGVYARVCIFIDWLETTMASY 242
                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trypsinogen 1.
Paralichthys olivaceus (Flounder).
                                                                                                                                                                                                                                                         199 VVCNGVLQ--GVVSWGYGCAE 217
                                                                                                                                                                                                                               181 VVCNGVLQGVGVVSWGYGCAE 201
                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity .....
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01.125;
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RESULT 2

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Gaps

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DB 13; Length 242;

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61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                               1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
                                                                                                                                                                                                                                                                                            21 IVGGKECSPYSQPHQVSLNSGYHFCGGSLVNENWVVSAAHCYKSRVEVRMGEHHIRVTEG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9W706 PRELIMINARY; PRT; 238 AA.

Q9W706;

Q9W706;

Q1.NOV-1999 (TREMBLrel. 12, Created)

O1-NOV-2099 (TREMBLrel. 12, Last sequence update)

O1-UNV-2002 (TREMBLrel. 21, Last annotation update)

Trypsinogen 2 (Fragment).

Paralichthys olivaceus (Flounder).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Actinopervygii, Neopterygii, Teleostei; Euteleostei; Paralichthys, Acanthoprerygii, Percomorpha; Pleuronectiformes; Pleuronectoidei; Paralichthyidae; Paralichthys.

NCBL_TAXID=8255;
                                                                                                                                                                                                                                                                                                                                                     81 KEQFISSSRVIRHPNYSSYNIDNDIMLIKLSKPATLNQYVQAVALPSSCAPACTMCTVSG
                                                                                                                                                                                                                                                                                                                                                                                                  121 WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=PANCREAS;
Suzuki T., Striastava A.S., Kurokawa T.;
Suzuki T., Striastava A.S., Kurokawa T.;
"Japanese flounder mRNA for trypsinogen 2.";
Submitted (JUL-1999) to the EMBL/Genbank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY $1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                         3,
                                                                                                                                                                                                      DB 13; Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4,
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                                                                                                                                                                                                                                       37; Indels
                                                                                                                                                  SIGNAL 1 13 POTENTIAL.
SEQUENCE 242 AA; 26201 MW; 3F4DE7CE80C4477C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 VVCNGELQ--GVVSWGYGCAERDHPGVYAKVCLFNDWLETSMANY 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 AA; 26071 MW; F2B8908085B8D062 CRC64;
                                                                                                                                                                                               77.5%; Score 897.5; DB 1
75.1%; Pred. No. 6.4e-87;
         InterPro; IPR001254; Ser_protease_Try.
PFan; PF00109; trypsin; IPRNTS; PR00722; CHWOTRYPSIN.
SMART; SM0020; Tryp.SPC; 1.
PR0SITE; PS50240; TRYPSIN DOM; I.
PROSITE; PS00134; TRYPSIN "HIS; UNKNOWN."
PROSITE; PS00135; TRYPSIN "SER; 1.
HYDROLAGE; Serine protease; Signal.
                                                                                                                                                                                                              Best Local Similarity 75.1%; Pred. No. 6.4e-
Matches 169; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS, SOI.125; --
InterPro; IPRO01314; Chymotrypsin.
InterPro; IPRO01254; Ser_protease_Try.
Pfam; PP00089; trypsin, 1.
PRNYS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp SPC; 1.
PROSITE; PS00124; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRYPSIN FAMILY.
EMBL; AB029751; BAA82363.1; -.
HSSP; P00763; 1DPO.
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Matches 169; Conservative
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                                                                                                                                                                                                   Query Match
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=PYLORIC CAECA;
MEDLINE=97104330; PubMed=8948488;
Genicot S., Rentier-Delrue F., Edwards D., Van Beeumen J., Gerday C.;
"Trypsin and trypsinogen from an antarctic fish: molecular basis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Gaps
                                                                                Wang K., Gan L., Lee I., Roach J., Hood L.,
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last annotation update)
101-UIN-2002 (TrEMBLrel. 21, Last annotation update)
11-VIPP in precursor (EC 3.4.21.4).
Parantochemia magellanica (Maori cod).
Bukaryota, Metazoa: Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Bueleostei, Meochemiorpia, Acanthopopterygii, Teleostei, Percomorpha, Perciformes, Notothemidae; Paranotothemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochim. Biophys. Acta 1298:45-57(1996).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                   237 AA; 25726 MW; 30D2DBAAC39080C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVCNNELQ--GVVSWGYGCAERDHPGVYAKVCLFNDWLESTWASY 237
                                                                                                                                                                                                                                                                                                                                                                                                      77.6%; Score 898.5; DB 1
76.0%; Pred. No. 4.9e-87;
                                                                                                                                          EMBL; U35747; AAAT501.1; --
HSSP; P35031; 181T.
MEROPS; S011.25; --
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Ser_protease_Try.
PRAM; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Trypsin; IPR0SITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN JOM; 1.
HWAT0lase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 AA.
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HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 76.08
Matches 171; Conservative
                  Tetraodontidae, Takifugu.
NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                     TRYPSIN FAMILY.
                                                                 SEQUENCE FROM N.A.
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Trypsinogen II.
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Q8QGW3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 IVGGYECQAHSQPHTVSLANSGYHFCGGSLVNENWVVSAAHCYKSRVEVERLGEHHIGQNEN 79
                                       TEGXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Trypainogen.

Trypainogen.

Buggraulis Japonicus (Japanese anchovy).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii, Neopterygii; Teleostei; Clupeomorpha; Engraulidae;

Engraulis.
                                                                                                                                                                                                                                                                                                                      78 TEQFISSSRVIRHENYSSYNINNDIMLIKLSEPATLNQYVQPVALPTSCAPAGTMCTVSG
                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 240;
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Interpro: IRR001314; Chymotrypain.
Interpro: IRR001314; Chymotrypain.
Interpro: IRR001314; Chymotrypain.
Interpro: IRR00139; Lrypain. 1.
PRINTS, PR00032; CHYMOTRYPSIN.
SWART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN ER; 1.
PHYDROJER; PS00135; TRYPSIN SR; 1.
Hydrolase; Scrine processe.
SEQUENCE 240 AA; 26026 MW; 299BI19BFF071464 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.5%; Score 886; DB 13; Length 2. Best Local Similarity 74.9%; Pred. No. 1e-85; Matches 167; Conservative 14; Mismatches 38; Indels
                                                                                                                        181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225
                                                                                                                                    196 VVCNGQLQ--GVVSWGYGCAQRDHPGVYAKVCIFIDWLERTMSSY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVCNGVLOGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
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                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                240 AA
                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=42892;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Anguilliformes, Anguillidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                         Engraulis japonicus (Japanese anchovy).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Engraulidae;
Engraulis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUS=PYLORIC CAECA;
Watabe S., Ahsan M.N., Funabara D.;
Watabe S., Ahsan M.N., Funabara D.;
"Anchovy trypsinogen mRNA.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL; AB041930; BA840330.1; -.
HSSP; PO0763; IDPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 VVCNGELQ--GIVSWGYGCAERDHPGVYAKVCLFNDWIDSTMAQY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225
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76.2%; Score 882; DB 13;
Best Local Similarity 73.8%; Pred. No. 2.8e-85;
Matches 166; Conservative 15; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; Enroresse_Try.
PRINTS; PR00072; CHYMOTRYPSIN.
SWART; SW00020; Tryp. SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
Hydrolase; Serine protease.
SEQUENCE 241 AA; 26282 WW; FE362D39CAEEI
             241
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
Trypsinogen (EC 3.4.21.4).
Q98TG9 PRELIMINARY;
Q98TG9;
01-JUN-2001 (TEMBLEEL 17,
01-JUN-2002 (TEMBLEEL 17,
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=42892;
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59 EGTEGXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTV 118
 59 EGTEOXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTV 118
 SGWGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSG 178
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLR--VRLGEHHIRVN 58
 24 IVGGSECAAHSQPWQVSLNIGYHFCGGSLINSQWVVSAAHCYQTASRISVRIGEHNIFVN 83
 21 IVGGYECAAHSQPWQVSLNIGYHFCGGSLISSEWVVSAAHCYQTASRISVRIGEHNIFVT
 119 SGWGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSG
 81 EGTEQRIQASKAIRHPQYSSATIDNDIMLIKLSSPATLNQYAQAVPLPSSCVGTGVMCTI
 Petromyzon marinus (Sea lamprey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
Petromyzontiformes, Petromyzontidae, Petromyzon.
 Roach J.C.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
TRYPSIN FAMILY.
 63.7%; Score 737.5; DB 13; Length 247; llarity 62.2%; Pred. No. 5.6e-70; Conservative 21; Mismatches 59; Indels 5;
 Roach J.C.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 179 GPVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 BECBD3069A071DCB CRC64;
 Last sequence update)
Last annotation update)
 247 AA
 PEAM, PF00089, trypein; I.
PRINTS: PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN_SER; 1.
 TRYPSIN A3
 POTENTIAL.
 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser protease Try.
Pfam; PF00089; trypsin; I
 Created)
 PRT;
 Hydrolase; Serine protease; Signal.
 EMBL; AF011899; AAB69655.1; -. EMBL; AF011352; AAB65411.1; -. HSSP; P00763; 1DPO.
 26295 MW;
 3 (TrEMBLrel. 05, C
3 (TrEMBLrel. 05, L
2 (TrEMBLrel. 21, L
 SEQUENCE FROM N.A.
TISSUE=ANTERIOR INTESTINE;
 Trypsinogen A3 precursor.
TRYPA3.
 PRELIMINARY;
 247 AA;
 SEQUENCE FROM N.A.
 Local Similarity
 NCBI_TaxID=7757;
 MEROPS; S01.128;
 01-JAN-1998
 01-JAN-1998
01-JUN-2002
 Matches 140;
 SEQUENCE
 Query Match
 042608;
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 119
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 119 SGWGNTWSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSG 178
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141 TGMGNITMANPAVSGDKLQCLEIPILSSSDCSNSY-PGMITSTMFCAGYLEGGKDSCQGDSG 199
 Kurokawa T., Suzuki T., Ohta H., Kagawa H., Tanaka H., Unuma T.;
"Expression of pancreatic enzyme genes during the early larval stage of Japanese eel, Angulla japonica.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ABO70720; BAB85634.1;
Hydrolase.
SEQUENCE 244 AA; 26317 MW; OEB3B68B9706D52D CRC64;
 Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSV--LRVRLGEHHIRVN 58
 21 IVGGYECEPHS@PWQASLNAGYHFCGGSLVNENWVVSAAHCYKSPSRLEVRLGEHHIGLN 80
 5; Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLR--VRLGEHHIRVN 58
 59 EGTEQXISSSSVKRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTV
 "The Molecular Evolution of the Vertebrate Trypsinogens.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN TAY.
EMBL; APOI1900; AB869656.1; -.
 Trypsingen Bl precursor (Fragment).

Trypsingen Bl precursor (Fragment).

Petromycon marinus (Sea lamprey).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

Petromyzontiformes; Petromyzontidae; Petromyzon.
 ,
2
 72.9%; Score 844.5; DB 13; Length 244; llarity 70.7%; Pred. No. 2.6e-81; Conservative 21; Mismatches 40; Indels 5;
 Ouery Match 63.9%; Score 740.5; DB 13; Length 244; Best Local Similarity 63.1%; Pred. No. 2.7e-70; Matches 142; Conservative 17; Mismatches 61; Indels 5;
 223
 200 GPVVCNGELQ--GVVSWGYGCAEQNHPGVYPKVCMFSDWLRTTMA 242
 25903 MW; C4582EE07E3B8007 CRC64;
 179 GPVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA
 Last sequence update)
Last annotation update)
 244 A.A.
 InterPro; IPRO01314; Chymotrypsin.
InterPro; IPRO01254; Ser_protease_Try.
Pfam; PP00089; trypsin; I
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00020; Tryp SPC; I.
PROSITE; PS50240; TRYPSIN DOM; I.
PROSITE; PS00134; TRYPSIN HIS; UNGNOWN I.
PHOTOLASE; Serine protease; Signal.
 POTENTIAL
 TRYPSIN
 Created)
 01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2002 (TrEMBLrel. 21,
 PRELIMINARY;
 244
 Similarity
 244 AA;
 SEQUENCE FROM N.A. Roach J.C.;
 NCBI_TaxID=7757;
 MEROPS; S01.128;
TISSUE=PANCREAS;
 Matches 159;
 Query Match
 SEQUENCE
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Gaps

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179 GPVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223

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TISSUE=TESTIS
 SEQUENCE
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 EGTEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTV 118
 SGWGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSG 178
 Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLR--VRLGEHHIRVN 58
 22 IVGGYECAAHSQPWQVSLANIGYHFCGGSLISSSBWVVSAAHCYQTASRISVRIGEHNIFVT 81
 Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 THE
 Petromyzon marinus (Sea lamprey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
Petromyzontiformes, Petromyzontidae, Petromyzon.
 ŝ
 63.6%; Score 736.5; DB 13; Length 245; 62.2%; Pred. No. 7.1e-70; ive 19; Mismatches 61; Indels 5;
 Roach J.C.;
"The Molecular Evolution of the Vertebrate Trypsinogens.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS TRYPSIN FAMILY.
EMBL; APO11901; AAB69657.1; -.
HSSP; P00763; 1DPO.
 201 GPVVCNGQLQ--GIVSWGRGCALPNYPGVYTKVCNYNSWIASTMA 243
 POTENTIAL.
TRYPSIN B2.
9A932508BB96C93B CRC64;
 179 GPVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 203 GPVVCNGELQ--GIVSWGRGCALPNYPGVYTKVCNYNAMIAQTIA 245
 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 Created)
Last sequence update)
Last annotation update)
 InterPro; JPR001314; Chymotrypain.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp SPc; 1.
PROSITE; PS00134; TRYPSIN_DM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_I.
Hydrolase; Serine protease; Signal.
NON TER 1
SIGNAL 13 POTENTIAL.
 247 AA
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 245
 PRT;
 Trypsinogen b2 precursor (Fragment) TRYPB2.
 PRT;
 26001 MW;
 (TrEMBLrel. 05, C
(TrEMBLrel. 05, L
(TrEMBLrel. 21, L
 Trypsinogen a2 precursor. TRYPA2.
 Matches 140; Conservative
 PRELIMINARY;
 PRELIMINARY;
 245
 245 AA;
 MEROPS; S01.128; -.
 Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=7757;
 01-JUN-2002
 01-JAN-1998
01-JUN-2002
 01-JAN-1998
 SEQUENCE
 Query Match
 042158;
 042158
 042160;
 042160
 53
 119
 RESULT 12
042160
 RESULT 13
 042158
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EGTEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTV 118
 178
 143
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVSAAHCYKSVLR--VRLGEHHIRVN 58
 24 IVGGSECAAHSQPWQVSLNIGYHFCGGSLINSQWVVSAAHCYQTASRIGSRIGEHNIFVN 83
 Gaps
 Also be a soluted in the accordance of the accordance of manual solutions of the accordance of manualian sperm and is released during acrosome reaction."; A homologue of pancreatic trypsin is localized in the acrosome of mammalian sperm and is released during acrosome reaction."; J. Blol. Chem. 274:29426-29432(1999).
 SEQUENCE FROM N.A.
STRAIN=CSYBL/60; TISSUE=PANCREAS;
STRAIN=21085560; Pubmed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 SGWGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSG
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Roach J.C.;
"The Molecular Evolution of the Vertebrate Trypsinogens.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
 ŝ
 DB 13; Length 247;
 Query Match
63.6%; Score 736.5; DB 13; Length
Best Local Similarity 61.8%; Pred. No. 7.1e-70;
Matches 139; Conservative 22; Mismatches 59; Indels
 203 GPVVCNGELQ--GIVSWGRGCALPNYPGVYTKVCNYNAWIAQTIA 245
 26309 MW; AD73E88531970324 CRC64;
 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
TESP4 (0910001819RIK protein) (Trypsinogen 9).
TC OR 0910001819RIK OR TRYPSINOGEN
 179 GPVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA
Petromyzontiformes; Petromyzontidae; Petromyzon.
NCBI_TaxID=7757;
 246 AA.
 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser protease_Try.
Pfam; PR00099; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN HIS; UNKNOWN_1.
PHOGISE; Serine protease; Signal.
 PŌTENTIAL.
TRYPSIN A2.
 PRT;
 EMBL; AF011898; AAB69654.1; -. HSSP; P00763; 1DPO.
 PRELIMINARY;
 247
 Mus musculus (Mouse)
 247 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 SEQUENCE FROM N.A
 MEROPS; S01.128;
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A Arakwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I., Saito T., Odazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Saito T., Cokazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Radda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann M., Gaasterland T., Gissi C., King B., Kochlwa H., Kachi B., Kochlwa H., Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrim L.M., Staubli F., Suzuki R., Tomta M., Wagner L., Washio T., & Sakrim L. Moffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fojita M., Gariboldi M., Businich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima U., Mazzarelli J., Sakamcto N., Saski H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F., Wynchaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Anachiaki V.
 STRAIN=129SVJ;
MEDLINE=99486155; PubMed=10506205;
Ohmura K., Kohno N., Kobayashi Y., Yamagata K., Sato S.,
Kashiwabara S., Baba T.;
"A homologue of pancreatic trypsin is localized in the acrosome of mammalian sperm is released during acrosome reaction.";
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Chen F., Rowen L., Hood L., Rothenberg E.V.;
"Differential transcriptional regulation of individual TCR Vbeta segments before gene rearrangement.";
J. Immunol. 166:1771-1780(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN PAMILY.
 "Functional annotation of a full-length mouse cDNA collection.";
 4;
 63.5%; Score 735; DB 11; Length 246;
 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-VUN-2002 (TrEMBLrel. 21, Last annotation update)
Pancreatic trypsin (0910001B19RIK protein) (Trypsinogen 8).
TD OR 0910001B19RIK OR TRYPSINOGEN.
 Indels
 26274 MW; B6A9F4C99079633F CRC64;
 55;
 62.1%; Pred. No. 1e-69;
 SEQUENCE FROM N.A. STRAIN-C57BL/6J; TISSUE-STOWACH, AND SPLEEN; MEDLINE-21085660; PUDMed-11217851;
 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001354; Ser_protease_Try.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp SPo; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
 MEDLINE=21103195; PubMed=11160223;
 EMBL, A8017032; BAA44761.1; -...
EMBL; AK008667; BAB25821.1; -...
EMBL; AK003064; BAB22542.1; -...
EMBL; AE000664; AA869056.1; -...
HSSP; PO0763; ISLU.
MEROPS; SOI.057; -...
 MGD; MGI:1913350; 0910001B19Rik
 Hydrolase; Serine protease
 Nature 409:685-690(2001).
 Query Match
Best Local Similarity 62.19
Matches 139; Conservative
 Mus musculus (Mouse).
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 246 AA;
 NCBI_TaxID=10090;
 Hayashizaki Y.
 SEQUENCE
 A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Ahizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ba Saito T., Odsazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., R. Heischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kubhi B., Loshima B., Kochiwa H., Kubi B., Staubi F., Fuzuki R., Panta B., Wagner L., Washio T., Ra Sakai K., Okido T., Furuko M., Aono H., Baldarelli R., Barsh G., Baraki K., Okido T., Fuzuki R., Carini L.M., Bult C., Fletcher C., Pujita M., Gariboldi M.F., Brownstein M.J., Bult C., Fletcher C., Pujita M., Gariboldi M.F., Brownstein M.J., Bult C., Fletcher C., Pujita M., Gariboldi M., Cordone P., Ring B., Kandid M., Rodriguez I., Sakamoto N.H., Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Natharaki Y., Thurna M., Marticker C., Milming L., Martickor J., Kawaji H., Kohtsuki S., Natharaki Y., Thurna M., Martickor J., Kandida K., Hasegawa Y., Kawaji H., Kohtsuki S., Natharaki J., Natharaki S., Natharaki J., Nathara
 <u>ب</u>
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKUTXPATLNQYVHAVALPTECAADATMCTVSG 120
 121 WGNTMS-SVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 24 IVGGYTCRENSIPYQVSLNSGYHFCGGSLINDQWVVSAAHCYKTRIQVRLGEHNINVLEG 83
 Gaps
 Chen F., Rowen L., Hood L., Rothenberg E.V.;
"Differential transcriptional regulation of individual TCR Vbeta
segments before gene rearrangement.";
J. Immunol. 166.1771-1780(2001)
-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN PAMILY: PAMILY
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 63.6%; Score 736; DB 11; Length 246;
 EMBL, AB0070561; BAA8187.1; -...
EMBL, AB017031; BAA74760.1; -...
EMBL, AB0070564; BAA85300.1; -...
EMBL, AB0070644; ABA85030.1; -...
EMBL, AB007664, AB86057.1; -...
EMBL, AB00764, AB86057.1; -...
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EMBL, AB00064, EMBCOST.1; -...
EMBCAPS; S01.059; -...
MCD, MCI.1913350, 0910001B19Rik.
EMCORP. IPRO01314; Chymotrypsin.
EMCORP. IPRO01354; Ser_procease_Try.
EMART: SMO0030; Lrypsin, 1.
EMART: SMO0030; Tryp SPC; 1.
EMART: SSC040; TRYPSIN HIS; UNKNOWN.1.
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EMPCSITE; PSC0135; TRYPSIN HIS; UNKNOWN.1.
 Score '30',
Pred. No. 8e-70;
...-**hes 55; Indels
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 62.1%; Preα.
Five 26; Mismatches
 246 AA.
 01-MAY-2000 (TrEMBLrel. 13, Created)
 MEDLINE = 21103195; PubMed = 11160223;
 Nature 409:685-690(2001).
 Conservative
 PRELIMINARY;
 Best Local Similarity
Matches 139; Conserv
 SEQUENCE FROM N.A.
 STRAIN=129;
 Query Match
 Q9R0T7;
 Q9R0T7
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 Gaps
 1 IVGGY-----ECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGE 52
 10 IVGGYSSTRYPIIECKAYSQPHQVSLNSGYHFCGGSLVNENWVVSAAHCYQSRVEVRLGE 69
 Sequence Seq
 Sequence 1
Sequence 2
Sequence 1
Sequence 1
 Sequence Sequence
 RESULT 1
US-08-467-155A-10
is Sequence 10, Application US/08467155A
is Patent No. 5736377
is GENERAL INFORMATION:
is APPLICANT: Band, Vimla
TITLE OF INVENTION:
is TITLE OF INVENTION:
is TITLE OF INVENTION:
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is TITLE OF INVENTION:
is TITLE OF INVENTION:
is TITLE OF INVENTION:
is CORRESPONDENCE ADDRESS:
is ADDRESSEE: 225 Franklin Street
 Indels 43;
 Query Match 71.1%; Score 823.5; DB 1; Length 271; Best Local Similarity 63.4%; Pred. No. 2.2e-86; Matches 168; Conservative 16; Mismatches 38; Indels 43;
 GITY: bc.
STATE: NA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DoS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CASSTRICATION DATA:
APPLICATION NUMBER: US/08/467,155A
FILING DATE: O6-JUN-1995
CLASSTRICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
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REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
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REFERENCE/DOCKET NUMBER: 30,398/100001
TELEFAK: 617/542-5070
TELEFAK: 617/542-5070
TELEFAK: 617/542-5070
 ALIGNMENTS
 not relevant
 LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
 TOPOLOGY: linear
MOLECULE TYPE: protein
 US-08-467-155A-10
661.5
661.5
661.5
661.5
619.5
619.5
619.5
549.5
549.5
849.5
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1 IVGGYECTXHSQAHQVSLNS.....GVYAKVXVLSGWVRDTMAXY 225
 Sequence 9, At
Sequence 9, At
Sequence 9, At
Sequence 9, At
Sequence 9, At
Sequence 2, At
Sequence 2, At
 Sequence 10,
Sequence 10,
 Sequence 36, Sequence 13, Sequence 5, Pequence 5, Pequence 9, Pequ
 Sequence 10,
Sequence 10,
Sequence 44,
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Sequence 9
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 GenCore version 5.1.3
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US-09-201-033-10
US-09-201-033-10
US-08-94-438-14
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US-09-106-468-9
 Total number of hits satisfying chosen parameters:
 262574 seqs, 29422922 residues
 SUMMARIES
 OM protein - protein search, using sw model
 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Gapop 10.0 , Gapext
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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 Length DB
 BLOSUM62
 Query
Match
 Post-processing:
 Title:
Perfect score:
 Scoring table:
 Score
 Database :
 Sequence:
 Searched:
 Run on:
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NQYVHAVALPTEGAADATMCTVSGWGNTMSSVXDGDKLQXLXLPILSHA-----DGA 148
 10 IVGGYSSTRYPIIECKAYSQPHQVSLNSGYHFCGGSLVNENWVVSAAHCYQSRVEVRLGE 69
 1 IVGGY------ECTXHSQAHQVSLNSGYHXCGGSLINXXWVSAAHCYKSVLRVRLGE
 NSYGPGMITQSMPCAGYLEGGKDSCQGDSGGPVVCNGVLQGVGVVSWGY-----GCA
 Query Match
71.1%; Score 823.5; DB 4; Length 271;
Best Local Similarity 63.4%; Pred. No. 2.2e-86;
Matches 168; Conservative 16; Mismatches 38; Indels 43
 53 HH-----IRVNEGTEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATL-
 DNA, AND RELATED
NOYVHAVALPTECAADATMCTVSGWGNTMSSVXDGDKLQXLXLPILSHA---
 COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALEMETIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,038
 GENERAL INFORMATION:
APPLICANT: Band, Vimla
TITLE OF INVENTION: NES-1 POLYBEPTIDES, DN
TITLE OF INVENTION: NOLECTIES AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
STREET: 225 Franklin Street
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clark Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/100002
TELECOMMUNICATION:
 247 EPGNPGVYAKVCIFNDWLTSTMATY 271
 201 ERDXPGVYAKVXVLSGWVRDTMAXY 225
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/628,198
 US-09-201-038-10; Sequence 10, Application US/09201038; Patent No. 6153387
 not relevant
 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 271 amino acids TYPE: amino acid STRANDEDNESS: not relevant
 617/542-8906
 MOLECULE TYPE: protein US-09-201-038-10
 TOPOLOGY: linear
 Boston
 FILING DATE:
 FILING DATE:
 TELEPHONE:
TELEFAX: 61
TELEX: 2001
 CITY: BOE
STATE: MJ
COUNTRY:
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 53 HH-----IRVNEGTEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATL----- 96
 43; Gaps
 1 IVGGY------ECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGE 52
 97 NOYVHAVALPTECAADATMCTVSGWGNTMSSVXDGDKLQXLXLPLLSHA------DCA 148
 10 IVGGYSSTRYPIIECKAYSQPHQVSLANSGYHFCGCSLVNENWVVSAAHCYQSRVEVKLGE
 Length 271;
 Indels
 GENERAL INFORMATION:

APPLICANT: Band, Vimla
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
TITLE OF INVENTION: NOLECULES AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flah & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
53 HH-----IRVNEGTEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATL
 OPERATION SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,198
PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,155
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T:
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/100002
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/542-5070
TELEFAX: 617/542-5070
 Query Match 71.1%; Score 823.5; DB 2; Best Local Similarity 63.4%; Pred. No. 2.2e-86; Matches 168; Conservative 16; Mismatches 38;
 COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 201 ERDXPGVYAKVXVLSGWVRDTMAXY 225
 247 EPGNPGVYAKVCIFNDWLTSTMATY 271
 Sequence 10, Application US/08628198
Patent No. 5843694
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SEQUENCE CHARACTERISTICS:
LENGTH:
271 amino acids
TYPE:
STRANDEDNES:
TOPOLOGY:
MOLECULE TYPE:
MOLECULE TYPE:
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 US-08-628-198-10
 CITY: BOE
STATE: MA
COUNTRY:
 US-08-628-198-10
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COUNTRY: U.S.A.

ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDLIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATA:
 Query Match 65.2%; Score 755; DB 2; Best Local Similarity 63.8%; Pred. No. 1.4e-78; Matches 143; Conservative 25; Mismatches 52
 APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT
TITLE OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
 NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFENCE/DOCKET NUMBER: B0801/7090
TELECHMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEPHONE: 617-720-4441
 US-08-978-404B-44

Sequence 44, Application US/08978404B
PARTENT NO. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
 247 EPGNPGVYAKVCIFNDWLTSTMATY 271
 FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
 201 ERDXPGVYAKVXVLSGWVRDTMAXY
 MOLECULE TYPE: No. 5968782e
 246 amino acids
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acid
 STRANDEDNESS: single
 amino acid
 linear
 Boston
 US-08-978-404B-44
 TOPOLOGY:
 STATE:
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 7;
130 NTYVQPVALPTSCAPAGTMCTVSGWGNTMSSTADKNKLQCLNIPILSYSSSTRYPIIDGN 189
 246
 97 NOYVHAVALPTECAADATMCTVSGWGNTMSSVXDGDKLQXLXLPILSHA------DCA 148
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 53 HH-----IRVNEGTEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATL----- 96
 149 NSYGPGMITQSMFCAGYLEGGKDSCQGDSGGPVVCNGVLQGVGVVSWGY-----GGA
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 Indels 43;
 DB 5; Length 271;
 Sequence 10, Application PC/TUS9607343
GENERAL INFORMATION:
APPLICANT: New England Medical Center Hospitals, Inc.
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS;
ADDRESSEE: Fish & Richardson P.C.
STEET: 225 Franklin Street
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07343
 Query Match 71.1%; Score 823.5; DB 5; Best Local Similarity 63.4%; Pred, No. 2.2e-86; Matches 168; Conservative 16; Mismatches 38;
 NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/100001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-9906
 247 EPGNPGVYAKVCIFNDWLTSTMATY 271
 201 ERDXPGVYAKVXVLSGWVRDTMAXY 225
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,155
FILING DATE: 06-UDN-1995
 TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
 not relevant
 ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 ATTORNEY/AGENT INFORMATION:
) TOPOLOGY: linear
) MOLECULE TYPE: protein
PCT-US96-07343-10
 CLASSIFICATION:
 Boston
 USA
 RESULT 4
PCT-US96-07343-10
 FILING DATE
 COUNTRY:
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 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 121 WGNTMSS-VXDGDKLQXLXLPILSHADCANSYGPGMITOSMFCAGYLEGGKDSCQGDSGG 179
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 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 84 DEQFINAAKIIKHPNYSSWTLNNDIMLIKLSSPVKLNARVAPVALPSACAPAGTQCLISG
 Length 246;
 Indels
PROTEASE THAT CLEAVES
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
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ATTORNEY/AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 4500
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
 Query Match
Best Local Similarity 60.3%
Matches 135; Conservative
 ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 , MOLECULE TYPE: protein US-08-956-267A-2
 TOPOLOGY:
 180
 RESULT 8
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 APPLICANT: COMPITTS, TRACEY L.
APPLICANT: COLDITTS, TRACEY L.
APPLICANT: COLDITTS, TRACEY L.
APPLICANT: GRANDOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: STUSSEL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWEN NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
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 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSWFCAGYLEGGKDSCQGDSGG 179
 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 1 IVGGYICEENSVPYQVSIANSGYHFCGGSLISEQ#VVSAGHCYKSRIQVRLGEHNIBVLEG 60
 Gaps
 1 IVGGYECTXHSQAHQVSINSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
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 Query Match 61.3%; Score 710; DB 4; Length 224; Best Local Similarity 60.3%; Pred. No. 1.7e-73; Matches 135; Conservative 31; Mismatches 54; Indels
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 STATE: ALL COUNTRY: USA
ZIP: GOO64-300
ZIP: GOO64-300
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIABLE
OPERATING SYSTEM: DOS
SOFTWARE: FRAESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
FILING DATE:
APPLICATION NUMBER: 35,441
REGISTRATION NUMBER: 35,441
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 35,441
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/938-1729
TELEROMONE: 847/938-1623
 ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CIIY: Abbott Park
 Sequence 34, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
 INPORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6232456e
 9,
 NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Lal
STREET: 100 Abbott P
 US-08-944-483-34
RESULT 6
US-08-944-483-34
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Sequence 2, Application US/08956267A

| Sequence 2, Application US/08956267A
| Patent No. 5945328
| GENERAL INFORMATION:
| APPLICANT: WOLDIKE, Helle Fabricius
| APPLICANT: KJELDSEN, Thomas Borglum
| TITLE OF INVENTION: (Trypsinogen)
| TITLE OF INVENTION: (Trypsinogen)
| TITLE OF INVENTION: (Trypsinogen)
| TITLE OF INVENTION: (Trypsinogen)
| TITLE OF INVENTION: (Trypsinogen)
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| TITLE OF INVENTION: (Trypsinogen)
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 121 WGNTWSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMPCAGYLEGGKDSCQGDSGG 179
 61 TEOXISSSVXRHPNYSSYNIXNDIMLIKLTXPATLNOYVHAVALPTECAADATMCTVSG 120
 Gapa
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
 25 IVGGYTCAANSIPYQVSLNSGSHFCGGGLINSQWVVSAAHCYKSRIQVRLGEHNIDVLEG
 Length 247;
 58; Indels
 US-08-766-982-13
US-08-766-982-13
Sequence 13, Application US/08766982
Patent No. 5948892
Patent No. 5948892
Patent No. 5948892
PATENTE OF INVENTION: Analogs of Macrophage Stimulating
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 13
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 204 PVVCNGQLQ--GIVSWGYGCAQRNRPGVYTKVCNYVNWIQQTIA 245
 61.1%; Score 707; DB 2;
60.3%; Pred. No. 4.4e-73;
tive 27; Mismatches 58
 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FREESC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,267A
FILING DATE: 22-OCT-1997
CLASSIFICATION: 435
 4500.204-US
```

us-10-036-371-8.rai

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35,441
 NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
 INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDENESS: single
 TOPOLOGY: linear MOLECULE TYPE: No. 6232456e
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
 TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 COMPUTER READABLE FORM MEDIUM TYPE: Diskett
 US-08-944-483-36
 RESULT 10
US-09-296-219-13
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 APPLICANT: COHEN, MAURICE
APPLICANT: COLPITS, TRACEY L.
APPLICANT: COLPITS, TRACEY L.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
APPLICANT: STROUPE, STEVEN D.
APPLICANT: STROUPE, STEVEN D.
APPLICANT: OF INVENTION: OP THE PROSTATE
TITLE OF INVENTION: OP THE PROSTATE
CORRESPONDENCE ADDRESS:
ADDRESSES: Abbott Laboratories
 ٠<u>.</u>
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 121 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMPCAGYLEGGKDSCQGDSGG 179
 121 WGNTASSGADYPDELQCLDAPVLSQAKCEASY-PGKITSNMFCVGFLEGGKDSCQGDSGG 179
 61 NEQFINAAKIIRHPQYDRKTLNNDIMLIKLSSRAVINARVSTISLPTAPPATGTKCLISG 120
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 1 IVGGYNCEENSVPYQVSLNSGYHFCGGSLINEQWVVSAGHCYKSRIQVRLGEHNIEVLEG 60
 Query Match 60.6%; Score 702; DB 2; Length 224; Best Local Similarity 60.3%; Pred. No. 1.4e-72; Matches 135; Conservative 26; Mismatches 59; Indels
 STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,982
FILING DATE:
CLASSIFICATION: S36
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-441
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
FENTANTH: 224 amino acids
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 ADDRESSE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
 Sequence 36, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
 : Abbott Laboratories
100 Abbott Park Road
 LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
 TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-766-982-13
CORRESPONDENCE ADDRESS:
 CITY: Abbott Park
 COUNTRY: USA
ZIP: 60064-3500
 ADDRESSEE:
 US-08-944-483-36
 STREET:
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61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNOYVHAVALPTECAADATMCTVSG 120
 61 NEQFINAAKIIRHPQYDRKTLNNDIMLIKLSSRAVINARVSTISLPTAPPATGTKCLISG 120
 121 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 4; Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 Query Match 60.6%; Score 702; DB 4; Length 224; Best Local Similarity 60.3%; Pred. No. 1.4e-72; Matches 135; Conservative 26; Mismatches 59; Indels
 Sequence 13, Application US/09296219
Patent No. 6246560
Fatent Nath, Robert C.
FITLE OF INVENTION: Protein
FITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Inc.
FITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Inc.
FITLE California
COUNTRY: USA
COMPUTER: California
MEDIUM TYPE: FIDPPY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/296,219
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 COMPUTER: ITEM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
 6183.US.01
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US-08-278-091-9
 LENGTH: 225
 RESULT 12
US-09-644-600-5
 TYPE: PRT
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 3,
 61 TEOXISSSVXRHPNYSSYNIXNDIMLIKLTXPATLNOYVHAVALPTECAADATMCTVSG 120
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 121 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLBGGKDSCQGDSGG 179
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 2 IVGGYNCEENSVPYQVSLANGGYHFCGGSLINEQMVVSAGHCYKSRIQVRLGEHNIEVLEG 61
 Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 Gaps
 OTHER INFORMATION: Serine protease catalytic domain of trypsin (Try) OTHER INFORMATION: homologous to similar domain in TADG-15
 4
 Length 225;
 Query Match 60.6%; Score 702; DB 4; Length 224; Best Local Similarity 60.3%; Pred. No. 1.46-72; Matches 135; Conservative 26; Mismatches 59; Indels
 60.6%; Score 702; DB 2; Length 22;
60.3%; Pred. No. 1.4e-72;
tive 26; Mismatches 59; Indels
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 180 PVVCNGQLQ--GVVSWGDGCAQKNKPGVYTKVYNYVKWIKNTIA 221
 FILING DATE:
CLASSIPICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-4*
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
 Query Match
Best Local Similarity 60.3*
Matches 135; Conservative
 LENGTH: 224 amino acids
TYPE: amino acid
 TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-296-219-13
 STRANDEDNESS: single
 TYPE: PRT
ORGANISM: Unknown
 US-09-027-337-5
 FEATURE:
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61 TEGXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 121 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 121
 1 IVGGYEÇTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 2 IVGGYNCEENSVPYQVSLNSGYHFCGGSLINEQWVVSAGHCYKSRIQVRLGEHNIEVLEG 61
 APPLICANT: LOOSMONE, Sheena M
APPLICANT: LOOSMONE, Sheena M
APPLICANT: LOOSMONE, Pale
APPLICANT: CHONG, Pale
APPLICANT: CHONG, Pale
APPLICANT: CALEIN, Machel H.
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: 23
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
 GENCEAL INC. GTALADOW.

GENCEAL INFORMATION:

APPLICANT: O'BLIEN, Timothy J.

APPLICANT: Tanimoto, Hirotoshi

ITLE OF INVENTION: TAGG-15: An Extracellular Serine Protease

TITLE OF INVENTION: Overexpressed in Carcinomas

FILE REFERENCE: D6064CIP/D

CURRENT FILING DATE: 1999-10-20

CURRENT FILING DATE: 1999-10-20

PRIOR FILING DATE: 1999-10-20

PRIOR FILING DATE: 1999-10-20

PRIOR FILING DATE: 1999-10-20

NUMBER OF SEQ ID NOS: 98

SEG ID NO S.

SEG ID NO S.
 Length 225;
 60.6%; Score 702; DB 4; Length 22:
60.3%; Pred. No. 1.46-72;
tive 26; Mismatches 59; Indels
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 181 PVVCNGQLQ--GVVSWGDGCAQKNKPGVYTKVVNYVKWIKNTIA 222
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA
 Sequence 9, Application US/08278091; Patent No. 5506139; GENERAL INFORMATION:
 ; Sequence 5, Application US/09644600 ; Patent No. 6451500
 ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 Query Match
Best Local Similarity 60.3%
Matches 135; Conservative
 CTHER INFORMATION: Trypsin
US-09-644-600-5
 ORGANISM: Homo sapiens
FEATURE:
 STATE: Ontario
COUNTRY: Canada
```

ص .. us-10-036-371-8.rai

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 121 WGNTMSS-VXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
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 1 IVGGYTCGANTVPYQVSLNSGYHFCGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVEG
 APPLICANT: YANGONNE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONEN, Raymond P.
APPLICANT: Michel H.
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
 Query Match 60.5%; Score 701; DB 1; Length 223; Best Local Similarity 60.3%; Pred. No. 1.8e-72; Matches 135; Conservative 29; Mismatches 56; Indels
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 180 PVVCSGKLQ--GIVSWGSGCAQKNKPGVYTKVCNYVSWIKQTIA 221
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/472,173
FILING DATE: 07-2UN-1995
 1038-495 MIS:vg
 ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
 US 08/278,091
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 FILING DATE: 21-UUL-1994
ATTORNEY AGENT INFORMATION:
NAME: STEWATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
TELECOMUNICATION INFORMATION:
TELECHONE: (416) 595-1163
INFORMATION FOR SEQ. 1D NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
 RESULT 15
US-08-472-173-9
Sequence 9, Application US/08472173
; Patent No. 5665353
; GENERAL INFORMATION:
 FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
 CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
 APPLICATION NUMBER:
 ; TOPOLOGY: linear
US-08-483-859-9
 FILING DATE: 07
CLASSIFICATION:
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 61 TEOXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNOYVHAVALPTECAADATMCTVSG 120
 121 WGNTMSS-VXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 61 NEQFISASKSIVHPSYNSNTLNNDIMLIKLKSAASLNSRVASISLPTSCASAGTQCLISG 120
 121 WGNTKSSGTSYPDVLKCLKAPILSDSSCKSAY-PGQITSNWFCAGYLEGGKDSCGGDSGG 179
 1 IVGGYTCGANTVPYQVSLNSGYHFCGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVEG 60
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: YANG, Yan-Ping
APPLICANT: GOMEN, Raymond P.
APPLICANT: CMEN, Michel H.
TITLE OF INVENTION: Radiod of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
TORESPONDENES: 2
CORRESPONDENE ADDRESS:
ADDRESSEE: SIM & MCBULNEY
 Query Match 60.5%; Score 701; DB 1; Length 223; Best Local Similarity 60.3%; Pred. No. 1.8e-72; Matches 135; Conservative 29; Mismatches 56; Indels
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,091
CLASSIFICATION: 435
CLASSIFICATION: 435
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTRARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,859
FILING DATE: 07-UNH-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 E: Sim & McBurney
Suite 701, 330 University Avenue
 ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416, 595-116, 116)
INFORMATION FOR SEQ ID NO: 9; SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acids
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 US-08-483-859-9
Sequence 9, Application US/08483859
Patent No. 565636
GENERAL INFORMATION:
 single
 COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 ; TOPOLOGY: linear
US-08-278-091-9
 Ontario
 STREET: Suite
CITY: Toronto
STATE: Ontario
 STRANDEDNESS:
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Search completed: February 12, 2003, 10:30:12 Job time : 49.3582 secs

time : 49.3582 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 12, 2003, 10:17:50; Search time 56.4179 Seconds (without alignments) 383.393 Million cell updates/sec Run on:

1 IVGGYECTXHSQAHQVSLNS......GVYAKVXVLSGWVRDTMAXY 225 US-10-036-371-8 1158 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

283224 Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|   |        | Description  | trypsin (8C 3.4.21 | (EC 3.4 | (EC 3 4 | (EC 3.4.2 | (EC 3.4. | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4.2 | (EC 3.4. | (EC 3.4. | (EC 3.4. | (EC 3.4. | (EC 3.4. | (EC 3.4. | (EC 3.4. | (EC 3  | (EC 3.4. | (EC 3.4. | (EC 3.4. | (EC 3  | (EC 3.4, | (EC 3  | (EC 3.4. | (EC 3.4.2 | (EC 3  | (EC 3.4.2 | (EC 2 4 2 | (EC 3.4. | trypsin (EC 3.4.21 |
|---|--------|--------------|--------------------|---------|---------|-----------|----------|-----------|-----------|-----------|----------|----------|----------|----------|----------|----------|----------|--------|----------|----------|----------|--------|----------|--------|----------|-----------|--------|-----------|-----------|----------|--------------------|
|   |        |              | ,                  |         |         |           |          |           |           |           |          |          |          |          |          |          |          |        |          |          |          |        |          |        |          |           |        |           |           |          |                    |
|   |        | ΩI           | S39047             | S39048  | 831776  | 831775    | 549489   | 831778    | TRDFS     | 831779    | TRRT1    | B25528   | TRDG     | TRRT2    | S13813   | A27547   | A35871   | B25852 | TRPGTR   | TRDGC    | A25852   | TRBOTR | 255067   | S33496 | 138363   | 855066    | S12764 | S05494    | J01472    | JQ1471   | T01779             |
|   |        | DB           | 7                  | ۲,      | 7       | 7         | 7        | 7         | Н         | 7         | ,-4      | N        | Н        | -        | 7        | 7        | 7        | ٦      | 7        | H        | Н        | Н      | 7        | 7      | ~        | 7         | 7      | 7         | ~         | 7        | 2                  |
|   |        | Match Length | 240                | 241     | 242     | 242       | 242      | 231       | 229       | 238       | 246      | 246      | 247      | 246      | 247      | 247      | 243      | 247    | 231      | 246      | 247      | 229    | 248      | 304    | 259      | 248       | 247    | 247       | 246       | 246      | 250                |
| * | Query  | Match        | ω.                 | Э.      | •       |           | 77.5     |           |           | S.        | 65.2     | m        | 'n       | ď        | •        | o.       | ,        | 61.3   | ä        | ä        | ö        |        |          | 6      | œ        | co        | ζ.     | œ.        | ۳.        | 53.2     |                    |
|   |        | Score        | 1086.5             | 1085.5  | 905.5   | 901.5     | 897.5    | 893.5     | 758.5     | 756       | 755      | 729      | 727      | 726      | 721      | 719      | 718      | 710    | 707      | 206      | 702      | 701    | 969      |        | 681.5    | 674       | 99     | 650.5     | ς.        | 616.5    | 995                |
|   | Result | No.          | 1                  | 7       | m       | 4         | S        | 9         | 7         | æ         | 6        | 10       | 11       | 12       | 13       | 14       | 15       | 16     | 17       | 18       | 19       | 20     | 21       | 22     | 23       | 24        | 25     | 26        | 27        | 28       | 29                 |

RESULT 2 S39048

| trypsin (BC 3.4.21 trypsin (BC 3.4.21 trypsin (BC 3.4.21 trypsin (BC 3.4.21 trypsin (BC 3.4.21 trypsin (BC 3.4.21 trypsin (BC 3.4.21 trypsin (BC 3.4.21 trypsin (BC 3.4.21 chymotrypsin (BC 3 75 nerve growth fa tissue kallikrein tissue kallikrein tissue kallikrein tissue kallikrein tissue kallikrein trypsin (BC 3.4.21 serine proteinase trypsin like prote tissue kallikrein | ALIGNMENTS | RESULT 1 S19047 Crypsin (EC 3.4.21.4) I - Atlantic cod Crypsin (EC 3.4.21.4) I - Atlantic cod) Crypsin (EC 3.4.21.4) I - Atlantic cod) Crypsin (EC 3.4.21.4) I - Atlantic cod) Crypsin (EC 3.4.21.4) I - Atlantic cod) Crypsin (EC 3.4.21.4) I - Atlantic cod) Crypsin (ED 3.904) Crypsin (ED 3.904) Aritle: Isolation and characterization of cDNAs from Atlantic cod encoding two different A.Recession: S19047; MUID:94039130; PMID:8223632 A.Recession: S19047; MUID:94039130; PMID:8223632 A.Residues: 1.240 cGUD A.Residues: 1.240 cGUD A.Residues: I.240 cGUD A.Residues: I.240 cGUD A.Cross-references: EMBL:X76886; NID:9450517; PIDN:CAA54214.1; PID:gli334752 C.Superfamily: trypsin homology crypsin                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Score 1086.5; DB 2; Length 240;<br>Pred: No. 4.96-99;<br>2; Mismatches 14; Indels 3; Gaps 2; | HCYKSVLRVRLGEHHIRVNEG 60                      | TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATWCTVSG 120<br> | WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP 180<br> | VVCNGVLQGVGVVSWGYGCABEDXDGVYAKVXVLSGMVRDTMAXY 225 |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------|-----------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|---------------------------------------------------|
| S31384<br>S54146<br>S340007<br>S35333<br>S35340<br>S40006<br>S40006<br>S40006<br>S40006<br>S40006<br>S72219<br>TRV21<br>A53968<br>TRWV3Y                                                                                                                                                                                                                                             | ALIG       | - Atlantic cod (Atlantic cod uence_revision 1 dmundsdottir, E. 91-1097, 1993. haracterization 47; MUID: 9403913; K76886; NID: 9403913; trypsin homology errine proteinase homology errine proteinase homology errine proteinase                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Score Pred. 1                                                                                | XCGGSLIN<br>     :<br> FCGGSLVSI              | DIMLIKL<br>                                                          | WGNTMSSYXDGDKLQXLXLPILSHADGANSY<br>                                  | XPGVYAKI<br>       <br>HPGVYAKI                   |
| 000000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                              |            | reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>r<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reior<br>reio | de de                                                                                        |                                               | X — I                                                                | 11.5                                                                 | ERD — ERD                                         |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                               |            | - Atla<br>(Atlar<br>quence<br>udmunda<br>091-100<br>Charact<br>047; M<br>L:X768E<br>trypsi<br>serine<br>n homel                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 93.8%;<br>91.6%;<br>vative                                                                   | QAHQVSLNSGYH<br>            <br> QAHQVSLNSGYH | PNYSSYN<br>       <br>PNYSSYN                                        | LOXLXLF<br>       <br>LOCLSLF                                        | SWGYGCA<br>       <br>SWGYGCA                     |
| 44444888888888888888888888888888888888                                                                                                                                                                                                                                                                                                                                               |            | 21.4) I smorthua s morthua s morthua s morthua s morthua s morthua s s s s s s s s s s s s s s s s s s s                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Query Match<br>Best Local Similarity 91.<br>Matches 206; Conservative                        | CTXHSQA<br>          <br> CTKHSQA             | SSSVXRH<br>       <br>SSSVIRH                                        | SVXDGDK                                                              | 106vgvv<br>        <br>10gvv                      |
| 529<br>474<br>474<br>467.5<br>467.5<br>467.5<br>474<br>474<br>474<br>474<br>474<br>474<br>474<br>47                                                                                                                                                                                                                                                                                  |            | EC 3.4<br>s: Gadus<br>(on Exploration S3)<br>con: S3)<br>con: S3)<br>con: S3)<br>con: S3<br>con: S3<br>con: S3<br>con: S4<br>con: S6<br>con: S6                                                                                                                                                                                                                                                                         | latch<br>cal Siπ<br>206;                                                                     |                                               |                                                                      |                                                                      |                                                   |
| 0 H G G G G G G G G G G G G G G G G G G                                                                                                                                                                                                                                                                                                                                              |            | RESULT 1 539047 C.Species: Gadus morh C.Species: Gadus morh C.Date: 20-May-1994 # C.Accession: S39047 E.Y. J. Blochem. 217, A.Y. Itle: Isolation an A.Reference number: S A.Accession: S39047 A.Rosidues: 1-240 cgul A.Rosidues: 1-240 cgul C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: trypsi: C.Superfamily: t                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Query Match<br>Best Local :<br>Matches 20:                                                   | 1 19                                          | 61                                                                   | 121                                                                  | 181                                               |
|                                                                                                                                                                                                                                                                                                                                                                                      |            | ######################################                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                              | · 중 음                                         | 8 6                                                                  | & 8                                                                  | 충 <u>음</u>                                        |

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cationic variants of tryps
 A/ACCESBAIOH: SOBOBOU
A/ACCESBAIOH: SOBOBOU
A/ACCESBAIOH: SOBOBOU
A/ACCESBAIOH: SOBOBOU
A/ACCESBAIOH: SOBOBOU
A/ACCESBAIOH: SOBOBOU
A/ACCESBAIOH: SEGEI
A/ACCESBAIOH: SEGEI
A/ACCESBAIOH: SEGEI
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A/ACCESBAIOH: SEGEI
A/ACCESBAIOH: SEGEI
A/ACCESBAIOH: SEGEI
A/ACCESBAIOH: SEGIIOH: trypsin (EC 3.4.21.4) I precursor - Atlantic salmon
C;Species: Salmo salar (Atlantic salmon)
C;Species: Salmo salar (Atlantic salmon)
C;Accession: S66660, 86661, 831775; 831777
R;Male, R.; Lorens, J.B.; Smalas, A.O.; Torrissen, K.R.
Bur. J Bloochen. 23, 677-685, 1995
A;Title: Molecular cloning and characterization of anionic and cationic vari
 C:Species: Paranotothenia magellanica
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
 A,Molecule type: mRNA
A,Residues: 1-242 <GEN>
A,Cross-references: EMBL:X82223; NID:9559507; PIDN:CAA57701.1; PID:9559508
 1 SEQFISSSRVIRHPNYSSYNIDNDIMLIKLSKPATLNTYVQPVALPTSCAPAGTMCTVSG 140
 141 WGNTMSSTADSNKLQCLNIPILSYSDCNNSY-PGMITNAMFCAGYLEGGKDSCQGDSGGP 199
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 9
 80
 Gapa
 21 IVGGYECKAYSQTHQVSLNSGYHFCGGSLVNENWVVSAAHCYKSRVEVRLGEHNIKVTEG
 121 WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
 ë,
 Length 242;
 Length 242;
 Indele
 trypsin (EC 3.4.21.4) precursor - Paranotothenia magellanica
 242
 181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225
 200 VVCNGELQ--GVVSWGYGCAEPGNPGVYAKVCIFNDWLTSTWASY
 7
 <SIG>
 DB 2;
 38,
 Ouery Match 77.8%; Score 901.5; DB 2
Best Local Similarity 75.1%; Pred. No. 6.8e-81;
Matches 169; Conservative 15; Mismatches 38
 8
 C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-13/Domain: slgnal sequence #status predicted <
F;14-242/Product: trypsin #status predicted <MAT>
F;21-235/Domain: trypsin homology <TRY>
 77.5%; Score 897.5;
 Query Matcn
Rest Local Similarity
 A, Accession: S66660
 Query Match
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 Lyppain (EC 3.4.21.4) IA precursor - Atlanic salmon C; Species: Salmo salar (Atlantic salmon)
C; Species: Salmo salar (Atlantic salmon)
C; Species: Salmo salar (Atlantic salmon)
C; Species: Salmo salar (Atlantic salmon)
C; Species: Salmo salar (Atlantic salmon)
C; Species: Salmo salar (Atlantic salmon)
C; Accession: S66659; S31776
Bur. J. Biochem. 232, 677-685, 1995
Bur. J. Biochem. 232, 677-685, 1995
A; Title: Molecular cloning and characterization of anioper and cationic variants of tryp
A; Reference number: S66659
A; Accession: S66659
A; Accession: S66659
A; Accession: S66659
A; MUD: 96035908; PMID: 7556223
A; Accession: S66659
A; MUD: 96035908; PMID: 7556223
C; Superfamily: Lrypsin homology
C; Keywords: hydrolase; Berine proteinase
C; Superfamily: Lrypsin in Expain homology
C; Keywords: hydrolase; Berine proteinase
F; 1-5, Domain: activation peptide #status predicted <APT>
F; 1-2, Domain: activation peptide #status predicted <APT>
F; 21-235, Domain: activation peptide #status predicted bends: #status predicted
F; 27-156, 45-61, 129-229, 136-202, 167-181, 192-216/ Disulfide bonds: #status predicted
F; 60, 104, 196/ Active site: His, Asp, Ser #status predicted
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A; Molecule type: mRNA
A; Residues: 1.241 • GUD>
A; Cross-references: RMBL:X76687; NID:9450519; PIDN:CAA54215.1; PID:91334753
C; Superfamily: trypsin; trypsin homology
C; Seywords: hydrolase; serine proteinase
P; 20-234, Domain: trypsin homology < TRX>
P; 59, 103, 195/Active site: His, Asp. Ser #status predicted
 SEQFISSSRVIRHPNYSSYNIDNDIMLIKLSKPATLMTYVQPVALPTSCAPAGTMCTVSG 140
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP 180
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP 180
 Gaps
 21 IVGGYECKAYSQAHQVSLNSGYHFCGGSLVNENWVVSAAHCYKSRVEVRLGEHNIKVTEG 80
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 Gaps
 9
 20 IVGGYECTRHSQAHQVSLANSGYHFCGGSLVSKDWVVSAAHCYKSVLRVRLGEHHIRVNEG 79
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
 3;
 ñ
 Length 241;
 Length 242;
 78.2%; Score 905.5; DB 2; Length : 75.6%; Pred. No. 2.8e-81; tive 15; Mismatches 37; Indels
 Score 1085.5; DB 2; Length
Pred. No. 6.2e-99;
2; Mismatches 14; Indels
 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225
 VVCNGELQ--GVVSWGYGCAEPGNPGVYAKVCIFNDWLISTMASY 242
 VVCNGVLQ--GVVSWGYGCAERDNPGVYAKVCVLSGWVRDTMASY 241
 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY
 Query Match 93.7%;
Best Local Similarity 91.6%;
Matches 206; Conservative
 Matches 170; Conservative
 Query Match
Best Local Similarity
 121
 181
 181
 140
 91
 80
 121
 199
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A/Molecule type: protein
A/Realduss 8-229 (TIT)-
A/Note: 119-pro was also found
R/Note: 119-pro was also found
R/Hermodson, M.A.; Tye, R.W.; Reeck, G.R.; Neurath, H.; Walsh, K.A.
FEBS Lett. 14, 222-224, 1971
A/Itle: Comparison of the amino terminal sequences of bovine, dogfish, and lungfish tryf
A/Reference number: A27719
 proteinase; zymc
 tryp
 Lypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)
C;Species: Salmo salar (Atlantic salmon)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: S66657; S31779
S;Male, R; Lorens, J.B.; Smalas, A.O.; Torrissen, K.R.
Eur. J. Biochem, 232, 677-685, 1995
A;Title: Molecular cloning and characterization of anionic and cationic variants of A;Reference number: S66657; MUID:96035908; PMID:7556223
 A;Accession: S66657
A;Accession: S66657
A;Accession: S66657
A;Accession: S66657
A;Coss-references: EMBL:X70074; NID:g64387; PIDN:CAA49679.1; PID:g64388
A;Cross-references: EMBL:X70074; NID:g64387; PIDN:CAA49679.1; PID:g64388
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-57/Domain: signal sequence (fragment) #status predicted <AFD-
F;16-238/Product: trypsin peptide #status predicted <APT-
F;16-238/Product: trypsin homology <FRYY-
F;16-231/Domain: trypsin homology <FRYY-
F;2-2152.40-56;124-225,131-198,163-177,188-212/Disulfide bonds: #status predicted
F;55,99,192/Active site: His, Asp, Ser #status predicted
 F;8-222/Domain: trypsin homology <TRY>
F;14-143,32-48,116-216,123-189,154-168,179-203/Disulfide bonds: #status predicted F;47,91,183/Active site: His, Asp, Ser #status predicted F;59,61,64,69/Binding site: calcium (Glu, Asp, Ala, Glu) #status predicted
 5
 .
ن
 120
 68 DETYIDSSMVIRHPNYSGYDLDNDIMLIKLSKPAALNRNVDLISLPTGCAYAGEMCLISG 127
 180
 Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 63
 A.Molecule type: protein
A.Residues: 1-21 «HER»
C.Superfamily: trypsin, trypsin homology
C.Keywords: hydrolase, pancreas; polymorphism; protein digestion; serine
R.1-7/Domain: activation peptide #status experimental «APT»
P.8-23/Product: trypsin #status predicted «MAT»
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 8 IVGGYECPKHAAPWTVSLNVGYHFCGGSLIAPGWVVSAAHCYQRRIQVRLGEHDISANEG
 61 TEQXISSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG
 121 WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP
 128 WGNTMDGAVSGDQLQCLDAPVLSDAECKGAY-PGMITNNAMCVGYMEGGKDSCQGDSGGP
 .,
B
 DB 1; Length 229;
 57; Indels
 51; Indels
 181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 A.Title: Amino acid sequence of dogfish trypsin.
A.Reference number: A00950; MUID:75146445; PMID:1092332
A.Accession: A00950
 Ouery Match 65.5%; Score 758.5; DB 1
Best Local Similarity 62.8%; Pred. No. 6.7e-67;
Matches 140; Conservative 23; Mismatches 57
 63.3%; Score 756; DB 2;
63.8%; Pred. No. 1.2e-66;
 63.8%; Pred. wo.
 Best Local Similari,
Matches 143; Conservative
 Query Match
Best Local Similarity
 A; Accession: B27719
 RESULT 8
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 Lypsin (EC 3.4.21.4) II precursor - Atlantic salmon (fragment)
C;Species: Salmo salar (Atlantic salmon)
C;Species: Salmo salar (Atlantic salmon)
C;Species: 22-Nov-1933 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: S6658; S31778
Ev. 22-Nov-1935 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: S6658; S31778
Ev. 3. Iorens, J.B.; Smalas, A.O.; Torrissen, K.R.
Ev. 3. Biochem. 232, G77-689, 1995
A;Title: Molecular cloning and characterization of anionic and cationic variants of tryp.
A;Recession: S6658
A;Molecular cloning and characterization of anionic and cationic variants of tryp.
A;Accession: S6658
A;Molecular Cype: mRNA
A;Residues: 1-231 cAMLA.
A;Cross-references: EMBL:X70073; NID:964385; PIDN:CA449678.1; PID:g64386
C;Superfamily: trypsin, trypsin homology
C;Keywords: Hydrolase; serine proteinase
F;1-4/Domain: signal sequence (fragment) #status predicted cAPT>
F;10-231/Product: trypsin 11 #status predicted cAPT>
F;10-231/Product: trypsin homology cTRY>
F;10-247/Domain: trypsin homology cTRY>
F;16-145,34-50.118-218,125-191,156-170,181-205/Disulfide bonds: #status predicted
F;49,93,185/Active site: His, Asp, Ser #status predicted
 5,
 ;
;
 trypsin (EC 3.4.21.4) precursor - spiny dogfish N;Alternate names: trypsinogen C;Species: Squalus acanthias (spiny dogfish) C;Decies: Squalus acanthias (spiny dogfish) C;Date: 31-May-1979 #sequence_revision 31-May-1979 #text_change 21-Jan-1997 C;Accession: A00900; B27719 C;Accession: A00900; B27719 R;Titani, K.; Ericsson, L.H.; Neurath, H.; Walsh, K.A. Biochemistry 14, 1358-1366, 1975
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 81 KEQFISSSRVIRHPNYSSYNIDNDIMLIKLSKPATLNQYVQAVALPSSCAPAGTMCTVSG 140
 121 WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP 180
 Gaps
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 80
 0 SEQFISSSRVIRHPNYSSYNIDNDIMLIKLSKPATLNTYVQPVALPTSCAPAGTMCTVSG 129
 WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP 180
 130 WGNTMSSTADKOKLQCLNIPILSYSDCNNSY-PGMITNAMPCAGYLBGGKDSCQGDSGGP 188
 Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 10 IVGGYECKAYSOPHQVSLNSGYHFCGGSLVNENWVVSAAHCYQSRVEVRLGEHNIQVTEG 69
 IVGGKECSPYSQPHQVSLNSGYHFCGGSLVNENWVVSAAHCYKSRVEVRMGEHHIRVTEG
 3;
 3.
 Length 231;
 Indels
 Indels
 181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225
 181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225
 Pred. No. 1.7e-80;
 38;
 DB 2;
 Pred. No. 3.9e-80
 77.2%; Score 893.5; D
74.7%; Pred. No. 3.9e-
live 16; Mismatches
 ilarity 75.1%; Pro
Conservative 16;
 Conservative
 Best Local Similarity
 Local Similarity
 Query Match
Best Local Simi
Matches 168;
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trypsin (EC 3.4.21.4) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Accession: B2528
R;Stevenson, B.J; Hagenbuerchle, O.; Wellauer, P.K.
R;Stevenson, B.J; Hagenbuerchele, O.; Wellauer, P.K.
Nucleic Acids Res: 14, 8307-8330, 188
A;Title: Sequence organisation and transcriptional regulation of the mouse elastase II as A;Reference number: A93646; MUID:87066713; PMID:3641189
A;Accession: B25528
A;Accession: B25528
A;Reference number: A93646; MUID:87066713; PMID:3641189
A;Residues: 1-246 c8TE>
A;Cross-references: GB:X04574; NID:954918; PIDN:CAA28243.1; PID:954919
C;Superfamily: trypsin, trypsin, homology protein digestion; serine proteinase
F;24-230/Domain: signal sequence #status predicted c5IG>
F;24-230/Domain: signal sequence #status predicted c5IG>
F;24-246/Product: trypsin #status predicted c5IG>
F;24-230/Domain: signal sequence #status predicted c5IG>
F;24-230/Domain: strypsin #status predicted c5IG>
F;24-230/Domain: signal sequence #status predicted c5IG>
F;24-230/Domain: signal sequence #status predicted c5IG>
F;24-230/Domain: signal sequence #status predicted c5IG>
F;24-230/Domain: signal sequence #status predicted c5IG>
F;31-307,200/Active after: His, Asp, Ser #status predicted
F;57,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
 24 IVGGYTCRESSVPYQVSLNAGYHFCGGSLINDQWVVSAAHCYKYRIQVRLGEHNINVLEG 83
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG
 121 WGNTMSS-VXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 PVVCNGELQ--GIVSWGYGCAQPDAPGVYTKVCNYVDWIQNTIA 244
 26,
 Query Match
Best Local Similarity 61.2%; Pred. No. 5.7e-64;
Matches 137; Conservative 27; Mismatches 56
 31; Mismatches
 Query Match
Best Local Similarity 61.6%;
Matches 138; Conservative 3
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 RESULT 11
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 trypein (EC 3.4.21.4) I precursor - rat

Livypsin (EC 3.4.21.4) I precursor - rat

NiAlternate names: trypsingon I

Cibbecies: Rattus norvegicus (Norway rat)

Cibbecies: Rattus norvegicus (Norway rat)

Cibbecies: Rattus norvegicus (Norway rat)

Cibbecies: Rattus norvegicus (Norway rat)

Cibbecies: Albochies 22657, M0048

Biol: Chem. 259, 14255-14244, 1984

A;Ttle: Structure of two related rat pancreatic trypsin genes.

A;Reference number: A22657; MUD:85054880; PMID:6094547

A;Accession: B22657

A;Accession: B22657

A;Accession: B22657

A;Accession: B22657

A;Accession: B22657

A;Accession: B22657

A;Accession: B22657

A;Accession: B22657

A;Accession: B22657

A;Accession: B22657

A;Accession: A246-45132

A;Cross-references: GB:J00778; MID:8206507; PIDN:AAA98518.1; PID:9206508

A;Accession: A00948

A;Accession: A00948

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A;Accession: A00948
 3
 61 TEOXISSSVXRHPNYSSYNIXNDIMLIKLTXPATLNOYVHAVALPTECAADATMCTVSG 120
 179
 121 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 24 IVGGYTCPEHSVPYQVSLNSGYHFCGGSLINDQWVVSAAHCYKSRIQVRLGEHNINVLEG 83
 TEGXISSSVXRHPNYSSYNIXNDIMLIKLTXPATLNOYVHAVALPTECAADATMCTVSG 120
 Gaps
 121 WGNTMSS-VXDGDKLQXLXLPILSHADCANSYGPGMITOSMFCAGYLEGGKDSCQGDSGG
 4
 Length 246;
 52; Indels
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 Query Match 65.2%; Score 755; DB 1; Best Local Similarity 63.8%; Pred. No. 1.6e-66; Matches 143; Conservative 25; Mismatches 52
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Length 246;

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trypsin (BC 3.4.21.4) precursor, anionic - dog
N;Alternate names: cationic trypsinogen
C;Species: Canis lugus familiaris (dog)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C;Accession: A26273
R;Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. S, 2669-2676, 1985
A;Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA seque?
A;Reference number: A26273; MUID:86284628; PMID:3841794
 ë,
 C,Superfamily: trypsin, trypsin homology
C;Keywords hydrolase; pancreas; protein digestion; serine proteinase; zymogen
C;Keywords hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: activation peptide #status predicted <APT>
F;24-23/Domain: activation peptide #status predicted <ENZ>
F;24-23/Domain: trypsin, anionic #status predicted <ENZ>
F;24-23/Domain: trypsin homology <TRX>
F;30-160,48-64,132-233,139-206,171-185,Disultide bonds: #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;63,107,200/Active site: His, Asp, Ser #status gredicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 A;Molecule type: mRNA
A;Residues: 1-247 <PIN>
A;Cross-references: GB:M11589; NID:g164094; PIDN:AAA30899.1; PID:g164095
 62.8%; Score 727; DB 1; Length 247; 61.6%; Pred. No. 9e-64;
```

RESULT 10

B25528

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anionic
 Crypsin (EC 3.4.21.4) precursor, cationic - rat
Cispecies: Raturs norvegicus (Norway rat)
Cibate: 30-dun-1988 #sequence_revision 30-dun-1988 #text_change 22-Jun-1999
CiAccession: A27547
RiFlecther, T.S. Alhaedeff, M. Craik, C.S.; Largman, C.
Biochemistry 26, 3081-3086, 1987
A;Title: Isolation and characterization of a cDNA encoding rat cationic trypsinogen.
A;Reference number: A27547; MUID:87271609; PMID:3607011
C;Species: Bos primigenius taurus (cattle)
C;Dace-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: S13813
R;Le Huerou, I.; Wicker, C.; Guilloteau, P.; Toullec, R.; Puigserver, A.
Eur., U Blochem. 193, 767-773, 1990
A;Title: Isolation and nucleotide sequence of CDNA clone for bovine pancreatic anion A;Reference number: S13813; MUID:91065383; PMID:1701147
A;Accession: S13813; MUID:91065383; PMID:1701147
A;Accession: S13813
A;Actaus: preliminary
A;Molecule type: mRNA
A;Residues: L-247 <4UNA
A;Residues: L-247 <4UNA
A;Residues: L-247 <4UNA
A;Residues: L-247 <4UNA
A;Residues: L-247 <4UNA
A;Residues: L-247 <4UNA
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A;Residues: L-247 <4UNA
A;Residues: L-247 <4UNA
A;Residues: L-24
 'n
 C;Superfamily: trypsin, trypsin homology
C;Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F;25-240/Domain: trypsin homology vRRv.
F;31-161,49-65,133-234,440-207,172-186/Disulfide bonds: #status predicted
F;64,108,201/Active site: His, Asp, Ser #status predicted
F;76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 121 WGNTMSS-VXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 85 GEQFIDAAKIIRHPSYNANTFDNDIMLIKLNSPATLNSRVSTVSLPRSCGSSGTKCLVSG 144
 WGNTWSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 24 IVGGYTCAENSVPYQVSLNAGYHFCGGSLINDQWVVSAAHCYQYHIQVRLGEYNIDVLEG 83
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 25 IVGGYTCQKNSLPYQVSLNAGYHFCGGSLINSQWVVSAAHCYKGRIQVRLGEHNIDVVFG 84
 A;Molecule type: mRNA
A;Residues: 1-247 <FLE>
A;Cross_references: GB:M16624; NID:g206498; PIDN:AAA41985.1; PID:g206499
 , ,
 62.3%; Score 721; DB 2; Length 247; llarity 60.7%; Pred. No. 3.5e-63; Conservative 30; Mismatches 54; Indels
 Length 247;
 Query Match 62.1%; Score 719; DB 2; Length 247 Best Local Similarity 61.2%; Pred. No. 5.5e-63; Matches 137; Conservative 26; Mismatches 57; Indels
 203 PVACNGQLQ--GIVSWGYGCAQKGKPGVYTKVCNYVDWIQETIA 244
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 Similarity
 A; Accession: A27547
 Best Local Sim
Matches 136;
 Query Match
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 A;Molecule type: DNA
Mresiduce; 1.246 c(RAA-
M. R. Residuce; 1.246 c(RAA-
M. MacDonald, R. J.; Stary, S. J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982
J. Biol. Chem. 257, 9724-9732, 1982
A;Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of A;Reference number: A00948; MUID:82265624; PMID:6896710
A;Accession: A00949
 Molecule type: mRNA
Residues: 9-246 <MAC>
:Comment: The trypsin II mRNA is present in much lower quantities than the trypsin I mR
 C.; MacDonald, R.J.; Rutter, W.J.
 A; Residues: 9-246 cMAC>
C; Comment: The trypsin II mRNA is present in much lower quantities than the tryp;
C; Genetics: 14/1; 67/2
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin homology
C; Reywords: hydrolaes; pancreas; protein digestion; serine proteinase; zymogen
E; 1-15/Domain: signal sequence #status predicted cAPT>
F; 24-24(Product: trypsin II #status predicted cAPT>
F; 24-24(Product: trypsin II #status predicted cAPT>
F; 24-24(Product: trypsin homology cTRY>
F; 24-39/Domain: trypsin homology cTRY>
F; 24-39/Domain: trypsin homology cTRY>
F; 24-160, 48-64, 132-233, 139-206, 171-185/Disulfide bonds: #status predicted
F; 53, 107, 200/Active site: His, Asp, Ser #status predicted
F; 55, 77, 80, 85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
 3,
 trypsin (EC 3.4.21.4) II precursor - rat
NiAlternate names: trypsinogen II
C;Species: Rattus norvegicus (Norway rat)
C;Species: 8xttus norvegicus (Norway rat)
C;Apecies: 05-Apr-1983 #sequence_revision 30-Sep-1987 #text_change 18-Jul-1997
C;Accession: A22657; A00949
B;Craik, C.S.; Choo, O.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, J. Biol. Chem. 259, 14255-14264, 1984
A;Title: Structure of two related rat pancreatic trypsin genes.
A;Reference number: A22657; MUID:85054880; PMID:6094547
 TEQXISSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 21 WGNTMSS-VXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 84 DEQFINAAKIIKHPNFDRKTLNNDIMLIKLSSPVKLNARVATVALPSSCAPAGTQCLISG 143
 83
 24 IVGGYTCQENSVPYQVSLNSGYHFCGGSLINDQMVVSAAHCYKSRIQVRLGEHNINVLEG 83
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
24 IVGGYTCEENSVPYQVSLNAGYHFCGGSLISDQWTVSAAHCYKSRIQVRLGEYNIDVLEG
 121 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG
 Length 246;
 57; Indels
 203 PVVCNGELQ--GIVSWGYGCAQRARPGVYTKVCNFVDWIQSTIA 244
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 180 PVVCNGVLQGVGVVSMGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 203 PYVCNGELQ--GIVSWGYGCALPDNPGVYTKVCNYVDWIQDTIA 244
 62.7%; Score 726; DB 1;
ilarity 62.1%; Pred. No. 1.1e-63;
Conservative 24; Mismatches 57;
 S13813
trypsin (EC 3.4.21.4) - bovine
 Query Match
Best Local Similarity
 Best Local Sim:
Matches 139;
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Lyppain (EC 3.4.21.4) precursor, pancreatic - African clawed frog C; Species: Xenopus laevis (African clawed frog)
C; Accession: A35871; S1217
C; Accession: A35871; S1217
C; Accession: A35871; S1217
C; Accession: A35871; MUID: 91007255; PMID: 2210372
C; Accession: A35871
A; Reference number: A35871; MUID: 91007255; PMID: 2210372
A; Accession: A35871
A; Reference number: A35871; MUID: 91007255; PMID: 2210372
A; Accession: A35871
A; Caccession: A35871

 ä
145 WGNTLSSGTNYPSLLQCLDAPVLSDSSCKSSY-PGKITSNMFCLGFLEGGKDSCQGDSGG 203
 Gaps
 1 IVGGYECTXHSQAHQVSINSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 4,
 Length 243;
 31; Mismatches 52; Indels
 204 PVVCNGQLQ--GVVSWGYGCAQKGKPGVYTKVCNYVNWIQQTVA 245
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTWA 223
 Query Match 62.0%; Score 718; DB 2; Best Local Similarity 61.2%; Pred. No. 6.7e-63; Matches 137; Conservative 31; Mismatches 52
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81 TEQFISSSKVIRHSGYNSYTLDNDIMLIKLSSPASLNAAVNTVPLPSGCSAAGTSCLISG 140

TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120

21 IIGGATCAKSSVPYIVSLNSGYHFCGGSLITNQWVSAAHCYKASIQVRLGEHNIALSEG 80

Search completed: February 12, 2003, 10:28:56 Job time : 57.4179 sec8

180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223

WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179

121

61

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(without alignments)
308.768 Million cell updates/sec
 February 12, 2003, 10:04:45; Search time 30.2239 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
 OM protein - protein search, using sw model
 Run on:
```

US-10-036-371-8 1158 Perfect score:

1 IVGGYECTXHSQAHQVSLNS.........GVYAKVXVLSGWVRDTMAXY 225 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 08 Maximum Match 1008

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | O gadine morthi | מול מול מ  | on les     | Salmo      | squalu     |            | rattus   |             | _      | 2 canis famil | 3 rattus norv | ~     |          |            |            |          | cani       |            |            | Ţ.        | gallus     | homo sa    | gallu      |            | 3 rattu  | ~        |          | 1 pleuronecte |            |        | anopheles | anopheles  | homo sapie |
|-----------|----------------|-----------------|------------|------------|------------|------------|------------|----------|-------------|--------|---------------|---------------|-------|----------|------------|------------|----------|------------|------------|------------|-----------|------------|------------|------------|------------|----------|----------|----------|---------------|------------|--------|-----------|------------|------------|
|           | Descr          | D1604           | 091041     | P35031     | P35032     | P00764     | P35033     | P00762   | P70059      | P07146 | P0687         | P0076         | 02946 | P08426   | P19799     | P07478     | P00761   | P06871     | P07477     | P00760     | 09062     | 09062      | P35030     | 090629     | P1595      | P12788   | P3282;   | P32821   | P35034        | Q9h2r5     | P35037 | P35036    | P3503      | 09p0g3     |
| SUMMARIES | ΙΩ             | TRY1 GADMO      | TRYX GADMO | TRY1 SALSA | TRY2 SALSA | TRYP_SQUAC | TRY3_SALSA | TRY1_RAT |             |        | TRY2_CANFA    | TRY2_RAT      |       | TRY3_RAT | TRY1 XENLA | TRY2_HUMAN | TRYP_PIG | TRY1_CANFA | TRY1 HUMAN | TRY1 BOVIN | TRYLCHICK | TRY2_CHICK | TRY4_HUMAN | TRY3 CHICK | TRY3_HUMAN | TRY4 RAT | TRYB RAT | TRYA_RAT | TRYP PLEPL    | KLKF HUMAN |        |           | TRY1_ANOGA | KLKE_HUMAN |
|           | Length DB      | 241 1           |            |            |            | 229 1      |            |          | 244 1       | 246 1  | 247 1         | 246           | 247 1 | 247 1    | 243 1      | 247 1      | 231 1    | 246 1      | 247 1      | 243 1      | 248 1     | 248 1      | 304 1      | 248 1      | 247 1      | 247 1    | 246 1    | 246 1    | 250 1         | 256 I      | 1 5/2  | 277 1     | 274 1      | 251 1      |
| de        | Query<br>Match | 93.8            | 93.7       |            |            | 65.5       |            |          |             | 63.0   | 62.8          | / . 79        | 62.3  | 62.1     | 0.79       | 61.3       | 61.1     | 61.0       | 9.09       | 60.5       |           |            |            |            |            |          |          | 33.2     |               |            |        |           | 8. S       |            |
|           | Score          |                 |            | 901.5      | 893.5      | 758.5      | 756        | 755      | 735         | 671    | 177           | 97/           | 177   | 61/      | 20 7 1     | 710        | /0/      | 706        | 702        | 701        | 697       | 693        | 169        | 4/0        | 000        | 000      | 01/10    | 0.010    | 529           | 1,11       |        | 0.70      |            | 460        |
|           | Result<br>No.  | 1               | 7          | m          | 4          | ı,         | ום         | 7        | <b>20</b> C | ,      | 7 -           | 1.            | 71    | 113      | <b>.</b>   | η,<br>1    | 9 5      | 17         | 87.        | 7.0        | 20        | 770        | 7 6        | 223        | <b>†</b> 2 | 070      | 9 10     | 4 0      | 0 7           | , ,        | 2 -    | 1 (       | 32         | 3.5        |

| P35041 anopheles g<br>Q9ubx7 homo sapien |                          | POOTS MUST MUST POOTS |            |         |                           |            |
|------------------------------------------|--------------------------|-----------------------|------------|---------|---------------------------|------------|
| TRY7_ANOGA<br>KLKB_HUMAN                 | CTRA GADMO<br>KLK6 HUMAN | KLK3 MOUSE            | KLK2 HUMAN | KLK PIG | KLKD HUMAN<br>TRYP ASTFI. | KLK7_HUMAN |
|                                          |                          |                       |            |         |                           | 1          |
| 267                                      | 263<br>244               | 261                   | 261        | 246     | 237                       | 253        |
| 39.6                                     | 38.8                     | 38.6                  | 38.1       | 37.4    | 37.3                      | 37.2       |
| 458                                      | 449.5                    | 447.5                 | 441.5      | 433.5   | 432.5                     | 431        |
| 3.5                                      | 37                       | 38                    | 4 0        | 4.2     | 4 4<br>6 4                | 45         |

## ALIGNMENTS

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RESULT 1
TRY1 GADMO STANDARD; PRT; 241 AA.

AC P16049; Q91040; Q92156;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 135, Last sequence update)
DT 15-JUN-2002 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 35, Last sequence update)
DF 15-JUN-2002 (Rel. 35, Last sequence update)
DF 15-JUN-2002 (Rel. 35, Last sequence update)
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DF 15-JUN-2002 (Rel. 35, Last sequence update)
DF 15-JUN-2002 (Rel. 35, Last sequence update)
DF 15-JUN-2002 (Rel. 35, Last sequence update)
DF 16-JUN-2002 SEQUENCE FROM N.A.
TISSUE-PAIOSIC caeca;
TISSUE-PAIOSIC caeca;
MEDLINE-9403913; PubMed-8223632;
Gudmundsdottir A., Gudmundsdottir E., Oskarsson S., Bjarnason J.B.,
Eakin A.E., Craik C.S.;
"Isolation and characterization of cDNAs from Atlantic cod encoding
two different forms of trypsinogen.";
[2]
Eur. J. Biochem. 217:1091-1097{1993}.
 Eur. J. Biochem, 180:85-94(1989).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 TISSUE=Pyloric caeca;
MEDLINE=89210867; PubMed=2707266;
Asgelrsson B., Fox J.W., Bjarnason J.B.;
"Purification and characterization of trypsin from the poikilotherm Gadus morhua.";
 MENOPS, 201151,
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSTE; PS50240; TRYPSIN DOM; I.
PROSTE; PS00135; TRYPSIN HIS; I.
PROSTE; PS00135; TRYPSIN HIS; I.
Bydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal; Multigene family.
 EMBL; X76886; CAA54214.1; -. PIR; S03570; S03570.
 SEQUENCE OF 20-58
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RESULT 3
TRY1_SALSA
ID _TRY1_SALSA
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ACT SITE
ACT SITE
ACT SITE
DISÜLFID
DISÜLFID
 DISULPID
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 7
 CHARGE RELAY SYSTEM (BY SIMILARITY).
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 61 TEQXISSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP 180
 140 WGNTMSSVADGDKLQCLSLPILSHADCANSY-PGMITQSMFCAGYLEGGKDSCQCDSGGP 198
 80 TEQYISSSSVIRHPNYSSYNINNDIMLIKLTKPATLNQYVHAVALPTECAADATMCTVSG 139
 Gapa
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 20 IVGGYECTKHSQAHQVSIANSGYHFCGGSLVSKDWVVSAAHCYKSVLAVRLGEHHIRVNEG 79
 TISSUE-Pyloric caeca;
MEDLINE-9403910; PubMed=8223632;
MEDLINE-9403910; PubMed=8223632;
MEDLINE-9403910; PubMed=8223632;
MEDLINE-9403910;
Eakin A.E., Craik C.S.;
Fakin A.E., Craik T.S.;
Fakin A.E.,
 1.NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsin X precursor (BC 3.4.21.4).
Gadus morbua (Atlantic cod).
Eukarymota; Metazoa; Chordata; Craniata; Vartebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadus.
 .
.
 DB 1; Length 241;
 14; Indels
 181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTWAXY 225
 TK -> EA (IN REF. 2).
F -> Y (IN REF. 2).
VSKD -> IN (IN REF. 2).
44EC9A0106AD1A68 CRC64;
 -> Q (IN REF. 2).
 Score 1086.5; DB 1,
Pred. No. 1.9e-104;
2; Mismatches 14;
 ACTIVATION PEPTIDE.
TRYPSIN 1.
 52 Vi
25941 MW;
 93.8%;
 Best Local Similarity 91.6%;
Matches 206; Conservative
 STANDARD;
 SEQUENCE FROM N.A.
 241 AA;
 NCBI_TaxID=8049;
 GADMO
 CONFLICT
CONFLICT
CONFLICT
SEQUENCE
 SIGNAL
PROPEP
CHAIN
ACT SITE
ACT SITE
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DISULFID
DISULFID
 DISULFID
 Query Match
 DISULPID
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REGUIRED FOR SPECIFICITY (BY SIMILARITY).
 139
 180
 120
 Gape
 79
 140 WGNTMSSVDDGDKLQCLNLPILSHADCANSY-PGMITQSMFCAGYLEGGKDSCQGDSGGP
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG
 80 TEQFISSSSVIRHPNYSSYNIDNDIMLIKLTEPATLNQYVHAVALPTECAADATMCTVSG
EMBL; X76887; CAA54215.1; -.
HSSP; P00763; 1DPO.
HSROPS; S01.151.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_procease_Try.
InterPro; IPR001254; Ser_procease_Try.
Pfam; PR00089; trypsin; 1.
PR05712; PR000972; Trypsin; 1.
PR057175; PS50240; TRYPSIN DOM; 1.
PR057175; PS60134; TRYPSIN DOM; 1.
PR057175; PS00134; TRYPSIN_ER; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
 20 IVGGYECTRHSQAHQVSLNSGYHFCGGSLVSKDWVVSAAHCYKSVLRVRLGEHHIRVNBG
 121 WGNTMSSYXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP
 Eukaryota, Euteazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 TISSUE=Pancreas;
MEDILINE=9603508; PubMed=7556223;
MEDILINE=9603508; PubMed=7556223;
MADILINE=9603508; PubMed=7.0., Torrissen K.R.;
MADICULINE cloning and characterization of anionic and cationic
"Molecular cloning and characterization of anionic and cationic
variants of trypsin from Atlantic salmon.";
Eur. J. Blochem. 232:677-685(1995).
 ..
m
 DB 1; Length
 14, Indels
 181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225
 241
 199 VVCNGVLQ--GVVSWGYGCAERDNPGVYAKVCVLSGWVRDTMASY
 Query Match
Best Local Similarity 91.6%; Pred. No. 2.4e-104;
Matches 206; Conservative 2; Mismatches 14;
 POTENTIAL.
ACTIVATION PEPTIDE.
TRYPSIN X.
 01-FFB-1994 (Rel. 28, Created)
01-FFB-1994 (Rel. 28, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
17-YPSIN 1 Drecureor (EC 3-4.21.4).
Salmo salar (Atlantic salmon).
 X-RAY CRYSTALLOGRAPHY (1.82 ANGSTROMS)
 MM,
 25976
 STANDARD;
 13
241
19
103
103
155
60
228
228
180
180
 191
189
141 AA;
 SEQUENCE FROM N.A.
 Multigene family.
 NCBI_TaxID=8030;
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 141 WGNTWSSTADSNKLQCLNIPILSYSDCNNSY-PGMITNAMFCAGYLEGGKDSCQ3DSGGP 199
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 Salmo salar (Atlantic salmon).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 ZR; 1.
Digestion; Pancreas; Zymogen; Signal;
 DB 1; Length 231;
 Indels
 181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225
 200 VVCNGELQ--GVVSWGYGCAEPGNPGVYAKVCIFNDWLTSTWASY 242
 CS4AlCAFE74FAE18 CRC64;
 ACTIVATION PEPTIDE
 77.2%; Score 893.5; DB 1
74.7%; Pred. No. 1.2e-84;
 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-UN 2002 (Rel. 41, Last annotation update)
Trypsin II precursor (EC 3.4.21.4) (Fragment)
 231 AA.
 16; Mismatches
 TRYPSIN II
 POTENTIAL
 PROSTE; JATES SET Drocease Try Pfam, PF00089; trypsin; 1. SMART, SMO0220; Tryp SPC, 1. PROSTE; PSC6240; TRYPSIN DOM; 1. PROSITE; PSC0134; TRYPSIN HIS; 1. PROSITE; PS00135; TRYPSIN HIS; 1.
 24823 MW;
 EMBL, X70073, CAA49678.1, -.
PIR, S31778, S31778.
HSSP, P35031, 1BIT.
MEROPS, S01.258, -.
 Hydrolase, Serine protease;
Multigene family.
 STANDARD;
 Conservative
 49
93
185
145
50
50
218
170
170
 SEQUENCE FROM N.A.
 231 AA;
 Similarity
 NCBI TaxID=8030;
 TRY2 SALSA
 Matches 168;
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 .;
7
 REQUIRED FOR SPECIFICITY (BY SIMILARITY)
 Proteins 20:149-166(1994).
--- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
--- SUBCELLULAR LOCATION: Extracellular.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 31 SEQFISSSRVIRHPNYSSYNIDNDIMLIKLSKRATLNITVQPVALPTSCAPAGTMCTVSG 140
 121 WGNTMSSVXDGDKLOXLKLPILSHADCANSYGPGMITQSMPCAGYLGGKDSCQGDSGGP 180
 Gaps
 MEDLINE-95148588; PubMed=1846025; Smalas A.O., Heimstad E.S., Hordvik A., Willassen N.P., Male R.; "Cold adaption of enzymes: structural comparison between salmon and
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 21 IVGGYECRAYSQTHQVSLNSGYHFCGGSLVNENWVVSAAHCYKSRVEVRLGEHNIKVTEG 80
 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Ser_protease_Try.
Pfam, PF00089; trypsin, 1.
SMART; SM00020; Tryp_SPc; 1.
PR0STIE; PS00134; TRYPSIN DOM; 1.
PROSTIE; PS00134; TRYPSIN DOM; 1.
PROSTIE; PS00134; TRYPSIN SER; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal; Multigene family; 3D-structure.
 "Structure determination and refinement of benzamidine-inhibited trypsin from the North Atlantic salmon (Salmo salar) at 1.82-A
 DB 1; Length 242;
 38; Indels
 33 T -> A (IN TRYPSINS IA/IB).
25958 MW; 43F5642498067E5A CRC64;
 CHARGE RELAY SYSTEM.
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 POTENTIAL.
ACTIVATION PEPTIDE.
TRYPSIN I.
 Score 901.5; DB 1
Pred, No. 1.9e-85;
5; Mismatches 38
 CRYSTALLOGRAPHY (1.82 ANGSTROMS).
 Acta Crystallogr. D 49:318-330(1993).
 77.8°,
75.18; Fr.
 EMBL; X70075; CAA49680.1; -.
EMBL; X70071; CAA49676.1; -.
EMBL; X70072; CAA49677.1; -.
 Smalas A.O., Hordvik A.;
 Matches 169; Conservative
 PIR, S31775, S31775.
PIR, S31776, S31776.
PIR, S31777; S31777.
PDB, 2TBS, 30-APR-94.
PDB, 1BIT, 01-NOV-94.
 242
60
104
196
156
 242 AA;
 Local Similarity
 bovine trypsins.'
 MEROPS; S01.151;
 ACT_SITE
ACT_SITE
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DISULFID
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Gaps

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1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
 STANDARD;
 PIR; S31779; S31779.
 HSSP, P00763; 1DPO.
 SEQUENCE FROM N.A.
 16
192
22
40
124
 TRY3 SALSA
P35033;
 ACT_SITE
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 TRY3_SALSA
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REQUIRED FOR SPECIFICITY (BY SIMILARITY).
 Gaps
 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATINQYVHAVALPTECAADATMCTVSG 120
 SEQFISSSRVIRHPNYSSYNIDNDIMLIKLSKPATLNTYVQPVALPTSCAPAGTMCTVSG 129
 WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP 180
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
NCBI_TaxID=7797;
٠<u>.</u>
 65.5%; Score 758.5; DB 1; Length 229; 62.8%; Pred. No. 9e-71; .ive 23; Mismatches 57; Indels 3;
 InterPro; Sullial; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PR00122; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_ESP; 1.
PROSITE; PS00135; TRYPSIN_ESP; 1.
PROSITE; PS00135; TRYPSIN_ESP; 1.
PROSITE; PS00135; TRYPSIN_ESP; 1.
PROFEP
 E83B83C5AD72FCE4 CRC64;
 181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225
 189 VVCNGELQ--GVVSWGYGCAEPGNPGVYAKVCIFNDWLTSTWATY
 Titani K., Ericsson L.H., Neurath H., Walsh K.A.; "Amino acid sequence of dogfish trypsin."; Biochemistry 14:1358-1366(1975).
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypain precursor (EC 3.4.21.4).
Squalus acanthias (Spiny dogfish).
 229 AA
 SEQUENCE OF 8-229.
MEDLINE=75146445; PubMed=1092332;
 24591 MW;
 Query Match
Best Local Similarity 62.8
Matches 140; Conservative
 STANDARD;
 229
47
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1183
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148
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1169
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 109 1
229 AA;
 SEQUENCE OF 1-21.
 TRYP SQUAC
P00764;
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 121 WGWTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP 180
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYYHAVALPTECAADATMCTVSG 120
 67
 Male R., Lorens J.B., Smalls A.O., Torrissen K.R.;
"Molecular cloning and characterization of anionic and cationic variants of trypsin from Atlantic salmon.";

Bur. J. Bloochem. 232:677-685(1995).

-i. CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lyg-|-Xaa.

-i. SUBCELLULAR LOCATION: Extracellular.

-i. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 Pfam; PF00089; trypsin; 1.
SMART; SM0020; tryp_SPc; 1.
PROSITE; PS50220; TRYPSIN DOM; 1.
PROSITE; PS50234; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN DEM; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal; NON TER
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 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last sequence update)
11-JUM-2002 (Rel. 41, Last annotation update)
Trypsin III precursor (EC 3.4.21.4) (Fragment).
Salmo salar (Atlantic salmon).
Salmo salar (Atlantic salmon).
Actinopterygii, Neopterygii, Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmo.
 SIMILARITY).
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8 İVGGYECPKHAAPWIVSLAVGYHFCGGSLİAPGWAVSAAHCYORRIQVRLGEHDISANEG
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 187 VVCNGMLQ--GIVSWGYGCAERDHPGVYTRVCHYVSWIHETIA 227
 181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 POTENTIAL.
ACTIVATION PEPTIDE.
TRYPSIN III.
TRYPSIN III.
CHARGE RELAY SYSTEM (CHARGE RELAY SYSTEM (CHARGE RELAY SYSTEM (BY SIMILARITY.
BY SIMILARITY.
 TISSUE=Pancreas;
MEDLINE=96035908; PubMed=7556223;
 EMBL; X70074; CAA49679.1; -.
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us-10-036-371-8.rsp

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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 Pfan, PF00089; trypsin; I
PRINTS, P60022; CHYWOTRPSIN.
SMART; SM00020; Tryp, SPC; I.
PROSITE; P500340; TRYPSIN DOM; I.
PROSITE; P500334; TRYPSIN DOM; I.
PROSITE; P500334; TRYPSIN SER; I.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
Multigene family; 3D-structure.
 REQUIRED FOR SPECIFICITY.
 ACTIVATION PEPTIDE.
TRYPSIN I, ANIONIC.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
 InterPro, IPR001314, Chymotrypsin.
InterPro, IPR001254; Ser_protease_Try.
 EMBL; V01273; CAA24580.1; -
EMBL; J00778; AAA98518.1; -
PIR; A00094; TRRTI.
PDB; 1TRM; 15-UL.93.
PDB; 1TRM; 16-UL.98.
PDB; 1BRA; 30-ARR-94.
PDB; 1BRC; 31-MY-94.
MEROPS; S01.094.
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198 BY SIMILARITY.
177 BY SIMILARITY.
212 BY SIMILARITY.
186 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
25389 MW; AE799880E8393023 CRC64;
 TEGXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNOYVHAVALPTECAADATMCTVSG 120
 179
 X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLURE-57229123; PubMed=3112942;
Sprang S., Standing T., Fletterick N.J., Stroud R.M., Finer-Moore J.,
Xuong N.-H., Hamlin R., Rutter W.J., Craik C.S.,
The three-dimensional structure of Asn102 mutant of trypsin: role of
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 75
 Rattus norvegicus (Rat).
Eukaryods, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
 Gaps
 McDonald R.J., Stary S.J., Swift G.H., "Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide Sequences of the cloned cDNAs "," Biol. Chem. 257:9724-9732(1982).
 16 IVGGYECRKNSASYQASLQSGYHFCGGSLISSTWVVSAAHCYKSRIQVRLGEHNIAVNEG
 121 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
<u>Tryp</u>sin I, anionic precursor (EC 3.4.21.4) (Pretrypsinogen I).
 SEQUENCE FROM N.A.
MEDLINE=85054880; PubMed=6054547;
Craik C.S., Choo Q.L., Swift G.H., Quinto C., McDonald R.J.,
Rutter W.J.;
 Length 238;
 51; Indels
 "Structure of two related rat pancreatic trypsin genes.";
J. Biol. Chem. 259:14255-14264(1984)
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 65.3%; Score 756; DB 1; 63.8%; Pred. No. 1.7e-70;
 63.8%; Prec.
tive 26; Mismatches
 246 AA.
 [1]
SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley;
MEDLINE=82265621, Pubmed-6896710;
 Similarity 63.8
 STANDARD;
 238 AA;
 Matches 143;
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 3,
 61 TEQXIBSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 24 IVGGYTCPEHSVPYQVSLNSGYHFCGGSLINDQWVVSAAHCYKSRIQVRLGEHNINVLEG 83
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
11-NOV-1997 (Rel. 41, Last sequence update)
12-JUN-2002 (Rel. 41, Last annotation update)
1rypsin precursor (EC 3.4.21.4)
1rypsin precursor (African clawed frog).
Xenopus laevis (African clawed frog).
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Fipidae;
Xenopodinae; Xenopus.
 121 WGNTMSS-VXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG
 ACTIVATION PEPTIDE (BY SIMILARITY).
TRYBEIN.
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
 4.
 Length 246;
 52; Indels
 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PP00089; trypsin, 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN IN I.
PROSITE; PS00135; TRYPSIN IN I.
Hydrolase; Serine protease; Digestion; Zymogen; Signal;
 234
244
24559 MW; GAPAODADI1943FB5 CRC64;
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 203 PVVCNGQLQ--GIVSWGYGCALPDNFGVYTKVCNFVGWIQDTIA 244
 Score 755; DB 1;
Pred. No. 2.2e-70;
 SIMILARITY
 25, Mismatches
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 EMBL; U72330; AAB17274.1; -.
HSSP; P00763; 1DPO.
 65.2%;
63.8%;
 tches 143; Conservative
 STANDARD;
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 232 2
236 2
245 2
246 AA;
 SEQUENCE FROM N.A.
 Multigene family.
 Similarity
 MEROPS; S01.258;
 NCBI_TaxID=8355;
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 121 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 61 TEQXISSSSYXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 STRAIN=A/J;

MEDLINE=87066713; PubMed=3641189;

Stevenson B.J., Hagenbuechle O., Wellauer P.K.;

Stevenson B.J., Hagenbuechle O., Wellauer p.K.;

Sequence organisation and transcriptional regulation of the mouse elastase II and trypsin genes.";

Nucleic Acids Res. 14:8307-8330(1986)

-! CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-! SUBCELDULAR LOCATION: Extracellular.
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 REQUIRED FOR SPECIFICITY (BY SIMILARITY)
 9
 81
 4; Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
 22 IVGGFTCAKNAVPYQVSLNAGYHFCGGSLINSQWVVSAAHCYKSRIQVRLGEHNIALNEG
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Trypsin II, anionic precursor (EC 3.4.21.4) (Pretrypsinogen II).
TRY2.
 Query Match
63.5%; Score 735; DB 1; Length 244;
Best Local Similarity 61.6%; Pred. No. 2.5e-68;
Matches 138; Conservative 33; Mismatches 49; Indels
 C63F29CB3300B323 CRC64;
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTWA 223
 201 PUVCNGQLQ--GVVSWGYGCAQRNYPGVYTKVCNFVTWIQSTIS 242
 BY SIMILARITY.
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 HSSP; P00763; 1DPO.
MEROPS; S01.064; -.
MGD; MGI:102759; Try2.
InterPro; 1PR001314; Chymotrypsin.
InterPro; 1PR001254; Ser protease_Try.
Pfam; PF00089; trypsin; I.
 26079 MW;
 EMBL; X04574; CAA28243.1; -. EMBL; X04577; CAA28245.1; -. PIR; B25528; B25528.
 STANDARD;
198
158
62
231
204
183
192
 Mus musculus (Mouse)
1988
28
130
137
169
194
244 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
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31; Mismatches
 246 AA
 PRT;
 26423 MW;
 EMBL; M11589; AAA30899.1;
PIR; A26273; TRDG.
HSSP; P00763; 1DPO.
 Matches 138; Conservative
 STANDARD;
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64
 Rattus norvegicus (Rat)
 247 AA;
 Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=10116;
 16
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 RESULT 11
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute on There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 121 WGNTMSS-VXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 Pinsky S.D., Laforge K.S., Scheele G.;
Pinsky S.D., Laforge K.S., Scheele G.;
"Differential regulation of trypsinogen mRNA translation: full-length
mRNA sequences encoding two oppositely charged trypsinogen isoenzymes
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 24 IVGGYTCRESSVPYQVSLNAGYHFCGGSLINDQWVVSAAHCYKXRIQVRLGEHNINVLEG 83
 Gaps
 in the dog pancreas.";
Mol. Cell. Biol. 5:2669-2676(1985).
-! - CATALYTIC ACTIVITY: Preferential
-! - SUBCELLULAR LOCATION: Extracellular.
-! - SUBCELLULAR LOCATION: Extracellular.
-! - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
 protease; Digestion; Pancreas; Zymogen; Signal.
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis
 63.0%; Score 729; DB 1; Length 246; 61.2%; Pred. No. 1.1e-67; Live 27; Mismatches 56; Indels
 CEF8C97AAC2D07AD CRC64;
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 203 PUVCNGELQ--GIVSWGYGCAQPDAPGVYTKVCNYVDWIQNTIA 244
 TRYPSIN II, ANIONIC.
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BY SIMILARITY.
 ACTIVATION PEPTIDE.
 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsin, anionic precursor (EC 3.4.21.4).
 247 AA
PRINTS, PR00722; CHYMOTRYPSIN, SMART; SM0020; Tryp SPC; 1. PROSITE; PS50240; TRYPSIN DOM; 1. PROSITE; PS00134; TRYPSIN,HIS; 1. PROSITE; PS00135; TRYPSIN,SER; 1. Hydrolase; Serine protease; Digesti
 SEQUENCE FROM N.A.
MEDLINE=86284628; Pubmed=3841794;
 26203 MW;
 Matches 137; Conservative
 STANDARD;
 63
200
160
160
64
233
206
220
 246 AA;
 Similarity
 NCBI_TaxID=9615;
 RESULT 10
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 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 121 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCCGDSGG 179
 144 WGNTLSSGTNYPELLOCLDAPILTOAQCEASY-PGQITENMICAGFLEGGKDSCQGDSGG 202
 Gaps
 83
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
MEROPS, 801.258;
InterPro; IRR001314; Chymotrypsin.
InterPro; IRR001314; Ser_protease_Try.
Piam; PR001089; trypsin; 1.
PRINTS; PR00122; CHYMOTRYREIN.
BRART; SM00202; TRYP SPC; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal; Signal.
 1 IVGGYECTXHSQAHQVSINSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
 24 IVGGYTCEENSVPYQVSLNAGYHFCGGSLISDQWVVSAAHCYKSRIQVRLGEYNIDVLEG
 21-JUL-1986 (Rel. 01, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsin II, anionic precursor (EC 3.4.21.4) (Pretrypsinogen II).
 MEDLINE-85054880; PubMed=6094547; Craik C.S., Choo Q.L., Swift G.H., Quinto C., McDonald R.J., Rutter W.J.; W.J., Structure of two related rat pancreatic trypsin genes."; J. Biol. Chem. 259:14255-14264(1984).
 62.8%; Score 727; DB 1; Length 247; 61.6%; Pred. No. 1.7e-67;
 51; Indels
 374E9D31D6DB8EAF CRC64;
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 203 PUVCNGELQ--GIVSWGYGCAQKNKPGVYTKVCNFVDMIQSTIA 244
 ACTIVATION PEPTIDE.
 J. Biol. Chem. 259:14255-14
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SEQUENCE OF 9-246 FROM N.A.
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 SPECIFICITY (BY SIMILARITY).
 Earnest T., Fauman B., Craik C.S., Stroud R.; "1.59-A structure of trypsin at 120 K: comparison of low temperature and room temperature structures."; Proteins 10:171-187(1991).
 Dischemistry 35:599-6009(1996).
Biochemistry 35:599-6009 (1996).
Biochemistry 35:599-6009 (1996).
Biochemistry 35:599-6009 (1996).
Biochemistry: Preferential cleavage: Arg-|-Xaa. Lys-|-Xaa. SUBCELLULAR LOCATION: Extracellular.
SUBCELLULAR LOCATION: TO PEPTIDASE FAMILY S1.
STRAIN=Sprague-Dawley, TISSUE=Pancreas;
MEDLINE=82265624; PubMed=6896710;
McDonald R.J., Stary S.J., Swift G.H.;
"Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of the cloned cDNAs.";
J. Biol. Chem. 257:9724-9732(1982).
 MEDLINE=96214506; PubMed=8634241;
Brinen L.S., Willett W.S., Craik C.S., Fletterick R.J.;
"X-ray structures of a designed binding site in trypsin show metal-
 Interpro; IPR001214; Chymotrypsin.
Interpro; IPR001224; Ser_protease_Try.
Ffam; PF00089; trypsin; 1.
Ffam; PF00089; trypsin; 1.
SNART; SM00020; Tryp SPC; 1.
PROSITE; PS00124; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal; Multigene family; 3D-structure.
 TRYPSIN II, ANIONIC.
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 ACTIVATION PEPTIDE.
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N -> D (IN REF. 1)
 X-RAY CRYSTALLOGRAPHY (1.59 ANGSTROMS).
MEDLINE-91351998; PubMed=1881877;
 K-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 AAA98517.1; JOINED.
 EMBL; V01274; CAA24581.1; -.
EMBL; L00131; AAA98517.1; -.
EMBL; L00130; AAA98517.1; JOII
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190
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195
84
 15LU; 11-JUL-96.
15LV; 11-JUL-96.
15LV; 11-JUL-96.
15LX; 11-JUL-96.
1DPO; 07-JUL-97.
37GI; 23-DEC-98.
 1ANB; 01-APR-97.
1ANC; 01-APR-97.
1AND; 01-APR-97.
 1AND; 01-APR-97.
1ANE; 01-APR-97.
1AMH; 24-DEC-97.
 dependent geometry
 MEROPS; S01.258;
 EMBL; L00130;
PIR; A22657; 7
PDB; 1ANB; 01-
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 HSSP; POUVOS,
REROES; SOLISS; ...
REROES; SOLISS; ...
InterPro; IPRO01214; Chymotrypain.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF000089; trypsin; 1.
DR PRO372; CHYMOTRYPSIN.
DR PROSTIE; PS00124; TRYPSIN DOM; 1.
DR PROSTIE; PS00134; TRYPSIN LS; 1.
DR PROSTIE; PS00134; TRYPSIN LS; 1.
DR PROSTIE; PS00134; TRYPSIN LS; 1.
DR Hydrolase; Serine protease; Digestion; Poperain.
FT SIGNAL 15 ACTIVATION PEPTIDE.
THYPSIN, ANIONIC.
 61 TEQXISSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 121 WGNTMSS-VXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 Eur J. Biochem. 193:767-773 (1990).

Fur J. Biochem. 193:767-773 (1990).

-!- CATALVITC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lyg-|-Xaa.

-!- SUBCELLULAR LOCATION: Extracellular.

-!- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1.
 4; Gaps
 24 IVGGYTCQENSVPYQVSLNSGYHFCGGSLINDQWVVSAAHCYKSRIQVRLGEHNINVLEG 83
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
 SEQUENCE FROM N.A.
STRAIN=Holstein-Friesian; TISSUE=Pancreas;
STRAIN=Holstein-Friesian; TISSUE=Pancreas;
STRAIN=91065383; Pubmed=1701147;
Ie Huerou I., Wicker C., Guilloteau P., Toullec R., Puigserver A.;
Is Huerou I., Wicker C., Guilloteau P., Toullec R., Povine
"Isolation and nucleotide sequence of cDNA clone for bovine
pancreatic anionic trypsinogen. Structural identity within the
 1 IVGGYECTXHSQAHQVSINSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
 DB 1, Length 246;
 88 V -> I (IN REF. 1).
26228 MW; ABD3630809AEE606 CRC64;
 180 PVVCNGVLQGVGVVSWGYGCABRDXPGVYAKVXVLSGWVRDTMA 223
 PVVCNGELQ--GIVSWGYGCALPDNPGVYTKVCNYVDWIQDTIA 244
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsin, anionic precursor (EC 3.4.21.4).
 EMBL; X54703; CAA38513.1; -.
HSSP; P00763; 1DPO.
 Matches 138; Conservative
 STANDARD;
 Bos taurus (Bovine).
 246 AA;
 Similarity
 NCBI_TaxID=9913;
 TRY2 BOVIN
Q29463;
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 ; Pred. No. 1.1e-
26; Mismatches
 PRT;
 SWART; SM00020; Tryp_SPc; 1.
PROSITE: PSSG240; TRYPEND DOM; 1.
PROSITE: FSG0134; TRYPSIN_HIS; 1.
PROSITE; PSG0135; TRYPSIN_HIS; 1.
 26269 MW;
 Matches 137, Conservative
 STANDARD;
 Xenopodinae; Xenopus.
 133
140
172
197
195
247 AA;
 Similarity
 SEQUENCE FROM N.A.
 Multigene family.
SIGNAL 1
 16
25
64
108
201
 NCBI_TaxID=8355;
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 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 121 WGNTMSS-VXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 Gaps
 144 WGNTLSSGVNYPDLLQCLVAPLLSHADCBASY-PGQITNNMICAGFLBGGKDSCQGDSGG 202
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 24 IVGGYTCAENSVPYGVSLNAGYHPCGGSLINDQWVVSAAHCYQYHIQVRLGEYNIDVLEG 83
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCET_TaxID=10116;
 Biochemistry 26:3081-3086(1987).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Trypsin III, cationic precursor (EC 3.4.21.4) (Pretrypsinogen III).
 84 GEOFIDASKIIRHPKYSSWTLDNDILLIKLSTPAVINARVSTLLLPSACASAGTECLISG
 MEDLINE=87271609; PubMed=3607011; Fletcher T.S., Alhadeff M., Craik C.S., Largman C.; "Isolation and characterization of a cDNA encoding rat cationic
 Score 721; DB 1; Length 247;
 54; Indels
 CHARGE RELAY SYSTEM.
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REQUIRED FOR SPECIFICITY.
 50A070495A7731DB CRC64;
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 203 PVACNGQLQ--GIVSWGYGCAQKGKPGVYTKVCNYVDWIQETIA 244
 7e-67;
 30; Mismatches
 247 AA
 Pred. No.
 InterPro; IPR001314; Chymotrypsin.
InterPro; IRR001284; Ser protease_Try.
Pfant; PF00089; trypsin; I
PRINTS; PR00722; CHYMOTRYPSIN.
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Σ
 62.3%;
60.7%;
 EMBL; M16624; AAA41985.1; -.
 26289
 Conservative
 STANDARD;
 63
200
107
160
64
233
206
185
195
 Rattus norvegicus (Rat).
 63
200
300
132
132
171
196
247 AA;
 Local Similarity
 P00763; 1DPO.
 SEQUENCE FROM N.A.
 MEROPS; S01.056; -
 Matches 136;
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 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 121 WGNTWSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 TISSUE=Pancreas, MEDLINE=91007255; PubMed=2210372; Shi Y.B., Brown D.D.; "Developmental and thyroid hormone-dependent regulation of pancreatic
 Gaps
 REQUIRED FOR SPECIFICITY (BY SIMILARITY)
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 genes in Xenopus laceris.;
Genes Dev. 4:1107-1113(1990).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLUIAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 25 IVGGYTCQKNSLPYQVSLNAGYHFCGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDVVVEG
Hydrolase, Serine protease; Digestion; Pancreas; Zymogen; Signal;
 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-UDN-2002 (Rel. 41, Last annotation update)
15-FUND precursor (St. 44.21.4).
Trypsin precursor (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 ACTIVATION PEPTIDE.
TRYPSIN III, CATIONIC.
THARGE RELAY SYSTEM (BY SIMILARITY)
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CHARGE RELAY SYSTEM (BY SIMILARITY)
 62.1%; Score 719; DB 1; Length 247;
 1.1e-66;
ches 57; Indels
 D74892BAA584E4A8 CRC64;
 204 PVVCNGQLQ--GVVSWGYGCAQKGKPGVYTKVCNYVNWIQQTVA 245
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 TRY1 XENLA
AC P1979;
DT 01-FEB-1991
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 121 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 199
 REQUIRED FOR SPECIFICITY (BY SIMILARITY) C588345A8837F8031 CRC64;
 Gaps
 TEQFISSSKVIRHSGYNSYTLDNDIMLIKLSSPASLNAAVNTVPLPSGCSAAGTSCLISG
 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
 SIMILARITY).
SIMILARITY).
SIMILARITY).
 "Cloning, characterization and nucleotide sequences of two cDNAs encoding human pancreatic trypsinogens.";
Gene 41:305-310(1986).
 [1]
SEQUENCE FROM N.A.
MEDLINE=86221712; PubMed=3011602;
Emi M., Nakamura Y., Ogawa M., Yamamoto T., Nishide T., Mori
 62.0%; Score 718; DB 1; Length 243; 61.2%; Pred. No. 1.4e-66;
 HSSP, P00763, 1DPO.
MEROPS, S01.151; --
Interpro. 1PR001314; Ser_protease_Try.
Interpro. 1PR001324; Ser_protease_Try.
Interpro. 1PR0010254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PR01NTS; PR00022; CHWOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DIM; 1.
PROSITE; PS00134; TRYPSIN JES; 1.
Hydrolase; Serine protease; Digestion; Signal;
 01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
1rypain II precursor (EC 3.4.21.4) (Anionic trypsinogen)
PRSS2 OR TRYP2.
HOMO sapiens (Human)
 52; Indels
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 BY SIMILARITY.

ACTIVATION PEPTIDE.

TRYPSIN.

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BY SIMILARITY.

 247 AA
 31; Mismatches
 email to license@isb-sib.ch)
 25492 MW;
 EMBL; X53458; CAA37538.1; -
 Query Match
Best Local Similarity 61.2%
Matches 137; Conservative
 STANDARD;
 15
20
243
243
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1197
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203
 191
 PIR, A35871; A35871.
 16
21
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60
104
1197
129
129
139
191
191
243 AA;
 Hydrolase; Serine
Multigene family.
 HUMAN
 or send an
 DISULFID
 ACT_SITE
ACT_SITE
DISULFID
DISULFID
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 SEQUENCE
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 RESULT 15
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ACTIVATION PEPTIDE.
TRYPSIN II.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
WHENDURED FOR SPECIFICITY (BY SIMILARITY).
MAY, 82BOP41EBBB3D5DB CRC64;
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 Gaps
 83
 9
 Clin. Chim. Acta 184:31-46(1989).
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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 24 IVGGYICEENSVPYQVSLNSGYHFCGGSLISEQWVVSAGHCYKSRIQVRLGEHNIEVLEG
 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PPR00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_BSR; 1.
PROSITE; PS00135; TRYPSIN_SRR; 1.
Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
 4.
MEDIJNE-90091010; PubMed=2598466; Kimland M.; Russick C., Marks W.H., Borgstroem A.; "Immunoreactive anionic and cationic trypsin in human serum.";
 Length 247;
 54; Indels
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 61.3%; Score 710; DB 1;
60.3%; Pred. No. 9.5e-66;
iive 31; Mismatches 54
 Search completed: February 12, 2003, 10:23:21 Job time : 31.2239 secs
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Matches 135; Conservative
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HSSP; P00763; 1DPO.
MEROPS; S01.258; -.
Genew; HGNC:9483; PRSS2.
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247 AA;
 Local Similarity
 Multigene family
 MIM; 601564; -
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Sequence:

Run on:

Searched:

Database

trypsin seri TRYI trypsin

Bos

KLK-L6 prote KLK-L6 prote

PRO1279 (UNQ secreted pro

TLSP.

PRO1279 poly

PRO protein,

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Trypsinogen-like p
Human spleen tryps
Human pancreatic t
Chimeric serine pr
Novel human kallik
Human protease, PR
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Human protease dom
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Bovine met-phe-try
Trypsinogen analog
 Bovine TRYP peptid
 Bovine trypsinogen
 Bovine trypsinogen
 Human trypsinogen.
 Prostate cancer-as
Human angiogenesis
Human PR01279 prot
 CASB12 polypeptide
CASB12 amino acid
Human serine prote
 Human trypsin seri
 Protein of the inv
 Human trypsinogen
 Pish; serine proteinase; pain; acute inflammation; chronic inflammation, arthritis; inflamed joint; bursitis; osteoarthritis; septic arthritis; retematoid arthritis; juvenile rheumatoid arthritis; libromyalgia; systemic lupus erythematosus; phlebitis; tendinitis; acus, eczeme, facial seborrhic eczema; foreskin infection; atthlete's foot; fistulae infection; ulcer; navel infection; scar, kelloid; boil; wart, allergic itch; hemorrhoid; wound; fungal infection; autoimmune disease.
 Bovine trypsin.
 TRYP protein.
 Human H
Human T
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 Amino acid sequence of cod trypsin isozymes.
 ALIGNMENTS
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AAY91926
AAB80953
AAY91925
AAR53638
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AAR51316
AAW57740
 AAY08894
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AAU68927
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AAB21305
AAB21305
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AAB21326
AAB21328
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 AAU12424
AAB66139
ABG61816
ABB95526
ABB84920
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 AAW81767
 AAU83684
 AAB11712
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 /label= Tyr,
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 /label= Asp,
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 Misc-difference 32
 Misc-difference 33
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 Misc-difference 64
 Gadus callarias.
 Misc-difference
 Misc-difference
 AAB31579;
 RESULT 1
 AAB31579
 75.73.78.55.
 Amino acid sequency Regrantis japonicu Engraulis japonicu Human amyloid beta Canine cationic tr Human trypsin hL a Human pancreatic t Porcine trypsinoge Canine anionic trypsinoge Partial trypsin se
 February 12, 2003, 10:03:55; Search time 151:119 Seconds (without alignments) 198.395 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 A Geneseq 101002:*

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1 IVGGYECTXHSQAHQVSLNS.....GVYAKVXVLSGWVRDTMAXY 225
 Description
 908470
 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 908470 seqs, 133250620 residues
 SUMMARIES
 OM protein - protein search, using sw model
 Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
 ABB04644
ABB04645
AAW64260
AAY78974
AAB35701
AAW08475
AAY78975
AAW78975
 AAB31579
 Gapop 10.0 , Gapext
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 В
 Length
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76.3
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Maximum DB 8
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181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225

VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY

181 121

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The specification describes a fish serine proteinase. The proteinases are useful as medicaments, for treating and preventing a disease in a human or an animal such as pain, acute inflammation, chronic dronic inflammation, arthritis, inflamed joints, bursitis, osteoarthritis, inflamed joints, bursitis, osteoarthritis, inflamed joints, bursitis, septic arthritis, inflamed loints, pursitis, septic arthritis, fibromyalgia, systemic lupus erythematosus, phlebitis, tendinitis, rash, psoriaafs, acne, eczema, facial sebornheic eczema of the hands, face or neck, foreskin infections, athlete's foot, fistulae infections, infections underthe and lergic itch, hemorrhoids, wounds, wound infections, wounds from burns, fungal infections and immunological and autoimmune diseases. They are also useful for removing dead or peeling skin from otherwise healthy skin, and for treating or preventing a classaste in which pathogenesis is caused by batteria, virus, fungus, parasite or a protozoan or a receptor mediated binding is involved.

The present sequence represents the amino acid sequence of cod trypsin
 Fish serine proteinase, useful as a cosmetic, medicament for treating eczema, psoriasis, arthritis, and in the manufacture of the medicament for treating, preventing pathogenic diseases involving receptor mediated binding
 'note= "Xaa is any amino acid or absent"
 ζg
 Disclosure; Page 13; 38pp; English
 Val,
 Gla
 Ser
 label= His, Asn
 Ser
 abel= Asp, Asn
 abel= Lys,
 label= Ala,
 abel= Val,
 label= Met,
 label= Asn,
 /label= Asn,
 15-JUN-2000; 2000WO-1S00005
 991S-0005086
 (BJAR/) BJARNASON J B.
 WPI; 2001-091493/10.
 Misc-difference 129
 225 AA;
 Misc-difference 82
 Misc-difference
 Misc-difference
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 Misc-difference
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 WO200078332-A2
 Bjarnason JB;
 18-JUN-1999;
 28-DEC-2000
 Sequence
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The present sequence represents a trypsinogen, which is a protease (I) isolated from Engraulis Japonicus (also called Engraulis japonica or Japanese anchovy). The present invention also describes: (I) a DNA cenceding (I), or encoding a protease consisting of an amino acid encoding (I), or encoding a protease consisting of an amino acid sequence in which part of the amino acid residue is replaced, inserted or deleted in the amino acid sequence encoded by the above DNA and ving a bio-activity substantially same as (I); (2) an expression vector in which he above DNA is recombined; (3) producing a sardine-derived protease in which a host cell transformed by the above containing substantially no other protein derived from fish; and containing substantially no other protein derived from fish; and (5) the preparation of a fish sauce in a short period while inhibiting the generation of a fish sauce in a short period while inhibiting protease prepared by the above method is not added in which at least one of a fish or a shellfish selected from the group consisting salts in a sa high salt concentration as above 8% to 24% and the protease prepared is an an aqueous solution containing salts in a salt and firsh salt concentration as above 8% to 24% and the protease prepared for the preparation of a fish sauce in a fis
 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 IVGGYECQAHSQPHTVSLNSGYHFCGGSLVNENWVVSAAHCYKSRVEVRLGEHHIGQNEN 79
 Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
 ₹.
 Protease; trypsinogen; sardine; Japanese anchovy; fish sauce
 Length 240;
 Indels
 Engraulis japonicus trypsinogen (aTry I) SEQ ID NO:1.
 76.5%; Score 886; DB 23;
llarity 74.9%; Pred. No. 1.8e-73;
Conservative 14; Mismatches 38;
 ABB04644 standard; Protein; 240 AA
 Claim 1; Fig 7; 32pp; Japanese.
 24-MAR-2000; 2000JP-0084302
 24-MAR-2000; 2000JP-0084302
 (first entry)
 (NISB) JAPAN TOBACCO INC.
 WPI; 2002-078276/11.
 Engraulis japonicus.
 Similarity
 new DNA sequence
 240 AA;
 N-PSDB; ABA04345.
 JP2001269173-A.
 short period
 Best Local Sim
Matches 167;
 04-MAR-2002
 02-OCT-2001.
 Sequence
 ABB04644;
 Query Match
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Gaps

Length 225; Indele

Query Match 97.6%; Score 1130; DB 22; Best Local Similarity 100.0%; Pred. No. 7.2e-96; Matches 225; Conservative 0; Mismatches 0;

121 WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP 180 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120

61 61

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WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP 140 WGNTMSNV-SGDKLQCLQIPILSDRDCKNSY-PGMITESMFCAGYLEGGKDSCQGDSGGP

121

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181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMAXY 225

198

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197

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The present sequence represents a trypsinogen, which is a procease (I) isolated from Engraulis japonicus (also called Engraulis japonicus (also called Engraulis japonicus or Japanese anchovy). The present invention also describes: (1) a DNA encoding (I), or encoding a procease consisting of an anino acid sequence in which part of the amino acid residue is replaced, inserted or deleted in the amino acid sequence encoded by the above DNA and having a bio-activity substantially same as (1); (2) an expression vector in which the above DNA is recombined; (3) producing a sardine-derived procease in which a host cell transformed by the above expression vector is cultured and (I) is recovered; (4) a protease containing substantially no other protein derived from fish; and (5) the preparation of a fish sauce in a short period while inhibiting the generation of an unpleasant smell compared to a case where the one of a fish or a shellfish selected from the group consisting of the above method is not added in which at least one of a fish or a shellfish selected from the group consisting of a shiph salt concentration as about 8 to 24% and the protease prepared by the above method is added to it and fermented for about 1 to 11 short nerion of a fish the preparation of a fish sauce in a short nerion of a fish sauce in a short nerion of a fish sauce in a short nerion of a fish sauce in a short nerion of a fish sauce in a
121 WGNTMSSVXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGGP 180
 140 WGNTMSNV-SGDKLQCLQIPILSDRDCDNSY-PGMITDAMFCAGYLBGGKDSCQGDSGGP 197
 Protease; trypsinogen; sardine; Japanese anchovy; fish sauce.
 Engraulis japonicus trypsinogen (aTry II) SEQ ID NO:2.
 198 VVCNGELQ--GVVSWGYGCAERDHPGVYAKVCIFTDWLQSTMA 238
 181 VVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 ABB04645 standard; Protein; 241 AA.
 Claim 1; Fig 8; 32pp; Japanese.
 24-MAR-2000; 2000JP-0084302.
 24-MAR-2000; 2000JP-0084302.
 (first entry)
 (NISB) JAPAN TOBACCO INC.
 Engraulis japonicus.
 WPI; 2002-078276/11.
 A new DNA sequence
 241 AA;
 N-PSDB; ABA04346.
 JP2001269173-A.
 04-MAR-2002
 02-OCT-2001
 ABB04645;
 Sequence
 Query Match
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3;
 This polypeptide comprises the human amyloid beta-protein precursor inhibitor (ABPI). The crystallographic structure of the complex of structure of the substrate-binding becket of mouse mast cell protease 7 (mMCP-7, see AAW4423)). The invention relates to mMCP-7 and related tryptase-7 proteases that can be used to prevent or inhibit fibrin clot formation. Such proceases can be used to treat disorders mediated by undesirable thrombus clot formation such as myocardial infarction and reocclusion following angloplasty of blood clots associated with pulmonary thromboembolism, deep vein thromboesis, cerebral embolism, renal vein and peripheral arterial
 Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 MCP-7; mast cell protease 7; tryptase-7; serine protease; amyloid beta-protein precursor inhibitor; human; blood clot; anticoagulant; myocardial infarction; reocclusion; thromboembolism; cerebral embolism; thrombosis; therapy.
 24 IVGGYTCPEHSVPYQVSLNSGYHFCGGSLINDQWVVSAAHCYKSRIQVRLGEHNINVLEG 83
 New compositions containing tryptase-7, e.g. mouse mast cell protease-7 - are used to treat clot formation in e.g. myocardial infarction, reocclusion following angioplasty or pulmonary
 7
 65.2%; Score 755; DB 19; Length 246; 63.8%; Pred. No. 1.9e-61; tive 25; Mismatches 52; Indels
VVCNGELQ--GIVSWGYGCAERDHPGVYAKVCLFNDWIDSTWAQY 240
 Human amyloid beta-protein precursor inhibitor.
 AAW64260 standard; Protein; 246 AA.
 (BGHM) BRIGHAM & WOMENS HOSPITAL.
 Example; Page 77; 92pp; English.
 96US-0032354.
 97WO-US21620.
 (first entry)
 Matches 143; Conservative
 WPI; 1998-333308/29.
 Similarity
 246 AA;
 thromboembolism
 Homo sapiens.
 25-NOV-1997;
 24-NOV-1998
 WO9824886-A1
 04-DEC-1996;
 11-JUN-1998.
 Stevens RL;
 thrombosis
 AAW64260;
 Query Match
Best Local S
 Sequence
 AAW64260
ID AAW6
 RESULT 4
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 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 20 IVGGYECQPYSQPHQVSLNSGYHFCGGSLISDSWVVSAAHCYKGRVEVRMGEHHIGMTEG 79
 4
 76.3%; Score 883; DB 23; Length 241; 74.2%; Pred. No. 3.4e-73; ive 14; Mismatches 40; Indels
 Conservative
 3est_Local Similarity
4atches 167; Conserv
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NEQFINSAKVIRHPNYNSWILDNDIMLIKLSSPAVLNARVATISLPRACAAPGTQCLISG 143
 121 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 JP2000253887-A.
 sapiena.
 11-MAR-1999;
 11-MAR-1999;
 19-SEP-2000,
 14-FEB-2001
 Sequence
 AAB35701;
 Query Match
 models
 180
 Ношо
 203
 AAB35701
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 3,
 This sequence represents the canine cationic trypsinogen amino acid sequence. The protein was isolated from the canine pancreas. The invention relates to monoclonal antibodies with specificity against canine trypsin, or canine trypsin-related substances. The antibodies are highly specific and can be used as reagent for quick and accurate detection and quantitation of canine trypsin and canine trypsin and canine trypsin and canine trypsin-like immunoreactants in various forms. The antibodies can be used in the diagnosis of diseases such as panoreatitis, panoreatic cancer, renal insufficiency and extrapancreatic hyposecretion.
 Anti-canine trypsin monoclonal antibody, useful as reagent for quick and accurate detection and quantitation of trypsin and/or trypsin-like immunoreactants in various forms in diagnosis e.g. of pancreatic
 Gaps
 202
 Cationic trypsinogen; dog; monoclonal antibody production; detect; diagnose; pancreatitis; pancreatic cancer; renal insufficiency; extrapancreatic hyposecretion.
 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG
 WGNTMSS - VXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG
 62.8%; Score 727; DB 21; Length 247; 61.6%; Pred. No. 7.1e-59;
 Indels
 203 PVVCNGQLQ--GIVSWGYGCALPDNPGVYTKVCNFVGWIQDTIA 244
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTWA 223
 Canine cationic trypsinogen amino acid sequence.
 31; Mismatches
 Claim 3; Page 63-64; 67pp; Japanese.
 Ź
 AAY78974 standard; protein; 247
 Yamada
 (FUJY) FUJI YAKUHIN KOGYO KK
 98JP-0236609.
 99WO-JP04299
 (first entry)
 Best Local Similarity 61.6
Matches 138; Conservative
 Ashida Y,
 WPI; 2000-206018/18
 Local Similarity
 247 AA;
 Canis familiaris.
 WO200009739-A1
 09-AUG-1999;
 10-AUG-1998;
10-MAR-1999;
 Waritani T,
 05-JUN-2000
 24-FEB-2000.
 Sequence
 AAY78974;
 Query Match
 diseases
 61
 84
 121
 AAY 78974 5

AAY 78974 5

AAY 78974 5

XXX AAY 78974 AAY 78974 AAY 78974 AAY 78974 AAY 78974 AAY 78974 AAY 78974 AAY 78974 AAY 78974 AAY 78974 AAY 7874 AAY
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TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120

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 Nucleotide sequence AAC66182 encodes human trypsin hL AAB35701, a serine protease. The invention relates to the human hL gene and protein sequences, to a recombinant vector containing the nucleotide sequence, and a host cell containing the vector. Human trypsin hL can be used for screening for serine protease inhibitors, in the preparation of a lung disease model animal, and for the development of an index marker of lung diseases caused by an anti-trypsin hL antibody.
 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 145 WGNTLSSGTNYPSLLQCLDAPVLSDSSCTSSY-PGKITSNMFCLGFLEGGKDSCQGDSGG 203
 25 IVGGYTCQRNALPYQVSLNSGYHFCGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDALEG 84
 protein used to screen
lung disease animal
 Gape
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
 Human; trypsin hL; serine protease; lung disease model animal.
 61.7%; Score 715; DB 21; Length 247; 61.6%; Pred. No. 8.9e-58; ive 23; Mismatches 59; Indels '
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 Novel gene encoding a serine protease and its for serine protease inhibitors and to prepare
 Human trypsin hL amino acid sequence.
¥
 Claim 2; Page 3-4; 17pp; Japanese.
AAB35701 standard; Protein; 247
 99JP-0065337.
 99JP-0065337.
 Best Local Similarity 61.6
Matches 138; Conservative
 WPI; 2000-658814/64.
 (first
 Local Similarity
 247 AA;
 (TTPH-) TT PHARMA
 N-PSDB; AAC66182
 180
 204
 121
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144 WGNTLSSGADYPDELQCLDAPVLSQAECEASY-PGKITNNMFCVGFLEGGKDSCQGDSGG 202
 An almost complete pig trypsinogen (AAW08475) lacking the very N-terminal end of the signal peptide is the product of a cDNA clone (AAY49818) isolated from a pig pancras cDNA library. The cDNA clone can be fused to a signal sequence (e.g. from the native enzyme or from a specified amylase gene) and used for prodn. of recombinant tryppin in transformed host cells, esp. filamentous fungus, e.g. secreted by Aspergillus niger. Levels of trypsin secreted by Aspergillus spp. are several-fold higher than those obtd. using other microbial systems.
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 Prodn. of trypsin or trypsingen in filamentous fungi - transformed with recombinant DNA comprising trypsingen sequence fused to signal sequence, provides higher level of expression than other expression
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 25 IVGGYTCAANSIPYQVSLNSGSHFCGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDVLEG
 121 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG
 Trypsinogen; trypsin; protease; filamentous fungus; Asperillus.
 Length 247;
 Indels
 203 PUVSNGELQ--GIVSWGYGCAQKORPGVTKVYNYVDWIKDTIA 244
 PUVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA
 58;
 61.1%; Score 707; DB 18;
60.3%; Pred. No. 4.8e-57;
live 27; Mismatches 58;
 AAW08475 standard; Protein; 247 AA.
 Example 2; Page 15; 28pp; English.
 96WO-DK00253.
 95DK-0000693.
 (first entry)
 Woldike HF;
 Conservative
 (NOVO) NOVO-NORDISK AS.
 WPI; 1997-077523/07.
 Porcine trypsinogen.
 Best Local Similarity
Matches 135; Conserv
 247 AA:
 N-PSDB; AAT49878
 Kjeldsen TB,
 WO9700316-A1.
 10-JUN-1996;
 16-JUN-1995;
 28-MAR-1997
 03-JAN-1997.
 Sus scrofa.
 AAW08475;
 Sequence
 Query Match
 systems
 180
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 The present invention relates to the isolation of CDNA sequences
(ABK44061-ABK44209) encoding human pancreatic tumour proteins. The
polymucleotide sequences encoding human pancreatic tumour proteins are
useful for stimulating an immune response in a patient and treating
competition and patient. A host cell that expresses these
composition comprising the protein encoded
patient. A composition comprising the protein may be used in the
composition comprising the protein may be used in the
protein, or an antibody that blinds to the protein may be used in the
compositions and/or treatment of diseases, particularly
pancreatic cancer. The sequences of the invention are also useful in
compositions, e.g. vaccines, for the diagnosis and
compositions, e.g. vaccines, for the diagnosis and
compositions cancer. Such compositions may be useful for
inhibiting the development of cancer in a patient, or as markers for
the progression of cancer. The polymucleotide sequences may also be used
as probes or primers for nucleic acid hybridisation assays.

ANU87689-AAU87694 represent human pancreatic tumour proteins.
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 Novel polynucleotide encoding pancreatic tumour polypeptides, useful in pharmaceutical compositions, e.g. vaccines, for treating pancreatic
 Human; pancreatic tumour protein; immune response; pancreatic cancer; development of cancer; cancer progression; cytostatic.
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 121 WGNTMSSVXD-GDKLOXLXLPILSHADCANSYGPGMITOSMFCAGYLEGGKDSCQCDSGG 179
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 24 IVGGYICEENSVPYQVSLNSGYHFCGGSLISEQWVVSAGHCYKSRIQVRLGEHNIEVLEG 83
 61.3%; Score 710; DB 23; Length 247; 60.3%; Pred. No. 2.6e-57;
 54; Indels
 Mismatches
 Claim 2; Page 164-165; 167pp; English.
 AAU87693 standard, Protein; 247 AA
 Human pancreatic tumour protein #5.
 31;
 06-AUG-2001; 2001WO-US24619.
 07-AUG-2000; 2000US-223130P. 30-JAN-2001; 2001US-265447P.
 15-MAY-2001; 2001US-291201P
 21-MAY-2002 (first entry)
 Xu J, Kalos MD;
 Matches 135; Conservative
 WPI; 2002-241741/29.
N-PSDB; ABK44208.
 (CORI-) CORIXA CORP.
 Local Similarity
 247 AA;
 WO200212331-A2.
 Homo sapiens.
 14-FEB-2002,
 AAU87693;
 Pyle RA,
 Sequence
 Query Match
 RESULT 7
 AAU87693
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Analysis of three-dimensional structures by generating combination of correspondence satisfying restriction condition, and calculating root mean square distance between elements in the combination of
 frypsin; three dimensional structure; protein structure analysis;
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 ABB83322 standard; protein; 223 AA.
 Disclosure; Fig 38; 65pp; English.
 Matsuzawa
 92JP-0021012.
92JP-0331703.
93US-0014867.
 2001US-0910054
 Conservative
 (first entry)
 Partial trypsin sequence
 Aikawa S,
 WPI; 2002-507172/54.
 (FUIT) FUJITSU LID
 Local Similarity
 223 AA;
 serine protease.
 US2002035434-A1
 correspondence
 23-JUL-2001;
 06-FEB-1992;
 Unidentified
 08-FEB-1993;
 30-AUG-2002
 Tomikawa M,
 Best Local Sim
Matches 135;
 21-MAR-2002.
 Sequence
 Query Match
 ABB83322;
 180
 121
 180
 RESULT 10
 4BB8332
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 This sequence represents the canine anionic trypsinogen amino acid sequence. The protein was isolated from the canine pancreas. The invention relates to monoclonal antibodies with specificity against canine trypsin, or canine trypsin-related substances. The antibodies are highly specific and can be used as reagent for quick and accurate detection and quantitation of canine trypsin and canine trypsin—like immunoreactants in various forms. The antibodies can be used in the diagnosis of diseases such as pancreatitis, pancreatic cancer, renal insufficiency and extrapancreatic hyposecretion.
 Anti-canine trypsin monoclonal antibody, useful as reagent for quick and accurate detection and quantitation of trypsin and/or trypsin-like immunoreactants in various forms in diagnosis e.g. of pancreatic
 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMPCAGYLEGGKDSCQGDSGG 179
 61 TEQXISSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 24 IVGGYTCSRNSVPYQVSLNSGYHFCGGSLINSQWVVSAAHCYKSRIQVRLGEYNIAVSEG 83
 Gaps
 Anionic trypsinogen; dog; monoclonal antibody production; detect; diagnose; pancreatitis; pancreatic cancer; renal insufficiency; extrapancreatic hyposecretion.
 61.0%; Score 706; DB 21; Length 246; 60.7%; Pred. No. 5.9e-57; tive 28; Mismatches 56; Indele
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTWA 223
 204 PVVCNGQLQ--GIVSWGYGCAQKNKPGVYTKVCNYVNWIQQTIA 245
 Canine anionic trypsinogen amino acid sequence.
 Claim 3; Page 64-65; 67pp; Japanese.
 AAY78975 standard; protein; 246 AA
 Yamada
 (FUJY) FUJI YAKUHIN KOGYO KK
 99JP-0063990.
 99WO-JP04299
 98JP-0236609
 (first entry)
 Conservative
 Waritani T, Ashida Y,
 Local Similarity
 WPI; 2000-206018/18.
 246 AA;
 Canis familiaris.
 WO200009739-A1.
 05-JUN-2000
 09-AUG-1999;
 LO-AUG-1998;
 10-MAR-1999;
 Matches 136;
 24-FEB-2000
 Sequence
 Query Match
 AAY78975;
 diseases
 144
 180
 203
 121
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The present invention relates to a method for analysis of three dimensional structures. The method involves generating a combination of correspondence satisfying a restriction condition between the elements belonging to a first and second point sets from among all candidates for the combination of correspondence, and calculating a root mean square distance between the elements corresponding in the combination of corresponding in the combination of corresponding in the combination of structures of molecules, particularly proteins. To illustrate the invention, the serine proteases trypain and elastase were used. The present sequence is a partial sequence for trypsin. The histidine and serine active sites of trypsin and elastase were analysed using the method of the invention.
 WGNTMSS-VXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 9
 Gaps
 9
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
 4
 Length 223;
 Indela
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 60.6%; Score 702; DB 23;
60.3%; Pred. No. 1.2e-56;
tive 29; Mismatches 56;
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The present invention relates to human tumour antigen-derived gene 15 (TABG-15) protein and coding sequence (see AAH21601 and AAB98500).

TABG-15 is an extracellular serine protease. It was found that TABG-15 is 9-20 residues that lack TABG-15 protein protein or its fragments of vaccinating an individual against TABG-15, having, suspected of having or at risk of getting cancer. Furthermore, the TABG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TABG-15.
 Novel extracellular serine protease, termed tumor antigen-derived gene
15 protein overexpressed in carcinomas and DNA encoding it, for
diagnosis, treatment, prevention of cancer, particularly breast,
121 WGNTASSGADYPDELQCLDAPVLSQAKCEASY-PGKITSNMFCVGFLEGGKDSCQGDSGG 179
 cytostatic; vaccine; ovarian tumour; cancer; trypsin;
lerived gene 15; serine protease.
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 121 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFÇAGYLEGGKDSCQGDSGG 179
 62 NEĢFINAAKIIRHPQYDRKTLNNDIMLIKLSSRAVINARVSTISLPTAPPATGTKCLISG 121
 Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 2 IVGGYNČEENSVPYQVSLNSGYHPCGGSLINEQWVVSAGHCYKSRIQVRLGEHNIEVLEG 61
 60.6%; Score 702; DB 22; Length 225;
60.3%; Pred. No. 1.3e-56;
iive 26; Mismatches 59; Indels 4
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 180 PUVCNGQLQ--GVVSWGDGCAQKNKPGVYTKVYNYVKWIKNTIA 221
 180 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 Human trypsin serine protease catalytic domain.
 ¥.
 Example 10; Fig 1; 130pp; English.
 AAB98503 standard; Protein; 225
 Human; TADG-15; cytostatic;
tumour antigen-derived gene
 99US-0421213.
 20-OCT-2000; 2000WO-US29095.
 (first entry)
 Query Match
Best Local Similarity 60.3³
Matches 135; Conservative
 H
 (UYAR-) UNIV ARKANSAS.
 Tanimoto
 WPI; 2001-381031/40.
 225 AA;
 WO200129056-A1.
 ovarian cancer
 Homo sapiens.
 20-0CT-1999;
 03-AUG-2001
 26-APR-2001.
 O'Brien TJ,
 AAB98503;
 Sequence
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 This invention describes a novel purified and isolated analogue of mature macrophage stimulating protein (MSP) having at least one unpaired cysteine residue substituted with another amino acid which modulates the proliferation or differentiation of the intestinal epithelium. The product of the invention binds to RON (a cell membrane protein tyrosine conditions which is a member of the cheek family) to promote the formation of kinase which is a member of the cheek family) to promote the formation of colon crypts. MSP analogues are useful for the treatment of conditions include thematopotetic disorders such as those involving a deficiency of megakaryocytes and gastrointestinal disorders such as ulcerative colitis, crohn's disease and infections. The MSP analogues are useful for maintaining and repairing the epithelial lining in the treatment of ancer, where the aggressive use of chemotherapeutic agents or the use of chack model body radiation may lead to gut toxicity. The MSP analogues, which cancer, which may lead to gut toxicity. The MSP analogues, which chave a higher activity than normal human MSP are effective at smaller charge and might are any be administered less frequently than human MSP. This sequence represents a human trypsin serine protease to domain which is used in a description of the method of the invention.
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 Macrophage stimulating protein; MSP; human; modulator; proliferation; differentiation; intestinal epithelium; colon crypt; treatment; cancer; haematopoietic disorder; megakaryocyte deficiency; gastrointestinal; chemotherapeutic agent; gut toxicity; serine protease; trypsin.
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLIXPATLNQYVHAVALPTECAADATMCTVSG 120
 61 NEQFINAAKIIRHPQYDRXTLANDIMLIKLSSRAVINARVSTISLPTAPPATGTKCLISG 120
 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCGGDSGG 179
 4; Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 888 - 1881 - 1881 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 - 1888 -
 Length 224;
 59; Indels
 Analogues of macrophage stimulating protein for treating gastrointestinal or haematopoietic disorders
 60.6%; Score 702; DB 20; 60.3%; Pred. No. 1.3e-56;
 Human trypsin serine protease protein domain.
 Mismatches
 Example 2; Column 27-30; 23pp; English.
 AAY31160 standard; protein; 224 AA.
 26;
 96US-0766982.
 96US-0766982.
 26-OCT-1999 (first entry)
 Conservative
 WPI; 1999-517975/43.
 Query Match
Best Local Similarity
Matches 135; Conserv
 (AMGE-) AMGEN INC.
 224 AA;
 Homo sapiens.
 16-DEC-1996;
 16-DEC-1996;
 USS948892-A.
 07-SEP-1999.
 AAY31160;
 Sequence
 Wahl RC;
 RESULT 11
 121
 AAY31160
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WO200053776-A2.
 01-APR-1999;
21-JUL-1999;
 11-MAR-1999;
 Homo sapiens
 32-FEB-2001
 14-SEP-2000.
 Sequence
 Query Match
 AAB21321;
 121
 180
 203
 AAB2132
RESULT
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 TRVI; trypsinogen; autocatalysis; cleavage; zymogenic precursor;
protease; peptide hormone; therapeutic protein; treatment; coagulation.
 185
 symogenic precursors of a protesse (in this invention trypsinogen), have their natural cleavable site replaced by a non-natural, autocatellytically cleavable site. Such protesses are reagents for producing peptide hormones and other therapeutic proteins by cleavage of their fusion proteins, and some also have therapeutic activity themselves, e.g. thrombin for treatment of coagulation disorders. The protesses are produced simply and in high yield without the need to add another protesse for cleavage, reducing costs and avoiding contamination of the final enzyme.
 61 TEQXISSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 126
 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 7 IVGGYNCEENSVPYQVSLNSGYHFCGGSLINEQWVVSAGHCYKSRIQVRLGEHNIEVLEG 66
 1 IVGGYEÇTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 Gaps
 This invention describes a method where autocatalytically cleavable,
 - useful
 4
 Length 230;
 Autocatalytically cleavable zymogenic protease precursors for cleaving fusion proteins and for therapeutic uses
 59; Indels
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTWA 223
 181 PVVCNGQLQ--GVVSWGDGCAQKNKPGVYTKVYNYVKWIKNTIA 222
 Query Match
60.6%; Score 702; DB 20;
Best Local Similarity 60.3%; Pred. No. 1.3e-56;
Matches 135; Conservative 26; Mismatches 59;
 Kopetzki E;
 Human TRYI trypsinogen variant protein
 AAW93488 standard; Protein; 230 AA
 Disclosure; Fig 1; 45pp; German.
 (HOFF) ROCHE DIAGNOSTICS GMBH
 Huber R,
 98WO-EP05094.
 97EP-0114513.
 (first entry)
 WPI; 1999-204669/17.
N-PSDB; AAX23298.
 Hopfner K,
 230 AA;
 Homo sapiens.
 12-AUG-1998;
 WO9910503-A1
 15-OCT-1997;
22-AUG-1997;
 11-JUN-1999
 04-MAR-1999.
 Sequence
 AAW93488;
 Bode W,
 180
 121
 186
 RESULT 13
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The present sequence is human trypsinogen, a member of the serine protease family. Kalikreins and kallikrein-like proteins are a subgroup of the serine protease enzyme family. They catalyse the selective cleavage of specific polypeptide precursors to release beptides with potent biological activity. Nucleic acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4, KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the treatment, monitoring and diagnosis of canners, especially prostrate cancer. They can also be used to identify a substance that can associate with or mediate the biological activity of the proteins. Antibodies can be used to treat conditions mediated by the kallikrein-like proteins.
 New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L protein mediated disorders, especially cancer.
 WGNTMSSVXD-GDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 61 TEQXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 143
 Gapa
 Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; trypsinogen;
kallikrein-like protein; serine protease;
cytostatic; cancer; prostrate cancer.
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG
 24 İVGGYNCEENSVPYQVSLNSGYHFCGGSLINEQWVVSAGHCYKSRIQVRLGEHNIEVLEG
 Length 247;
 Indels
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA
 60.6%; Score 702; DB 21;
ilarity 60.3%; Pred. No. 1.46-56;
Conservative 26; Mismatches 59;
AAB21321 standard; Protein; 247 AA.
 Example 4; Fig 17; 184pp; English
 99US-0124260.
99US-0127386.
99US-0144919.
 (MOUN) MOUNT SINAI HOSPITAL.
 09-MAR-2000; 2000WO-CA00258
 Yousef GM, Diamandis EP;
 Best Local Similarity
Matches 135; Conserva
 WPI; 2000-587440/55.
 247 AA;
 Human trypsinogen.
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us-10-036-371-8.rag

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 This sequence is used in the creation of a database containing the information for amino acid sequence of protein with at least 1 bloological function with added a score on importance of expression of the biological information for each amino acid residue. The database is polypeptide based on the homology of amino acid sequence, e.g. sterio publication of protein, and includes retrieval and evaluation of high homologous relationship for the determination of mostly resembling protein. The database allows for correct and rapid retrieval and protein and protein and polypeptide having biological functions.
 DHFR; dihydrofolic acid reductase, protein function; trypsin; bovine; ribonuclease; myoglobin; database; homology; resemblance.
 61 TEOXISSSSVXRHPNYSSYNIXNDIMLIKLTXPATLNQYVHAVALPTECAADATMCTVSG 120
 61 NEQFISASKSIVHPSYNSNTLNNDIMLIKLKSAASLNSRVASISLPTSCASAGTQCLISG 120
 121 WGNTMSS-VXDGDKLQXLXLPILSHADCANSYGPGMITQSMFCAGYLEGGKDSCQGDSGG 179
 Gaps
 1 IVGGYECTXHSQAHQVSLNSGYHXCGGSLINXXWVVSAAHCYKSVLRVRLGEHHIRVNEG 60
 1 VGGYTCGANTVPYQVSENSGYHFCGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVEG 60
 Determination of protein biological function - comprises use of amino acid sequences database containing the relevant information
 4
 PVVCNGVLQGVGVVSWGYGCAERDXPGVYAKVXVLSGWVRDTMA 223
 (IYAK-) IYAKU BUNSHI SEKKEI KENKYUSHO KK.
 Search completed: February 12, 2003, 10:22:29
Job time : 152.119 secs
 AAW81767 standard; peptide; 223 AA.
 Example 1; Fig 1; 11pp; Japanese.
 Bovine TRYP peptide fragment.
 97JP-0093577.
 97JP-0093577
 (first entry)
 Query Match 60.5%
Best Local Similarity 60.3%
Matches 135; Conservative
 WPI; 1999-018384/02.
 223 AA;
 JP10287696-A.
 11-APR-1997;
 11-APR-1997;
 29-JAN-1999
 27-0CT-1998
 Bos taurus.
 AAW81767;
 Sequence
 180
 180
AAW81767
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